(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
7 December 2000 (07.12.2000)

PCT

(10) International Publication Number
WO 00/73469 A2

(51) International Patent Classification⁷: C12N 15/54, 9/12, 15/11, 5/12, C07K 16/40, A61K 38/00, G01N 33/68

(21) International Application Number: PCT/US00/14842

(22) International Filing Date: 26 May 2000 (26.05.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/136,503 28 May 1999 (28.05.1999) US

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(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *Without international search report and to be republished upon receipt of that report.*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 00/73469 A2

(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

DESCRIPTION

PROTEIN KINASES

FIELD OF THE INVENTION

The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

BACKGROUND OF THE INVENTION

The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be or to describe prior art to the invention.

Cellular signal transduction is a fundamental mechanism whereby external stimuli that regulate diverse cellular processes are relayed to the interior of cells. One of the key biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins, which enables regulation of the activity of mature proteins by altering their structure and function.

Protein phosphorylation plays a pivotal role in biological signal transduction. Among the biological functions controlled by protein phosphorylation are the following: cell division; differentiation and death (apoptosis); cell motility and cytoskeletal structure; control of DNA replication, transcription, splicing and translation; protein translocation events from the endoplasmic reticulum and Golgi apparatus to the membrane and extracellular space; protein nuclear import and export; regulation of metabolic reactions, etc. Abnormal protein phosphorylation is widely recognized to be causally linked to the etiology of many diseases including cancer as well as immunologic, neuronal and metabolic disorders.

The most common phospho-acceptor amino acid residues are serine, threonine and tyrosine. Phosphorylation in histidine has also been observed in bacteria. The presence of a phosphate moeity modulates protein function in multiple ways. A common mechanism includes changes in the catalytic properties (V_{max} and K_m) of an enzyme leading to its activation or inactivation. A second widely recognized mechanism involves promoting protein-protein interactions. An example of this is the tyrosine autophosphorylation of the

ligand-activated EGF receptor tyrosine kinase. This event triggers the high-affinity binding to the phosphotyrosine residue on the receptor's C-terminal intracellular domain to the SH2 motif of the adaptor molecule Grb2. Grb2 in turn binds through its SH3 motif to a second adaptor molecule, such as SHC. The formation of this ternary complex acivates the signaling events that are responsible for the biological effects of EGF. Serine and threonine phosphorylation events have also being recently recognized to exert their biological function through protein-protein interaction events mediated by the high-affinity binding of phosphoserine and phosphothreonine to WW motifs present in a large variety of proteins (Lu, P.J. *et al.* (1999) Science 283:1325-1328). A third important outcome of protein phosphorylation is changes in the subcellular localization of the substrate. As an example, nuclear import and export events in a large diversity of proteins are regulated by protein phosphorylation (Drier E.A. *et al.* (1999) Genes Dev 13: 556-568).

Protein kinases are one of the largest families of eukaryotic proteins with several hundred known members. These proteins share a 250-300 amino acid domain that can be subdivided into 12 distinct subdomains that comprise the common catalytic core structure. These conserved protein motifs have recently been exploited using PCR-based and bioinformatic strategies leading to a significant expansion of the known kinases. Multiple alignment of the sequences in the catalytic domain of protein kinases and subsequent parsimony analysis permits their segregation into a dendrogram reflecting the relatedness of their catalytic domains (Fig. 1). In this manner, related kinases are clustered into distinct branches or subfamilies including: tyrosine kinases, cyclic-nucleotide-dependent kinases, calcium/calmodulin kinases, cyclin-dependent kinases and MAP-kinases, serine-threonine kinase receptors, and several other less defined subfamilies.

We have recently completed a systematic analysis of the protein kinases present in *C. elegans*, the multicellular organism whose entire DNA sequence has been determined. We identified 473 unique kinase profiles including 398 full-length conventional kinases, and 20 additional proteins that may function as atypical protein kinases. (Plowman G.D. *et al.* (1999), Proc. Natl. Acad. Sci. 96:13603-13610).

Using parsimony analysis, the protein kinases may be divided into 4 major groups: AGC, CAMK, CMGC and tyrosine kinases. In addition, there are a number of minor yet distinct families, including the STE and casein kinase 1, families related to worm- or

fungal-specific kinases, and a family designated "other" to represent several smaller families. In addition, we designate an "atypical" family to represent protein kinases whose catalytic domain has little or no primary sequence homology to conventional kinases, including the A6 kinases and PI3 kinases.

The AGC kinases are basic amino acid-directed enzymes that phosphorylate residues found proximal to Arg and Lys. Examples of this group are the cyclic nucleotide-dependent kinases, G protein kinases, NDR or DBF2 and the ribosomal S6 kinases.

The CAMK group kinases are also basic amino acid-directed kinases. They include the Ca2+/calmodulin-regulated and AMP-dependent protein kinases, myosin light chain kinases, checkpoint 2 kinases (CHK2) and EMK-related protein kinases. The EMK family of STK are involved in the control of cell polarity, micotubule stability and cancer. One member of the EMK family, C-TAK1 has been reported to control entry into mitosis by activating Cdc25C which in turn dephosphorylates Cdc2.

CMGC group kinases are "proline-directed" enzymes phosphorylating residues that exist in a proline-rich context. They include the cyclin-dependent kinases (CDKs), mitogen-activated kinases (MAPKs), GSK3s and CLKs. Most CMGC kinases have larger-than-average kinase domains owing to the presence of insertions within subdomains X and XI.

The tyrosine kinase group encompass both cytoplasmic (i.e. src) as well as transmembrane receptor tyrosine kinases (i.e. EGF receptor). These kinases play a pivotal role in the signal transduction processes that mediate cell proliferation, differentiation and apoptotis.

Group members that define smaller, yet distinct phylogenetic branches of conventional kinases include the elongation factor 2 kinases (EIFKs); homologues of the yeast sterile family kinases (STE) which refers to 3 classes of kinases which lie sequentially upstream of the MAPKs; mixed lineage kinases (MLKs); Lim-domain containing kinases (LIMKs); Calcium-calmodulin kinase kinases (CAMKK), dual-specific tyrosine kinases (DYRK), integrin receptor associated kinase (IRAK); testis-specific kinases (TSK); UNC-51 related kinases (UNC); several families that are close homologues to worm (C26C2.1, YQ09, ZC581.9, YFL033c, C24A1.3), Drosophila (SLOB), or yeast (YDOD_sp, YGR262_sc) kinases, and others that are "unique" and don't cluster into any obvious family.

SUMMARY OF THE INVENTION

Through a search of the EST database for homologies to the conserved catalytic kinase domain of protein kinases, hundreds of mammalian members of known and previously unidentified protein kinase families and groups have been identified as part of the present invention. Multiple alignment and parsimony analysis of the catalytic domain reveals that approximately half of these protein kinases cluster into 10 known groups, with the other half perhaps defining novel groups. Classification in this manner has proven highly accurate not only in predicting motifs present in the remaining non-catalytic portion of each protein, but also in their regulation, substrates, and signaling pathways. The present invention includes the partial or complete sequence of new protein kinases, their classification, predicted or deduced protein structure, and a strategy for elucidating their biologic and therapeutic relevance.

Thus, a first aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,

SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to nucleic acid is meant a polymer of nucleotides conjugated to each other, including DNA and RNA, that is isolated from a natural source or that is synthesized. The isolated nucleic acid of the present invention is unique in the sense that it is not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular (*i.e.*, chromosomal) environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only nucleotide chain present, but that it is essentially free (about 90 - 95% pure at least) of non-nucleotide material naturally associated with it, and thus is distinguished from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of the total DNA or RNA present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other DNA or RNA present, or by a preferential increase in the amount of the specific DNA or RNA sequence, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other DNA or RNA sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term "significant" is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other nucleic acids of about at least 2 fold, more preferably at least 5 to 10 fold or even more. The term also does not imply that there is no DNA or RNA from other sources. The other source DNA may, for example, comprise DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term distinguishes from naturally occurring events, such as viral infection, or tumor type

growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately 10^6-fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

By a "kinase polypeptide" is meant 10 (preferably 20, more preferably 40, most preferably 75) or more contiguous amino acids set forth in an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,

SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof as described herein. For sequences for which the full-length sequence is not given, the remaining sequences can be determined using methods well-known to those in the art and are intended to be included in the invention. In certain aspects, polypeptides of 100, 200, 300 or more amino acids are preferred. The kinase polypeptide can be encoded by a full-length nucleic acid sequence or any portion of the full-length nucleic acid sequence, so long as a functional activity of the polypeptide is retained. By "functional" domain is meant any region of the polypeptide that may play a regulatory or catalytic role as predicted from amino acid sequence homology to other proteins or by the presence of amino acid sequences that may give rise to specific structural conformations (*i.e.*, coiled-coils). For some purposes, polypeptide domains are preferred, including, but not limited to, N-terminal, catalytic/kinase and C-terminal.

The amino acid sequence will be substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID

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ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 or portions of or the entire corresponding full-length amino acid sequences.

By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues between two sequences (either full-length or a defined domain) by the total number of residues in the known sequence, or the domain of the known sequence, and multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have replacements and substitutions, have a lower degree of identity. "Gaps" are spaces in an alignment that can result from aligning a novel sequence with a known sequence when the novel sequence has additions or deletions of amino acids in comparison with the known sequence. These gaps do not factor into the assessment of % identity using the sbove calculation.

Those skilled in the art will recognize that several computer programs are also available for determining sequence identity using standard parameters, for example, Blast (Altschul, *et al.* (1997) Nucleic Acids Res. 25:3389-3402), Blast2 (Altschul, *et al.* (1990) J. Mol. Biol. 215:403-410), and Smith-Waterman (Smith, *et al.* (1981) J. Mol. Biol. 147:195-197).

In preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding a kinase polypeptide comprising a nucleotide sequence that: (a) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID

NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID

NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (e) is the complement of the nucleotide sequence of (d); (f) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID

NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.) A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID

NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ

ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID

NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,

SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (g) is the complement of the nucleotide sequence of (f); (h) encodes a polypeptide having an amino acid sequence selected from the group consisting

of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,

SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID

NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,

SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more of the domains selected from the group consisting of a N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (i) is the

complement of the nucleotide sequence of (h). The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.

The term "complement" refers to two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if all of the nucleotides of the first sequence are complementary to all of the nucleotides of the second sequence.

The term "domain" refers to a region of a polypeptide that contains a particular function. For instance, N-terminal or C-terminal domains of signal transduction proteins can serve functions including, but not limited to, binding molecules that localize the signal transduction molecule to different regions of the cell or binding other signaling molecules directly responsible for propagating a particular cellular signal. Some domains can be expressed separately from the rest of the protein and function by themselves, while others must remain part of the intact protein to retain function. The latter are termed functional regions of proteins and also relate to domains.

The term "N-terminal domain" refers to the extracatalytic region located between the initiator methionine and the catalytic domain of the protein kinase. The N-terminal domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the N-terminal boundary of the catalytic domain. Depending on its length, the N-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose N-terminal domain has been shown to play a regulatory role is PAK65, which contains a CRIB motif used for Cdc42 and rac binding (Burbelo, P.D. *et al.* (1995) J. Biol. Chem. 270, 29071-29074). The N-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the amino-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. Further, in some cases, portions of the N-terminal domains of the protein kinases of the invention have not been identified since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined and using the approaches described herein the N-terminal domain can be identified.

The term "catalytic domain" or "kinase domain" refers to a region of the protein kinase that is typically 25-300 amino acids long and is responsible for carrying out the phosphate transfer reaction from a high-energy phosphate donor molecule such as ATP or GTP to itself (autophosphorylation) or to other proteins (exogenous phosphorylation). The catalytic domain of protein kinases is made up of 12 subdomains that contain highly conserved amino acid residues, and are responsible for proper polypeptide folding and for catalysis. The catalytic domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database. The catalytic/kinase domains of the protein kinases of the invention are identified in Table 2, herein. Further, in some cases, the complete sequence of the catalytic/kinase domains of the protein kinases of the invention may not have been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the catalytic/kinase domain can be identified.

The term "catalytic activity", as used herein, defines the rate at which a kinase catalytic domain phosphorylates a substrate. Catalytic activity can be measured, for example, by determining the amount of a substrate converted to a phosphorylated product as a function of time. Catalytic activity can be measured by methods of the invention by holding time constant and determining the concentration of a phosphorylated substrate after a fixed period of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

The term "substrate" as used herein refers to a molecule phosphorylated by a kinase of the invention. Kinases phosphorylate substrates on serine/threonine or tyrosine amino acids. The molecule may be another protein or a polypeptide.

The term "C-terminal domain" refers to the region located between the catalytic domain and the carboxy-terminal amino acid residue of the protein kinase. The C-terminal domain can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C-terminal boundary of the catalytic domain or of any functional C-terminal extracatalytic domain. Depending on its length and amino acid composition, the C-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose C-terminal

domain may play a regulatory role is PAK3 which contains a heterotrimeric G_b subunit-binding site near its C-terminus (Leeuw, T. *et al.* (1998) Nature, 391, 191-195). The C-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the carboxy-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. In some cases, the C-terminal domains of the protein kinases of the invention have not been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the C-terminal domain can be identified.

The term "signal transduction pathway" refers to the molecules that propagate an extracellular signal through the cell membrane to become an intracellular signal. This signal can then stimulate a cellular response. The polypeptide molecules involved in signal transduction processes are typically receptor and non-receptor protein tyrosine kinases, receptor and non-receptor protein phosphatases, SRC homology 2 and 3 domains, phosphotyrosine binding proteins (SRC homology 2 (SH2) and phosphotyrosine binding (PTB and PH) domain containing proteins), proline-rich binding proteins (SH3 domain containing proteins), nucleotide exchange factors, and transcription factors.

The term "coiled-coil structure region" as used herein, refers to a polypeptide sequence that has a high probability of adopting a coiled-coil structure as predicted by computer algorithms such as COILS (Lupas, A. (1996) Meth. Enzymology 266:513-525). Coiled-coils are formed by two or three amphipathic α-helices in parallel. Coiled-coils can bind to coiled-coil domains of other polypeptides resulting in homo- or heterodimers (Lupas, A. (1991) Science 252:1162-1164). Coiled-coil-dependent oligomerization has been shown to be necessary for protein function including catalytic activity of serine/threonine kinases (Roe, J. *et al.* (1997) J. Biol. Chem. 272:5838-5845). Coiled-coil regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "proline-rich region" as used herein, refers to a region of a protein kinase whose proline content over a given amino acid length is higher than the average content of this amino acid found in proteins (*i.e.*, >10%). Proline-rich regions are easily discernable by visual inspection of amino acid sequences and quantitated by standard computer

sequence analysis programs such as the DNAStar program EditSeq. Proline-rich regions have been demonstrated to participate in regulatory protein -protein interactions. Among these interactions, those that are most relevant to this invention involve the "PxxP" proline rich motif found in certain protein kinases (*i.e.*, human PAK1) and the SH3 domain of the adaptor molecule Nck (Galisteo, M.L. *et al.* (1996) J. Biol. Chem. 271:20997-21000). Other regulatory interactions involving "PxxP" proline-rich motifs include the WW domain (Sudol, M. (1996) Prog. Biophys. Mol. Bio. 65:113-132). Proline rich regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "spacer region" as used herein, refers to a region of the protein kinase located between predicted functional domains. The spacer region has no detectable homology to any amino acid sequence in the database, and can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C- and N-terminal boundaries of the flanking functional domains. Spacer regions may or may not play a fundamental role in protein kinase function. Precedence for the regulatory role of spacer regions in kinase function is provided by the role of the src kinase spacer in inter-domain interactions (Xu, W. *et al.* (1997) Nature 385:595-602). Spacer regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "insert" as used herein refers to a portion of a protein kinase that is absent from a close homolog. Inserts may or may not by the product alternative splicing of exons. Inserts can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNAStar program Megalign. Inserts may play a functional role by presenting a new interface for protein-protein interactions, or by interfering with such interactions. Insert regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "C-terminal tail" as used herein, refers to a C-terminal domain of a protein kinase, that by homology extends or protrudes past the C-terminal amino acid of its closest homolog. C-terminal tails can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNAStar program Megalign. Depending on its length, a C-terminal tail may or may not play a regulatory role in kinase function. C-terminal tail regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides, more preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 50 contiguous nucleotides, most preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 100 contiguous nucleotides. In some instances, the conditions may prevent hybridization of nucleic acids having more than 5 mismatches in the full-length sequence.

By stringent hybridization assay conditions is meant hybridization assay conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM NaH_2PO_4, pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart solution at 42 °C overnight; washing with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C. Under some of the most stringent hybridization assay conditions, the second wash can be done with 0.1X SSC at a temperature up to 70 °C (pg. 421, Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein including any figures, tables, or drawings.). However, other applications may require the use of conditions falling between these sets of conditions. Methods of determining the conditions required to achieve desired hybridizations are well-known to those with ordinary skill in the art, and are based on several factors, including but not limited to, the sequences to be hybridized and the samples to be tested.

In other preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding kinase polypeptides, further comprising a vector or promoter effective to initiate transcription in a host cell. The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding a kinase polypeptide and a transcriptional termination region functional in a cell. Specific

vectors and host cell combinations are discussed herein. The recombinant nucleic acid can also contain the full-length sequence encoding the protein kinase, or a domain, for example.

The term "vector" relates to a single or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding a kinase can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

The term "transfecting" defines a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field, detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

The term "promoter" as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different organisms. For example, in prokaryotes, the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35,

SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, encodes an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID

NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, a functional derivative thereof, or at least 10, 20, 40, 50, 75, 100, 200, 300 or 500 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID

NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length sequences or derivatives thereof. The nucleic acid may be isolated from a natural source by cDNA cloning or by subtractive hybridization. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the nucleic acid may be synthesized by the triester method or by using an automated DNA synthesizer.

The term "mammal" refers preferably to such organisms as mice, rats, rabbits, guinea pigs, sheep, and goats, more preferably to cats, dogs, monkeys, and apes, and most preferably to humans.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a kinase polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acid encoding kinase polypeptides are provided in Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides, even more preferably 2 out of 20 nucleotides or most preferably 1 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a kinase polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 10 (preferably 25, more preferably 50, most preferably 75) or more contiguous amino acids selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,

SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof. In particular, a unique nucleic acid region is preferably of mammalian origin and preferably human.

A second aspect of the invention features a nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,

SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the nucleic acid probe encodes a kinase polypeptide that is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167,

SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. The nucleic acid probe contains a nucleotide base sequence that will hybridize to a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ

ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, or a functional derivative thereof.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID

NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or functional derivatives thereof.

Methods for using the probes include detecting the presence or amount of kinase RNA in a sample by contacting the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to kinase RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for a kinase polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson *et al.*, in Nonisotopic DNA Probe Techniques, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

In a third aspect, the invention describes a recombinant cell or tissue comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,

SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In such cells, the nucleic acid may be under the control of the genomic regulatory elements, or may be under the control of exogenous regulatory elements including an exogenous promoter. By "exogenous" it is meant a promoter that is not normally coupled *in vivo* transcriptionally to the coding sequence for the kinase polypeptides.

The polypeptide is preferably a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID

NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence. By "fragment," is meant an amino acid sequence present in a kinase polypeptide. Preferably, such a sequence comprises at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,

SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or of the corresponding full-length amino acid sequence, or a functional derivative thereof.

In a fourth aspect, the invention features an isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ

ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to a polypeptide is meant a polymer of amino acids (2 or more amino acids) conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of non-amino acid material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level

this level should be at least 2-5 fold greater (*e.g.*, in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

In preferred embodiments, the kinase polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. Preferably, the kinase polypeptide contains at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous

amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof.

In preferred embodiments, the kinase polypeptide comprises an amino acid sequence having (a) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ

ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ

ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (c) an amino acid sequence of a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (d) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, an insert, and a C-terminal tail. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.)

The polypeptide can be isolated from a natural source by methods well-known in the art. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the polypeptide may be synthesized using an automated polypeptide synthesizer. The isolated, enriched, or purified kinase polypeptide is preferably selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ

ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242A.

In some embodiments the invention includes a recombinant kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,

SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. By "recombinant kinase polypeptide" is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (*e.g.*, present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a fifth aspect, the invention features an antibody (*e.g.*, a monoclonal or polyclonal antibody) having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain or fragment where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ

ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In preferred embodiments, the antibody binds specifically to domains of kinase polypeptides, that are defined *supra*.

By "specific binding affinity" is meant that the antibody binds to the target kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody fragments are polypeptides that contain regions that can bind other polypeptides. The term "specific binding affinity" describes an antibody that binds to a kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions.

The term "polyclonal" refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

"Monoclonal antibodies" are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art (Kohler *et al.*, Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term "antibody fragment" refers to a portion of an antibody, often the hyper variable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hyper variable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a kinase polypeptide or domains of a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by probing the sample with the antibody under conditions suitable for kinase-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the

kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the kinase as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

An antibody or antibody fragment with specific binding affinity to a kinase polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

Antibodies having specific binding affinity to a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

In a sixth aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain, where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID

NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; and where the domains are defined as above. By "hybridoma" is meant an immortalized cell line that is capable of secreting an antibody, for example an antibody to a kinase of the invention. In preferred embodiments, the antibody to the kinase comprises a sequence of amino acids that is able to specifically bind a kinase polypeptide of the invention.

In a seventh aspect, the invention features a kinase polypeptide binding agent able to bind to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. The binding agent is preferably a purified antibody that recognizes an epitope present on a kinase polypeptide of the invention. Other binding agents include molecules that bind to kinase polypeptides and analogous molecules that bind to a kinase polypeptide. Such binding agents may be identified by using assays that measure kinase binding partner activity, such as those that measure PDGFR activity.

The invention also features a method for screening for human cells containing a kinase polypeptide of the invention or an equivalent sequence. The method involves identifying the novel polypeptide in human cells using techniques that are routine and standard in the art, such as those described herein for identifying the kinases of the invention (*e.g.*, cloning, Southern or Northern blot analysis, in situ hybridization, PCR amplification, etc.).

In an eighth aspect, the invention features methods for identifying a substance that modulates kinase activity comprising the steps of: (a) contacting a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,

SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance; (b) measuring the activity of said polypeptide; and (c) determining whether said substance modulates the activity of said polypeptide.

The term "modulates" refers to the ability of a compound to alter the function of a kinase of the invention. A modulator preferably activates or inhibits the activity of a kinase of the invention.

The term "activates" refers to increasing the cellular activity of the kinase. The term inhibit refers to decreasing the cellular activity of the kinase. Kinase activity is preferably the interaction with a natural binding partner.

The term "modulates" also refers to altering the function of kinases of the invention by increasing or decreasing the probability that a complex forms between the kinase and a natural binding partner. A modulator preferably increases the probability that such a complex forms between the kinase and the natural binding partner, more preferably increases or decreases the probability that a complex forms between the kinase and the natural binding partner depending on the concentration of the compound exposed to the

kinase, and most preferably decreases the probability that a complex forms between the kinase and the natural binding partner.

The term "complex" refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules bound to one another. For instance, a protein tyrosine receptor protein kinase, GRB2, SOS, RAF, and RAS assemble to form a signal transduction complex in response to a mitogenic ligand.

The term "natural binding partner" refers to polypeptides, lipids, small molecules, or nucleic acids that bind to kinases in cells. A change in the interaction between a kinase and a natural binding partner can manifest itself as an increased or decreased probability that the interaction forms, or an increased or decreased concentration of kinase/natural binding partner complex.

The term "contacting" as used herein refers to mixing a solution comprising the test compound with a liquid medium bathing the cells of the methods. The solution comprising the compound may also comprise another component, such as dimethyl sulfoxide (DMSO), which facilitates the uptake of the test compound or compounds into the cells of the methods. The solution comprising the test compound may be added to the medium bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

In a ninth aspect, the invention features methods for identifying a substance that modulates kinase activity in a cell comprising the steps of: (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,

SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) adding a test substance to said cell; and (c) monitoring a change in cell phenotype or the interaction between said polypeptide and a natural binding partner.

The term "expressing" as used herein refers to the production of kinases of the invention from a nucleic acid vector containing kinase genes within a cell. The nucleic acid vector is transfected into cells using well known techniques in the art as described herein.

In a tenth aspect, the invention provides methods for treating a disease or abnormal condition by administering to a patient in need of such treatment a substance that modulates the activity of a polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID

NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the disease is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer. Also included are metabolic disorders, such as diabetes mellitus, and reproductive disorders, such as infertility.

Preferably, the disease or disorder is selected from the group consisting of rheumatoid arthritis, artherosclerosis, autoimmune disorders, and organ transplantation. Preferably the disease or disorder is selected from the group consisting of immune-related diseases and disorders, myocardial infarction, cardiomyopathies, stroke, renal failure, and oxidative stress-related neurodegenerative disorders. Most preferably, the immune-related diseases and disorders are selected from the group consisting of rheumatoid arthritis, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation.

Substances useful for treatment of disorders or diseases preferably show positive results in one or more in vitro assays for an activity corresponding to treatment of the disease or disorder in question Substances that modulate the activity of the polypeptides

preferably include, but are not limited to, antisense oligonucleotides and inhibitors of protein kinases.

The term "preventing" refers to decreasing the probability that an organism contracts or develops an abnormal condition.

The term "treating" refers to having a therapeutic effect and at least partially alleviating or abrogating an abnormal condition in the organism.

The term "therapeutic effect" refers to the inhibition or activation factors causing or contributing to the abnormal condition. A therapeutic effect relieves to some extent one or more of the symptoms of the abnormal condition. In reference to the treatment of abnormal conditions, a therapeutic effect can refer to one or more of the following: (a) an increase in the proliferation, growth, and/or differentiation of cells; (b) inhibition (*i.e.*, slowing or stopping) of cell death; (c) inhibition of degeneration; (d) relieving to some extent one or more of the symptoms associated with the abnormal condition; and (e) enhancing the function of the affected population of cells. Compounds demonstrating efficacy against abnormal conditions can be identified as described herein.

The term "abnormal condition" refers to a function in the cells or tissues of an organism that deviates from their normal functions in that organism. An abnormal condition can relate to cell proliferation, cell differentiation or cell survival. An abnormal condition may also include irregularities in cell cycle progression, i.e., irregularities in normal cell cycle progression through mitosis and meiosis.

Abnormal cell proliferative conditions include cancers such as fibrotic and mesangial disorders, abnormal angiogenesis and vasculogenesis, wound healing, psoriasis, diabetes mellitus, and inflammation.

Abnormal differentiation conditions include, but are not limited to neurodegenerative disorders, slow wound healing rates, and slow tissue grafting healing rates.

Abnormal cell survival conditions relate to conditions in which programmed cell death (apoptosis) pathways are activated or abrogated. A number of protein kinases are associated with the apoptosis pathways. Aberrations in the function of any one of the protein kinases could lead to cell immortality or premature cell death.

The term "aberration", in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term "administering" relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the complements of the sequences and fragments; and (b) detecting the presence or amount of the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from the group consisting of rheumatoid arthritis, artherosclerosis, autoimmune disorders, organ transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative stress-related neurodegenerative disorders, metabolic disorder including diabetes, reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof. Hybridization conditions should be such that hybridization occurs only with the kinase genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

Hybridization conditions should be such that hybridization occurs only with the genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

The diseases for which detection of kinase genes in a sample could be diagnostic include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in comparison to normal cells. By "amplification" is meant increased numbers of kinase

DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

"Amplification" as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang et al. (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon

& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker et al., EPO Publication No. 0 520 722 A1; Jones et al., U.S. Patent No. 4,447,608; Kabbe et al., U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker et al., Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin et al., Br. J. Cancer 53:361-368 (1986); Fernandes et al., Cancer Research 43:1117-1123 (1983); Ferris et al. J. Org. Chem. 44(2):173-178; Fry et al., Science 265:1093-1095 (1994); Jackman et al., Cancer Research 51:5579-5586 (1981); Jones et al. J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus et al., J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell et al., Magnetic Resonance in Medicine 17:189-196 (1991); Mini et al., Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece et al., Cancer Research 47(11):2996-2999 (1977); Sculier et al., Cancer Immunol. and Immunother. 23:A65 (1986); Sikora et al., Cancer Letters 23:289-295 (1984); and Sikora et al., Analytical Biochem. 172:344-355 (1988), all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle et al., J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke et al., J. Med. Chem. 36:425-432 (1993); and Burke et al. BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., " J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

formulated in animal models to achieve a circulating concentration range that initially takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors and major organs can also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be deter-mined using detection methods such as X-ray, CAT scan and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, Journal of American Veterinary Medical Assoc., 202:229-249, 1993). Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness or toxicity. Gross abnormalities in tissue are noted and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

In a final aspect, the invention features a method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein the method comprises: (a) comparing a nucleic acid target region encoding the kinase polypeptide in a sample, where the kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID

NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding the kinase polypeptide, or one or more fragments thereof; and (b) detecting differences in sequence or amount between the target region and the control target region, as an indication of the disease or disorder. Preferably, the disease or disorder is selected from the group consisting of immune-related diseases and disorders, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders, and cancer. Immune-related diseases and disorders include, but are not limited to, those discussed previously.

The term "comparing" as used herein refers to identifying discrepancies between the nucleic acid target region isolated from a sample, and the control nucleic acid target region. The discrepancies can be in the nucleotide sequences, *e.g.* insertions, deletions, or point mutations, or in the amount of a given nucleotide sequence. Methods to determine these discrepancies in sequences are well-known to one of ordinary skill in the art. The "control" nucleic acid target region refers to the sequence or amount of the sequence found in normal cells, *e.g.* cells that are not diseased as discussed previously.

The term also includes anti-sense molecules drawn thereto.

The invention has been described broadly and generically herein. Each of the narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. For example, in some instances the nucleotide sequence of particular kinase polypeptides may not be part of a preferred embodiment.

The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

BRIEF DESCRIPTION OF THE FIGURES

Figures 1A to 1BB shows the amino acid sequences of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

Figures 2A to 2MMMM shows the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID

NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates in part to kinase polypeptides, nucleic acids encoding such polypeptides, cells containing such nucleic acids, antibodies to such polypeptides, assays utilizing such polypeptides, and methods relating to all of the foregoing. The present invention is based upon the isolation and characterization of new kinase polypeptides. The polypeptides and nucleic acids may be produced using well-known and standard synthesis techniques when given the sequences presented herein.

I. The Nucleic Acids of the Invention

Included within the scope of this invention are the functional equivalents of the herein-described isolated nucleic acid molecules. The degeneracy of the genetic code permits substitution of certain codons by other codons that specify the same amino acid and hence would give rise to the same protein. The nucleic acid sequence can vary

substantially since, with the exception of methionine and tryptophan, the known amino acids can be coded for by more than one codon. Thus, portions or all of the kinase genes of the invention could be synthesized to give a nucleic acid sequence significantly different from one selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121. The encoded amino acid sequence thereof would, however, be preserved.

In addition, the nucleic acid sequence may comprise a nucleotide sequence which results from the addition, deletion or substitution of at least one nucleotide to the 5'-end and/or the 3'-end of the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID

NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a derivative thereof. Any nucleotide or polynucleotide may be used in this regard, provided that its addition, deletion or substitution does not alter the amino acid sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, that is encoded by the nucleotide sequence. For example, the present invention is intended to include any nucleic acid sequence resulting from the addition of ATG as an initiation codon at the 5'-end of the inventive nucleic acid sequence or its derivative, or from the addition of TTA, TAG or TGA as a termination codon at the 3'-end of the inventive nucleotide sequence or its derivative. Moreover, the nucleic acid molecule of the present invention may, as necessary, have restriction endonuclease recognition sites added to its 5'-end and/or 3'-end.

Such functional alterations of a given nucleic acid sequence afford an opportunity to promote secretion and/or processing of heterologous proteins encoded by foreign nucleic acid sequences fused thereto, for example. All variations of the nucleotide sequence of the kinase genes of the invention and fragments thereof permitted by the genetic code are, therefore, included in this invention.

Further, it is possible to delete codons or to substitute one or more codons with codons other than degenerate codons to produce a structurally modified polypeptide, but one which has substantially the same utility or activity as the polypeptide produced by the unmodified nucleic acid molecule. As recognized in the art, the two polypeptides are

functionally equivalent, as are the two nucleic acid molecules that give rise to their production, even though the differences between the nucleic acid molecules are not related to the degeneracy of the genetic code. This is discussed further in the "Functional Derivatives" section, herein.

Finally, many of the nucleic acid molecules of the invention are provided as a partial sequence only (Fig. 2A through 2QQ). However, it is standard for one of ordinary skill in the art to obtain a full-length sequence when provided with a partial sequence. Similarly, when provided with a partial or full-length sequence it is standard for one of ordinary skill in the art to obtain nucleic acid sequence coding for homologous proteins. Therefore, these nucleic acid molecules are also part of the invention.

The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore presumably define new protein kinase groups.

Additional characteristics may be found, *inter alia*, in the tables, namely Table 1, Table 2, Table 3 and Table 4, shown below.

II. Nucleic Acid Probes, Methods, and Kits for Detection of Protein Kinases.

A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory, Sambrook, Fritsch, & Maniatis, eds., 1989).

In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences that correspond to N-terminal, kinase or C-terminal portions, for example, of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid probes may be used as primers in a polymerase chain reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press,

Michael, *et al.*, eds., 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art ("Molecular Cloning: A Laboratory Manual", 1989, *supra*). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b) detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to

radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or steptavidin).

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

III. <u>DNA Constructs Comprising a Protein Kinase Nucleic Acid Molecule and Cells Containing These Constructs.</u>

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The polypeptide may be purified from cells that have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding a kinase of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a kinase of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and a sequence encoding a kinase of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a kinase of the invention, or (3) interfere with the ability of the gene sequence of a kinase of the invention to be transcribed by the promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence.

Thus, to express a gene encoding a kinase of the invention, transcriptional and translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a kinase of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells. Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for kinases of the invention. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include γgt10, γgt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

To express a kinase of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the kinase of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage λ, the *bla* promoter of the β-lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage λ (P_L and P_R), the *trp*, *recA*, *λacZ*, *λacI*, and *gal* promoters of *E. coli*, the α-amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the ς-28-specific promoters of *B. subtilis* (Gilman *et al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic

promoters are reviewed by Glick (Ind. Microbiot. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev. Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the kinase polypeptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO or CHO-K1, or cells of lymphoid origin and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332, which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used (Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of kinases of the invention in insect cells (Jasny, Science 238:1653, 1987; Miller *et al.*, In: Genetic Engineering, Vol. 8, Plenum, Setlow *et al.*, eds., pp. 277-297, 1986).

Any of a series of yeast expression systems can be utilized which incorporate promoter and termination elements from the actively expressed sequences coding for glycolytic enzymes that are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational modifications. A number of recombinant DNA strategies exist utilizing strong promoter sequences and high copy number plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian genes and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). Several possible vector systems are available for the expression of kinases of the invention in a mammalian host.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of kinases of the invention in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer *et al.*, J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, Nature (London) 290:304-31, 1981); and the yeast gal4 gene sequence promoter (Johnston *et al.*, Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver *et al.*, Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon that encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes a kinase of the invention (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (*i.e.*, AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the kinase of the invention coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as the kinase of the invention coding sequence).

A nucleic acid molecule encoding a kinase of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule. Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (Mol. Cell. Biol. 3:280-, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector;

the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColEl, pSC101, pACYC 184, πVX; "Molecular Cloning: A Laboratory Manual", 1989, *supra*). Bacillus plasmids include pC194, pC221, pT127, and the like (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall *et al.*, J. Bacteriol. 169:4177-4183, 1987), and streptomyces bacteriophages such as φC31 (Chater *et al.*, In: Sixth International Symposium on Actinomycetales Biology, Akademiai Kaido, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John *et al.* (Rev. Infect. Dis. 8:693-704, 1986), and Izaki (Jpn. J. Bacteriol. 33:729-742, 1978).

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, Miami Wntr. Symp. 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast Saccharomyces: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, Cell 28:203-204, 1982; Bollon *et al.*, J. Clin. Hematol. Oncol. 10:39-48, 1980; Maniatis, In: Cell Biology: A Comprehensive Treatise, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, *i.e.*, transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene(s) results in the production of a kinase of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

IV. The Proteins of the Invention

A variety of methodologies known in the art can be utilized to obtain the polypeptides of the present invention. The polypeptides may be purified from tissues or cells that naturally produce the polypeptides. Alternatively, the above-described isolated nucleic acid fragments could be used to express the kinases of the invention in any organism. The samples of the present invention include cells, protein extracts or membrane extracts of cells, or biological fluids. The samples will vary based on the assay format, the detection method, and the nature of the tissues, cells or extracts used as the sample.

Any eukaryotic organism can be used as a source for the polypeptides of the invention, as long as the source organism naturally contains such polypeptides. As used herein, "source organism" refers to the original organism from which the amino acid sequence of the subunit is derived, regardless of the organism the subunit is expressed in and ultimately isolated from.

One skilled in the art can readily follow known methods for isolating proteins in order to obtain the polypeptides free of natural contaminants. These include, but are not limited to: size-exclusion chromatography, HPLC, ion-exchange chromatography, and immuno-affinity chromatography.

Further, the polypeptides of the invention include the full-length polypeptides that can be identified from the full-length or partial sequences encoded by SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,

SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 (Figure 1). In addition, the polypeptides of the invention include the domains of these polypeptides, including, but not limited to, the N-terminal, kinase/catalytic, and C-terminal domains.

The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore presumably define new protein kinase groups.

Additional characteristics are shown in, *inter alia*, the tables, namely Table 1, Table 2, Table 3 and Table 4, provided below.

V. Antibodies, Hybridomas, Methods of Use and Kits for Detection of Protein Kinases

The present invention relates to an antibody having binding affinity to a kinase of the invention. The polypeptide may have an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or a functional derivative thereof, or at least 9 contiguous amino acids thereof (preferably, at least 20, 30, 35, or 40 or more contiguous amino acids thereof). Alternatively, the antibody may bind to a part of the polypeptide not provided in the sequences above, but that is present in the full-length sequence of the polypeptide and that is easily obtained using methods standard in the art. Further, the antibody may bind specifically to particular domains of one or more of the kinases of the invention, including, but not limited to, the N-terminal, kinase/catalytic, or C-terminal domains.

The present invention also relates to an antibody having specific binding affinity to a kinase or kinase domain of the invention. Such an antibody may be isolated by comparing its binding affinity to a kinase of the invention with its binding affinity to other polypeptides. Those that bind selectively to a kinase of the invention would be chosen for use in methods requiring a distinction between a kinase of the invention and other

polypeptides. Such methods could include, but should not be limited to, the analysis of altered kinase expression in tissue containing other polypeptides.

The kinases of the present invention can be used in a variety of procedures and methods, such as for the generation of antibodies, for use in identifying pharmaceutical compositions, and for studying DNA/protein interaction.

The kinases of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting.

The present invention also relates to a hybridoma that produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line that is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth *et al.*, J. Immunol. Methods 35:1-21, 1980). Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal that is immunized, the antigenicity of the polypeptide and the site of injection.

The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or β-galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Agl4 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell that produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", *supra*, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, *see* Stemberger *et al.*, J. Histochem. Cytochem. 18:315, 1970; Bayer *et al.*, Meth. Enzym. 62:308-, 1979; Engval *et al.*, Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro, in vivo*, and *in situ* assays to identify cells or tissues that express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby *et al.*, Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro, in vivo*, and *in situ* assays as well as in immunochromotography.

Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides (Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspczak *et al.*, Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the kinases of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a kinase polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Altered levels of a kinase of the invention in a sample as compared to normal levels may indicate disease.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock *et al.* ("Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents that are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

VI. Isolation of Compounds That Interact With Protein Kinases

The present invention also relates to a method of detecting a compound capable of binding to a protein kinase of the invention, comprising incubating the compound with a kinase of the invention and detecting the presence of the compound bound to the kinase. The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts.

The present invention also relates to a method of detecting an agonist or antagonist of kinase activity or kinase binding partner activity comprising incubating cells that produce a kinase of the invention in the presence of a compound and detecting changes in the level of kinase activity or kinase binding partner activity. The compounds thus identified would produce a change in activity indicative of the presence of the compound.

The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts. Once the compound is identified it can be isolated using techniques well known in the art.

The present invention also encompasses a method of agonizing (stimulating) or antagonizing kinase associated activity in a mammal comprising administering to said mammal an agonist or antagonist to a kinase of the invention in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of kinase activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize kinase associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al*).

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin,

naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No.4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris *et al.* J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.* J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J.

Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*, Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); Sikora *et al.*, Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432 (1993); and Burke *et al.* BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen *et al.*, Clin. Exp. Immunol. 91:141-156 (1993); Anafi *et al.*, Blood 82:12:3524-3529 (1993); Baker *et al.*, J. Cell Sci. 102:543-555 (1992); Bilder *et al.*, Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton *et al.*, Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert *et al.*, Experimental Cell Research 199:255-261 (1992); Dong *et al.*, J. Leukocyte Biology 53:53-60 (1993); Dong *et al.*, J. Immunol. 151(5):2717-2724 (1993); Gazit *et al.*, J. Med. Chem. 32:2344-2352 (1989); Gazit *et al.*, " J. Med. Chem. 36:3556-3564 (1993); Kaur *et al.*, Anti-Cancer Drugs 5:213-222 (1994); Kaur *et al.*, King *et al.*, Biochem. J. 275:413-418 (1991); Kuo *et al.*, Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall *et al.*, J. Biol. Chem. 264:14503-14509 (1989); Peterson *et al.*, The Prostate 22:335-345 (1993); Pillemer *et al.*, Int. J. Cancer 50:80-85 (1992); Posner *et al.*, Molecular Pharmacology 45:673-683 (1993); Rendu *et al.*, Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring *et al.*, J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda *et al.*, Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

VII. Biological Significance, Applications and Clinical Relevance of Novel Protein Kinases

For each protein kinase in this application, we provide a classification of the protein class and family to which it belongs, a summary of non-cataltyic protein motifs, a profile of its expression in several hundred tissue and cell sources, and a chromosomal location. This information can be used to suggest potential function, regulation or therapeutic utility for each of the proteins.

The kinase classification and protein domains often reflect pathways, cellular roles, or mechanisms of up- or down-stream regulation. Also disease-relevant genes often occur in families of related genes. For example if one member of a kinase family functions as an oncogene, a tumor suppressor, or has been found to be disrupted in an immune, neurologic, cardiovascular, or metabolic disorder, frequently other family members may play a related role.

The expression analysis organizes kinases into groups that are transcriptionally upregulated in tumors and those that are more restricted to specific tumor types such as melanoma or prostate. This analysis also identifies genes that are regulated in a cell cycle dependent manner, and are therefore likely to be involved in maintaining cell cycle checkpoints, entry, progression, or exit from mitosis, oversee DNA repair, or are involved in cell proliferation and genome stability. Expression data also can identify genes expressed in endothelial sources or other tissues that suggest a role in angiogenesis, thereby implicating them as targets for control of diseases that have an angiogenic component, such as cancer, endometriosis, retinopathy and macular degeneration, and various ischemic or vascular pathologies. A proteins' role in cell survival can also be suggested based on restricted expression in cells subjected to external stress such as oxidative damage, hypoxia, drugs such as cisplatinum, or irradiation. Metastases-associated genes can be implicated when expression is restricted to invading regions of a tumor, or is only seen in local or distant metastases compared to the primary tumor, or when a gene is upregulated during cell culture models of invasion, migration, or motility.

Chromosomal location can identify candidate targets for a tumor amplicon or a tumor-suppressor locus. Summaries of prevelant tumor amplicons are available in the literature, and can identify tumor types to experimentally be confirmed to contain amplified copies of a kinase gene which localizes to an adjacent region.

Based on these criteria several kinases immediately stand out as being of potential therapeutic relevance. The protein kinases can be divided into the following disease-relevant categories (nucleotide Seq ID #s in parentheses):

Tumor associated: Mok (SEQ ID NO:NO:57), EPK2, AA316804 (SEQ ID NO:11), AA435956 (SEQ ID NO:NO:48), AA278842 (SEQ ID NO:88), AA599286 (SEQ ID NO:89), AA826850 (SEQ ID NO:3), HRI (SEQ ID NO:73), MLK4 AA232253 (SEQ ID NO:82), AA883975 SGK 235 (SEQ ID NO:95), AA311714 (SEQ ID NO:101), MPSK1 (SEQ ID NO:110), R19609 (Seq ID111), AA383293 (SEQ ID NO:26).

Prostate-specific: AA234451 (SEQ ID NO:47), TSK4 (SEQ ID NO:93), RIP4 (SEQ ID NO:84), KIAA0965 (SEQ ID NO:8).

Oncogenic or proliferation associated: KIAA0781 (SEQ ID NO:38), AA789239 (SEQ ID NO:52), CCRK (SEQ ID NO:54), CLK4 (SEQ ID NO:55), H85389 (SEQ ID NO:97).

Neuronal restricted: CAMKKB (SEQ ID NO:66)

Hematopoietic expressed: PTK9L (SEQ ID NO:22), DRAK2 (SEQ ID NO:29), AI025291 (SEQ ID NO:94)

Angiogenic or endothelial expressed: DRAK1 (SEQ ID NO:31), MAK-V (SEQ ID NO:40), TRAD (SEQ ID NO:44), MOK (SEQ ID NO:57), AA08847 (SEQ ID NO:78), HGP_66444466 (SEQ ID NO:79), RSK4 (SEQ ID NO:16).

Cell cycle regulated: AA454060 (SEQ ID NO:45), KIAA0999 (Mitotic – SEQ ID NO:32), AA579641 (Mitotic – SEQ ID NO:60), AA305176 (Mitotic – SEQ ID NO:6), AA018361 (S1 phase – SEQ ID NO:100).

VIII. Transgenic Animals.

A variety of methods are available for the production of transgenic animals associated with this invention. DNA can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (*e.g.*, the nucleus of a two-cell embryo) following the initiation of cell division (Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442, 1985). Embryos can

be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term. Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan *et al.*, *supra*). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout (Experientia 47: 897-905, 1991). Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sanford *et al.*, July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. Females are placed with males, and the mated females are sacrificed by CO_2 asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice (Hammer *et al.*, Cell 63:1099-1112, 1990).

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art (Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987).

In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, the gene encoding neomycin resistance is physically linked to the sequence(s) of the invention.

Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination (Capecchi, Science 244: 1288-1292, 1989). Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner *et al.* (Nature 338: 153-156, 1989), the teachings of which are incorporated herein in their entirety including any drawings. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science 244:1281-1288, 1989; and Simms *et al.*, Bio/Technology 6:179-183, 1988).

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding a kinase of the invention or a gene effecting the expression of the kinase. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introduction of a kinase, or regulating the expression of a kinase (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode human STE20-related kinases. Native expression in an animal may be reduced by providing an amount of anti-sense RNA or DNA effective to reduce expression of the receptor.

IX. Gene Therapy

Protein kinases of the invention, or their genetic sequences will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated

positive initial results. The basic science of gene therapy is described in Mulligan (Science 260:926-931, 1993).

In one preferred embodiment, an expression vector containing protein kinase coding sequence is inserted into cells, the cells are grown *in vitro,* and then are infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous gene encoding kinases of the invention in such a manner that the promoter segment enhances expression of the endogenous kinase gene (for example, the promoter segment is transferred to the cell such that it becomes directly linked to the endogenous kinase gene).

The gene therapy may involve the use of an adenovirus containing kinase cDNA targeted to a tumor, systemic kinase increase by implantation of engineered cells, injection with kinase-encoding virus, or injection of naked kinase DNA into appropriate tissues.

Target cell populations may be modified by introducing altered forms of one or more components of the protein complexes in order to modulate the activity of such complexes. For example, by reducing or inhibiting a complex component activity within target cells, an abnormal signal transduction event(s) leading to a condition may be decreased, inhibited, or reversed. Deletion or missense mutants of a component, that retain the ability to interact with other components of the protein complexes but cannot function in signal transduction may be used to inhibit an abnormal, deleterious signal transduction event.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, several RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (*e.g.*, cDNA) encoding recombinant kinase of the invention protein into the targeted cell population (*e.g.*, tumor cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., 1989; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y., 1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in a reconstituted system *e.g.*, liposomes or other lipid systems for delivery to target cells (*e.g.*, Felgner *et al.*, Nature 337:387-8,

1989). Several other methods for the direct transfer of plasmid DNA into cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins (Miller, *supra*).

In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection (Capecchi, Cell 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is precipitated with $CaPO_4$ and taken into cells by pinocytosis (Chen *et al.*, Mol. Cell Biol. 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu *et al.*, Nucleic Acids Res. 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner *et al.*, Proc. Natl. Acad. Sci. USA. 84:7413-7417, 1987); and particle bombardment using DNA bound to small projectiles (Yang *et al.*, Proc. Natl. Acad. Sci. 87:9568-9572, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The admixture of adenovirus to solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene (Curiel *et al.*, Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic acid molecule into a cell. Gene transfer is commonly performed to enable the expression of a particular product encoded by the gene. The product may include a protein, polypeptide, anti-sense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic

acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In another preferred embodiment, a vector having nucleic acid sequences encoding a protein kinase polypeptide of the invention is provided in which the nucleic acid sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression are set forth in International Publication No. WO 93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, a method of gene replacement is set forth. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene that is missing or defective in the animal.

X. Administration of Substances

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures, or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used, and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be formulated in animal models to achieve a circulating concentration range that initially

takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors, and major organs can be also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan, and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition, and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, *Journal of American Veterinary Medical Assoc., 202*:229-249, 1993). Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness, or toxicity. Gross abnormalities in tissue are noted, and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

EXAMPLES

The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of the protein kinases of the invention.

EXAMPLE 1: Isolation of cDNA clones Encoding Novel Mammalian Protein Kinases Materials and Methods Identification from cDNA databases and isolation of clones encoding novel protein kinases

Novel kinases were identified from the public EST databases using a Hidden Markov model, abbreviated HMM (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531). The model was built with 70 mammalian and yeast kinase catalytic domain sequences. These sequences were chosen from a comprehensive collection of kinases such that no two sequences had more than 50% sequence identity. ESTs were translated in six open reading frames and were searched against the model. ESTs that had a score of at least 10 against the HMM were then masked for repetitive sequences and vectors and were clustered using MSA. The resulting contigs were searched against known kinases to identify EST clones that encode novel kinases.

Approximately 40% of the ESTs encoding potentially novel kinases did not correspond to the correct EST upon sequence analysis. Most of these discrepancies were resolved by ordering additional clones, however, 14 remained unavailable. These 14 ESTs were amplified from a variety of single-stranded cDNA sources with primers derived from the corresponding EST entry as shown on Table 5. The PCR product was subcloned into a bluescript vector, digested to confirm the presence of a correct size insert and sequenced. Full sequencing of EST and PCR was carried out using a cycle sequencing Big-dye kit

with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Table 5: Primers used to clone PCR products corresponding to novel kinases

	ID#	ID#	Parent	5' primer	3' primer
sp	na	aa	Sequence	Sequence*	Sequence*
H	33	153	2R22-5-11	GAGATCGRNTTYAARGARTTYGA	TGTCACNCCNAGNSWCCANAYRTT
M	81	200	5R57_10_2_m TESK2_m	GCTGCTGGACAGTGACTTGTATTT	GAAAGCAAAGCCTTCACACCTT
H	67	187	5R69_17_2_h	CTCTCACCTCAGGAACTGG	GCTTGCGGATCTTCTCA
H	46	166	SGK309_h	GACATCCTGCCGGCCAACTACG	CGGCCCTGGAGCTGCATCACTA
M	67	228	5R72_16_2_h	TGCGCGACACCATTGACCAG	CTCAGGGCTTACATACAGAG
H	45	165	5R72_8_2_h	AAAGGAGAACTACATTTTGAAAAT	CTTCATCATCTCTAATACATTGGTTGG
H	41	161	Z36720	CAAATTAAGATCATTGACTTTGGG	GGAAACAAAGTCCTTGGCCTC
H	115	234	AL031652 – Pak6	GTGGACATCTGGTCCCTCG	GTAGGTCCTTCACTCTTGGAG

- degenerate oligonucleotide residue designation:

N= A,C,G ot T

R= A or G

Y= C or T

S = C or G

W= A or T

Full-length sequence extension of protein kinases using cDNA and genomic databases

Extension of partial cDNA sequences to encompass the full-length open-reading frame was carried out by iterative blastn searching of the cDNA databases listed in Table 6. All blastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of –3 and reward for a nucleotide match of 1. The gapped blast algortihm is described in: (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and

PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402).

Table 6. Databases used for cDNA-based sequence extensions

Database	Database Date
LifeGold templates	Feb 2000
LifeGold compseqs	Feb 2000
LifeGold compseqs	Mar 2000
LifeGold compseqs	Apr 2000
LifeGold fl	Feb 2000
LifeGold flft	Apr 2000
NCBI human Ests	May 2000
NCBI murine Ests	May 2000
NCBI nonredundant	May 2000

Extension of partial cDNA sequences to encompass the full-length open-reading frame was also carried out by iterative searches of genomic databases. Three methods were used. The first method made use of the Smith-Waterman algorithm to carry out protein-protein searches of the closest homologue or orthologue to the partial kinase. The target databases consisted of Genescan and open-reading frame (ORF) predictions of all human genomic sequence derived from the human genome project (HGP) as well as from Celera. The complete set of genomic databases searched is shown in Table 7 below. Genomic sequences encoding potential extensions were further assessed by blastp analysis against the NCBI nonredundant to confirm the novelty of the hit. The extending genomic sequences were incorporated into the cDNA sequence after removal of potential introns using the Seqman program from DNAStar. The default parameters used for Smith-Waterman searches were as shown next. Matrix: blosum 62; gap-opening penalty: 12; gap extension penalty: 2. Genescan predictions were made using the Genescan program as detailed in (Chris Burge and Sam Karlin "Prediction of Complete Gene Structures in Human Genomic DNA", JMB (1997) 268(1):78-94). ORF predictions from genomic DNA were made using a standard 6-frame translation.

The second method for genomic sequence-based extensions made use of tBlastn searches of the homologue or orthologue to the partial kinase against the cDNA databases listed in Table 7. The recognition of significant hits in these databases made possible to identify bridging partial cDNA clones. The iterative application of the two methods made possible the assemblage of the virtual full-length sequence for a large number of the kinases presented in this application. All tblastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of −3 and reward for a nucleotide match of 1.

The last method for defining cDNA extensions from genomic sequence used iterative searches of genomic databases through the Genescan program to predict exon splicing and the Genewise program (http://www.sanger.ac.uk/Software/Wise2/) to predict potential ORFs based on homology to the closest orthologue/homologue.

Table 7. Databases used for genomic-based sequence extensions

Database	Number of entries	Database Date
Celera v. 1-5	5,306,158	Jan 19/00
Celera v. 6-10	4,209,980	Mar 24/00
Celera v. 11-14	7,222,425	Apr 24/00
Celera v. 15	243,044	May 14/00
HGP all Genescan	25,885	Apr 04/00
HGP; Phase 0	4,944	May 04/00
HGP; Phase 1	28,478	May 05/00
HGP; Phase 2	1,508	May 04/00
HGP; Phase 3	9,971	May 05/00

Virtual Extensions

Human AA826850 (SEQ ID NO: 3, SEQ ID NO:124)

Blastn analysis of the partial AA826850 sequence revealed an extension to encompass the complete ORF in the Incyte EST 238299.1. A frame-shift correction at position 595 of this EST (marked by X in NA sequence) generated an uninterrupted ORF.

Human AA960957 (SEQ ID NO: 4, SEQ ID NO:125)

Since the initial filing of this application, the partial AA960957 sequence appeared in the public database as the full-length gene for a protein kinase encoded by a gene that maps adjacent to the evc (AJ250839) (ellis-van creveld syndrome and weyers acrodental dysostosis) gene from 4p16.1.

Human 5R79-46-1_h (SEQ ID NO: 5, SEQ ID NO:126)

Blastn analysis of the partial 5R79-46-1 sequence revealed an extension to encompass the complete ORF in the Incyte EST 463894.6. Since the initial filing of this application, the full-length virtual 5R79-46-1 appeared in the public database as the full-length gene for the TANK-binding kinase (TBK1) (Pomerantz,J.L. and Baltimore,D. (1999) EMBO J. 18 (23), 6694-6704). TBK1 participates in NF-kB activation through the formation of a signaling complex with TRAF2 and TANK.

Human AA305176 (SEQ ID NO: 6, SEQ ID NO:127)

Blastn analysis of the partial AA305176 sequence revealed an extension to encompass the complete ORF in the Incyte EST 220937.1.

Human AA256100 (SEQ ID NO: 8, SEQ ID NO:129)

Blastn analysis of the partial AA256100 sequence revealed an extension to encompass the complete ORF through the assembly of three partial clones: Incyte EST 480815.6, KIAA0965 (BAA76809) and AA256100.

Human AA210825 (SEQ ID NO: 9, SEQ ID NO: 130)

Blastn analysis of the partial AA210825 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte EST 014721.7, and the NCBI EST's AW01158 and AA210825. An insertion of two "N's" at positions 1915 and 1916 generated an uninterrupted ORF. Blastx analysis indicated the possibility of a start Met in the range of 400-450 nucleotides (i.e. compared to the closest homolog, human PKCmu (CAA53384.1). However, no Met was found in this region; rather ORF ends in an in-frame stop preceeded by the sequence "RGLLAPGDPPCPPPNPAPATPPSSRLPTELFSNFCDS". It is possible that part of the sequence covered by nucleotide positions 1-400 derived from AW01158 comes from an intron, explaining the absence of a start Met.

Human AA127299 (SEQ ID NO:10, SEQ ID NO:131)

No entries in the database extended this sequence. The 1684 bp insert of this EST contains a 1369 bp intron at the 3' end. Blastx and SW analysis of the 315 bp coding

region revealed homology to the extracatalytic C2 domain of PKC. This EST, may or may not encode a kinase.

Human AA316804 (SEQ ID NO:11, SEQ ID NO:132)

Since the initial filing of this application, the partial AA316804 sequence appeared in the public database as the full-length gene for the PKC family protein kinase EPK2 or PKCnu (AB015982).

Human H19102 (SEQ ID NO:14, SEQ ID NO:135)

Genewise and Genescan analyses of the partial H19102 sequence revealed an extension from the HGP phase 3 contig 3810672 to encompass the complete catalytic domain of this EST. Blastn analysis against the non-redundant database revealed that this gene is found in the cosmid AC005726 from chromosome 17. H19102 may encode a dual catalytic kinase given the homology to S6 kinase. Analysis of genomic sequence upstream of the 5' end of H19102 revealed a non-kinase gene oriented in the same polarity as H19102 suggestive of the start Met for H19102 being close to the 5' end of the H19102 sequence. From this analysis it is deduced that the second catalytic domain of H19102, if present, is most likely located within the 47334-185,215 bp region of the genomic sequence of AC005726.

Human AA476563 (SEQ ID NO:15, SEQ ID NO:136)

Since the initial filing of this application, the partial AA476563 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KC1 (NM_012424) (Zhang, H. et al Genomics (1999) 61, 314-318), which is an S6 kinase mapping to 12q12-q13.1.

Human AA626690 (SEQ ID NO:16, SEQ ID NO:137)

Since the initial filing of this application, the partial AA626690 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KA6 (AF184965) (Yntema,H.G et al (1999) Genomics 62, 332-343), an S6 kinase commonly deleted in patients with complex X-linked (Xq21.1) mental retardation.

Human AI215680 (SEQ ID NO: 17, SEQ ID NO:138)

Since the initial filing of this application, the partial AI215680 sequence appeared in the public database as the full-length gene encoding a hypothetical protein (AAD30182) from the locus AC006530.4 from chromosome 14.

Human AA887783 (SEQ ID NO:21, SEQ ID NO:142)

Blastn analysis of the partial AA887783 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte 415390R6 and the NCBI EST's AA887783 and N94726. Since the initial filing of this application, the nearly full-length virtual AA887783 sequence appeared in the public database as the full-length gene encoding SGK3 (AF169035), a serum- and glucocorticoid-induced protein kinase (Kobayashi,T. et al (1999) Biochemical J. 344, 189-197.

Human R47805 (SEQ ID NO:22, SEQ ID NO:143)

A cDNA clone encoding the full-length ORF of R47805 was isolated using R47805 as a screening probe. A full-length form for R47805 has also appeared in the public database as

PTK9L (NM_007284), an A6-related protein kinase.

Human H60215 (SEQ ID NO:23, SEQ ID NO:144)

Blastn analysis of the partial H60215 sequence revealed an extension to encompass the complete ORF in the public EST AI275726. This was confirmed through the full insert sequencing of this EST (2,310 bp) which corresponds to the sequence under SEQ ID NO:144.

A different stop codon was predicted for AI275726 compared to H60215 due to a single nucleotide insertion at position 1586 in AI275726. Evidence for the extra nucleotide comes from EST AI191922.

SGK324_h orthologue of W30246_m (SEQ ID NO:24 , SEQ ID NO:145)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding to the human orthologue of murine W30246. Exons predicted from the following sequences were used for contig construction: Celera 17000189645083, 17000057549105 and 11000501939981; Incyte142404.1, HGP_7249119, Incyte 7196489H1, Celera 11000501939981, 17000028165594; Incyte 7249119_3, Celera 17000035772368, 11000502081575 and 17000140274329. The latter Celera sequence provides the N-terminus.

Human AA383293 (SEQ ID NO:26, SEQ ID NO:147)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding for AA383293. Exons predicted from the following sequences were used for contig construction: (numbers in parenthesis

refer to the aa sequence of the closest homolog (RU2S, NP_057440) used for the Smith-Waterman query): N-term from Incyte 6010175_2 (14-97), Incyte 6981981 (134-184) 7596749 (186-232) Celera 17000020789545 (243-301) CAB75619.1 (310-341)--(56-145 DCX homology) 6010175_2 , Celera 17000030058129 (241-262 DCX homology).

Human AA021445 (SEQ ID NO:32, SEQ ID NO:152)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. Contig reconstruction was as follows: nucleotides1-802 from KIAA0999 (AB023216); nucleotides 803-4321 from full-insert sequence of AA021445. A pairwise alignment between the AA021445 and KIAA0999 revealed three inserts in the extracatalytic C-terminus of 48, 48 and 161 aminoacids. In addition, both AA021445 and KIAA0999 have 15 copies of a CAG repeat. Trinucleotide repeats are often found in genes that linked to neurodegenerative diseases.

Human 2R22-55-1 (SEQ ID NO:33, SEQ ID NO:153)

Blastn analysis revealed an extension in the Incyte EST clone 321074.1 to encompass the complete ORF corresponding to 2R22-55-1.

Human orthologue of AA544838_m (SEQ ID NO:36, SEQ ID NO:156)

tBlastn analysis identified the partial human KIAA0135 (U79240) clone as the human orthologue of murine AA544838. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte406786.5, KFZp430051 and KIAA0135 (U79240).

Human orthologue of AI785735_m (SEQ ID NO:38, SEQ ID NO:158)

tBlastn analysis identified the partial human KIAA0781 (AB018324) clone as the human orthologue of murine AI785735. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte 986123.37 KIAA0781 (AB018324).

Human AA207220 (SEQ ID NO: 39, SEQ ID NO:159)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. The full ORF was reconstructed from Incyte 402740.1 and AA207220. Frame corrections: deletion of 441 and 595 over Inc402740.1 seq based on blastx to keep frame open; two n insertions 940, 941 over AA207220 to keep frame open.

Human AA426580 (SEQ ID NO:40, SEQ ID NO:160)

Since the initial filing of this application, the partial AA426580 sequence appeared in the public database as the full-length gene encoding MAK-V (AJ271722) from chromosome 21q22.1.

Human 5R79-54-1 (SEQ ID NO: 41, SEQ ID NO:161)

Genewise and Genescan analyses of the partial 5R79-54-1 sequence revealed an extension from genomic sequence to encode the full ORF for 5R79-54-1.

Human orthologue of AA542015_m (SEQ ID NO: 42, SEQ ID NO:162)

tBlastn analysis identified KIAA1297 (AB037718). Blastn extended the KIAA1297 sequence to provide the C-terminus through the Incyte 224074.1 EST. The partial ORF consists of a dual catalytic domain flanked by 6 Ig domains and 2 fibronectin repeats. Based on homology to the bt drosophila protein (AAF59316.1), the human form of AA542015 is expected to be missing 16 Ig domains.

Human R19772 (SEQ ID NO:44, SEQ ID NO:164)

The full-length ORF for R19772 was isolated by screening a cDNA library using a probe derived from R19772. Since the initial filing of this application, the R19772 sequence appeared in the public database as the full-length gene encoding Trio (Duet) (AB011422). CDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 8. Isoforms for R19772

Kestrl Name	Kestrl AA Acc #	Isoform type	Source	Description*
Trad (Duet)	R19772	B	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762
		C	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762

				Deletion of 32 aa (160-191)
		D	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)
		E	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)

* reference amino acid position are with respect to sequence of Trad (AB011422)

Human AA435956 (SEQ ID NO:48, SEQ ID NO:168)

Blastn analysis revealed an extension to encompass the nearly complete catalytic region of AA435956. 5' end sequence extension was provided by genomic locus AC007242.3_h (range 44880-43801). Based on blastx analysis, the extended sequence encodes is full-length at the C-terminus.

Human AA397553 (SEQ ID NO: 51, SEQ ID NO:171)

Since the initial filing of this application, the partial AA397553 sequence appeared in the public database as the full-length gene encoding CRK7 (AF227198), a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters.

Human AA789239 (SEQ ID NO: 52, SEQ ID NO:172)

Since the initial filing of this application, the partial AA789239 sequence appeared in the public database as the full-length gene encoding NKIAMRE (AF130372), a novel kinase deleted in human leukemia.

Human AA631990 (SEQ ID NO:55, SEQ ID NO:175)

Blastn analysis revealed an extension to encompass the full-length ORF for AA631990. The full ORF was reconstructed from 253847.5 and AA631990 and AA207220. Frame corrections: delete 1 C at 1380, delete 2N's at 2033/2034.

Human AA557536 (SEQ ID NO:56, SEQ ID NO:176)

Blastn analysis revealed an extension to encompass full-length ORF for AA557536. The full ORF was reconstructed from AA557536, celera 11000504061899 and the Incyte 097089.1 EST. An 85bp intron was removed from AA557536.

Human N34132 (SEQ ID NO: 63, SEQ ID NO:183)

Full sequencing of EST N34132 (1.3 kb) confirmed that this cDNA encodes a novel NEK-subfamily kinase. Blast analysis against the EST database showed that four

EST sequences (AA283140, AA283140, AA282911 and N53011) extended the sequence of N34132 at the 3' end to form a 2.31 kb contig. Blast analysis of the new contig against the nonredunat public database showed that the N34132 extended contig overlapped (100% identity) over 228 bp at its 3' end with human KIAA0344 (AB002342), a 5, 787 bp cDNA encoding a 1246 aa polypeptide. The 5' 790 bp of the KIAA0344 cDNA (encoding the 58 N-terminal protein sequence) were found to be divergent with respect to the extended 2.32 kb N34132 contig. Evidence that the extended N34132 contig (2.31kb) and KIAA0344 (AB002342) belong to the same gene is the following. First, blast analysis of the nucleotide sequences for N34132 and KIAA0344 against the NRN database confirmed that these cDNA's are transcribed from the same genomic locus defined by two overlapping BACs (AC004765 and AC004803) from chromosome 12p13.3. Second, full sequence determination of a PCR fragment amplified from single-stranded cDNA confirmed the junction between the extended N34132 contig and KIAA0344_h (AB002342). The 462 PCR product was amplified with primers CTCCTCAACAGACAGTGCAG (5' primer) and GACATTCTACTACTCGGTCTC (3' primer) designed from the N34132 extended contig and KIAA0344 sequences, respectively. The region of N34132 containing the start Met was isolated by PCR from a testis cDNA library (Clontech).

Human 5R69-17-2 (SEQ ID NO:67, SEQ ID NO:187)

The full-length ORF for 5R69-17-2 was isolated by screening a cDNA library using a probe derived from 5R69-17-2.

Human H85811 (SEQ ID NO:68, SEQ ID NO:188)

Tblastn, Smith-Waterman and blastn analyses using cDNA databases revealed an extension to encompass full-length ORF for H85811. The full ORF was reconstructed from Incyte ESTs 202971.8, 034583.3 and 034583.1 and public ESTs H85811 and AI570599.

Human R43524 (SEQ ID NO:73, SEQ ID NO:192)

Blastn analysis revealed an extension to encompass the complete catalytic region and the C-terminus of R43524. Since the initial filing of this application, the partial R43524 sequence appeared in the public database as the full-length gene encoding the heme-regulated initiation factor 2-alpha kinase (HRI) (AF181071).

Human AA088547 (SEQ ID NO:78, SEQ ID NO:197)

Genewise and Genescan analyses of genomic databases revealed an extension to encompass the complete ORF for AA088547.

Human orthologue of AA139478_m (SEQ ID NO:80, SEQ ID NO:199)

Tblastn identified the Incyte 211475.1 as the potential full-length human orthologue of murine AA139478

Human AA232253 (SEQ ID NO:82, SEQ ID NO:201)

The full-length ORF for AA232253 was isolated by screening a cDNA library using a probe derived from AA232253. Since the initial filing of this application, the AA232253 sequence appeared in the public database as the full-length gene encoding SLK (AB011422). SLK is a stress-regulated mixed lineage kinase-like protein that activation of Rac and induction of apoptosis. cDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 9. Isoforms for AA232253

Kestrl Name	**Kestrl AA Acc #**	**Isoform type**	**Description***
MLK4	AA232253	MLK4	Substitution of C for W at 346
		MLK4B	Different Cterm (332-800); seq in MLK4B is as shown in *

* C-terminus specific to MLK4B

LPLAARMSEESYFESKTEESNSAEMSCQITATSNGEGHGMNPSLQAMMLMGFGDI
FSMNKAGAVMHSGMQINMQAKQNSS
KTTSKRRGKKVNMALGFSDFDLSEGDDDDDDDGEEEDNDMDNSE

Human H97685 (SEQ ID NO:84, SEQ ID NO:203)

Blastn analysis revealed an extension to encompass the full-length ORF for H97685. The full ORF was reconstructed from Incyte 474824.1 and the public ESTs H97685 and M62021.

Human AI052250 (SEQ ID NO:87, SEQ ID NO:206)

Blastn analysis revealed an extension to encompass the full-length ORF for AI052250. The full ORF was reconstructed from Incyte 396868.1, the public partial cDNA FLJ10074 (minus intron) and the public ESTs and the public ESTs AI052250 and H97685, AI499220 and M62021.

Human AA278842 (SEQ ID NO:88, SEQ ID NO:206)

A nearly full-length cDNA (FL4F12) for AA278842 was isolated by screening a cDNA library using a probe derived from AA278842. A full-length virtual ORF was generated using FL4F12 and AA278842.

Human AA599286 (SEQ ID NO:89, SEQ ID NO:208)

Since the initial filing of this application, the partial AA599286 sequence appeared in the public database as a full-length ORF (AK000342).

Human AA425725 (SEQ ID NO:90, SEQ ID NO:209)

Since the initial filing of this application, the partial AA425725 sequence appeared in the public database as MSSK1, a serine kinase gene located from human chromosome Xq28.

Human SGK022 orthologue of AA060026_m (SEQ ID NO:91, SEQ ID NO:210)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases databases revealed a potential human orthologue for murine AA060026. The full-length ORF for SGK022 was reconstructed from genomic locus AC022307.

Human AA399669 (SEQ ID NO:93, SEQ ID NO:212)

Blastn analysis revealed an extension to encompass the full-length ORF for AA399669. The full ORF was reconstructed as follows: sequence 1-1007 from AL136295.2; sequence1008-2319 from AA399669 and Incyte 428177.1.

Human AA883975 (SEQ ID NO:95, SEQ ID NO:214)

Genescan and Genewise analyses of the genomic databases revealed an extension for AA883975 to encompass the full-length ORF

Human AA905446 (SEQ ID NO:96, SEQ ID NO:215)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases databases revealed an extension for AA905446 to encompass the full-length ORF. For the Smith-Waterman analysis murine STK22 (NP_033462) was used as the closest orthologue. Contig formation: range 162133-163687 from HGP_h 6921333_9; removed intron (146-893) predicted from blastx analysis.

Human H29974 (SEQ ID NO: 97 SEQ ID NO:216)

Blastn analysis revealed an extension to encompass a complete catalytic ORF for AA399669. The nearly full-length ORF was reconstructed using Incyte 213829.1 and H29974.

Human AA215311 (SEQ ID NO:99, SEQ ID NO:218)

Blastn analysis revealed an extension to encompass the full-length ORF for AA21531. The full ORF was reconstructed from Incyte 067584.1, 022456.1, AA215311 and the reverse complement of CPG_043208.

Human AA018361 (SEQ ID NO:100, SEQ ID NO:219)

The full-length ORF for AA018361 was isolated by screening a cDNA library using a probe derived from AA018361. This yielded clone Sug4-30. Clone Sug4-30, like multiple, independent cDNA clones contained a 181bp intron. The existence of intron-less RNA's was confirmed by a PCR reaction that generated a product that upon sequence analysis skipped the intron region. The full-length virtual ORF for AA018361 was generated through a contig between AL117482 (seq 1-367) and the sequence for clone Sug4-30.

Human orthologue of AA396601_m (SEQ ID NO:106, SEQ ID NO:225)

tBlastn and Smith-Waterman analyses of genomic sequence revealed an extension to encompass the full catalytic region for the human orthologue of AA396601. The ORF was reconstructed from Incyte 018653.9 (7261449H1, 6891740J1) and genomic sequence CPG_040010.

Human orthologue of AA671275_m (SEQ ID NO:108, SEQ ID NO:227)

Since the initial filing of this application, a potential human orthologue for murine AA671275 appeared in the public database as the full-length ORF for vaccinia related kinase 3 (BAA90769).

Human H05721 (SEQ ID NO:111, SEQ ID NO:230)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for H05721.

Human AI086865 (SEQ ID NO:112, SEQ ID NO:231)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AI086865. The full-length ORF was reconstructed from Celera 17000102901516, Incyte 243269.1 and public AL1377531.

Human AA836348 (SEQ ID NO:113, SEQ ID NO:232)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AA836348.

Human R86668 (SEQ ID NO:14, SEQ ID NO:233)

The full-length ORF for R86668 was isolated by screening a cDNA library using a probe derived from R86668. Since the initial filing of this application, the R8668 sequence appeared in the public database as the full-length gene mitogen-activated protein kinase kinase kinase 6 (MAP3K6) (NM_00467).

Human 2R41-9-4 (SEQ ID NO: 16, SEQ ID NO:235)

The full-length virtual ORF for 2R41-9-4 was generated using genomic sequence to provide the Nterminus for the partial ORF predicted from clone 2R41-9-4

Table 10. Sequences deleted from the provisional patent due to duplication with other genes in the patent

Prov. SEQ ID NO: (na)	Prov. SEQ ID NO: (aa)
160	196
213	214
215	216
122	126
119	123
148	184
4	20
7	23
205	206
14	30
15	31
35	56
42	63
51	72
44	65
77	91

78	92
79	93
80	94
157	193

Results

Table 1 documents the results from the analysis of the nucleic acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family "and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "ORF Start", "ORF End", "ORF Length" refer to the open reading frame range and length as calculated by standard nucleic acid translation programs such as MapDraw (DNAStar). "DNA Repeats" refers to regions of low complexity sequence or repetitive elements such as Alu, LINE, SINE, and LTR sequences. The chromosomal location (CHR localization) for 37 of the 110 novel protein kinases is shown on Table 1 (NA, not available). The methods for determining chromosomal position are outlined below, in Example 2.

Table 2 documents the results from the analysis of the amino acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family "and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "nraa Score", "ID match aa", "Identity", "Similar", "nraa Match Acc#", Description" refer to the data obtained using a Smith-Waterman search of the amino acid sequence against the non-

redundant protein database (Matrix: Pam100; gap open/extension penalties 14/1). "Kinase Domain Start", "Kinase Domain End", "Profile Start" and "Profile End" refer to data obtained using a Hidden-Markov Model to define catalytic range boundaries. The profile has a length of 261 amino acids, corresponding to the complete protein kinase catalytic domain. Proteins in which the profile recognizes a full length catalytic domain have a "Profile Start" of 1 and a "Profile End" of 261. The boundaries of the catalytic domain within the overall protein are noted in the "Kinase Domain Start" and "Kinase Domain End" columns.

The following abbreviations were used for kinases:

ASK	Apoptosis signal-regulating kinase
CaMK	Ca2+/calmodulin-dependent protein kinase
CCRK	Cell cycle-related kinase
CDK	Cyclin-dependent kinase
CK	Casein kinase
DAPK	Death-associated protein kinase
DM	myotonic dystrophy kinase
Dyrk	dual-specificity-tyrosine phosphorylating-regulated kinase
GAK	Cyclin G-associated kinase
GRK	G-protein coupled receptor
GuC	Guanylate cyclase
HIPK	Homeodomain-interacting protein
IRAK	Interleukin-1 receptor-associated kin
MAPK	Mitogen activated protein kinase
MAST	Micotubule-associated STK
MLCK	Myosin-light chain kinase
MLK	Mixed lineage kinase
NIMA	NimA-related protein kinase
PKA	cAMP-dependent protein kinase
RSK	Ribosomal protein S6 kinase
RTK	Receptor tyrosine kinase

SGK	Serum and glucocorticoid-regulated kinase
STK	serine threonine kinase
ULK	UNC-51-like kinase

The following abbreviations were used for species

H	Human
M	Murine
R	Rat
FV	Fowlpox virus
MT	M. thermoautotrophicum
CE	Caenorhabditis elegans
DM	Drosophila melanogaster
OS	Oryza sativa
SP	Schizosaccharomyces pombe
TP	Tetrahymena pyriformis
PI	Petunia inflata
NC	Neurospora crassa
MSV	Medicago sativa
MSV	Moloney murine sarcoma virus
SA	Squalus acanthias
CS	Cucumis sativus
GM	Glycine max
LL	Lilium longiflorum
TV	Trichomonas vaginalis
MP	Mycoplasma pneumoniae
DD	Dictyostelium discoideum
SC	Saccharomyces cerevisiae
MT	Methanobacterium thermoautotrophicum

Domain and Motif Identification

A Hidden Markov model (HMM) (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. (1994). Hidden Markov models in computational biology: Applications to protein modeling. J. Mol. Biol., 235:1501-1531) was used to identify, both catalytic and extracatalytic domains. Table 4 shows extra-catalytic domains that were identified using the HMM program. Other domains such as coiled-coil and pest motifs were identified as described next.

Potential coiled-coil domains were identified using the COILS program (www.ch.embnet.org/software/COILS_form.html). The matrix used was MTIDK with windows of 14, 21, 28 amino acids. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region.

Protein sequences containing potential pest motifs were identified using the program PESTfind (www.at.embnet.org/embnet/tools/bio/PESTfind/). PEST regions in proteins are by definition sequences that tend to be rich in proline, glutamic or aspartic acid, argininine and histidine; they have been associated with increased protein turnover rates (Rogers S. *et al.* (1986) Science 234, 364-368. The algorithm defines PEST sequences as hydrophilic stretches of amino acids greater than or equal to 12 residues in length. Such regions contain at least one P, one E or D and one S or T. They are flanked by lysine (K), arginine (R) or histidine (H) residues, but positively charged residues are disallowed within the PEST sequence. PESTfind produces a score ranging form about -50 to +50. By definition, a score above zero denotes a possible PEST region; a value greater than +5 defines a high probability that there is a PEST domain.

Identification of potential coiled-coil domains and PEST domains in N34132

Potential coiled-coil domains were identified in N34132 (SEQ ID NO:183) using the COILS program. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region. The amino acid positions within N34231 scoring for potential coil-coil regions are shown below.

Table 11 coiled-coil domains predicted for N34132

Coiled-coil Region	Amino acid range	Length (aa)
1	124-147	24
2	437-451	15
3	495-526	32
4	1,723-1,749	27

Potential PEST domains were identified in N34132 using PESTfind, a value greater than +5 defines a high probability that there is a PEST domain. The amino acid positions within N34132 scoring for potential PEST regions are shown below.

Table 12 Potential Pest domains identified in N34132

PEST Region	Score	Amino acid range	Amino Acid Length
1	+ 4.91	54-95	42
2	+11.4	537-570	34
3	+31.08	1293-1304	12
4	+10.15	1543-1565	23
5	+ 6.17	1698-1732	35

EXAMPLE 2. Chromosomal Localization of Novel Mammalian Protein Kinases

Materials and Methods

Several sources were used to find information about the chromosomal localization of each of the genes described in this patent. First, the accession number for the nucleic acid sequence was used to query the Unigene database. The site containing the Unigene search engine is: http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html. Information on map position within the Unigene database is imported from several sources, including the Online Mendelian Inheritance in Man (OMIM, http://www.ncbi.nlm.nih.gov/Omim/searchomim.html), The Genome Database (http://gdb.infobiogen.fr/gdb/simpleSearch.html), and the Whitehead Institute human physical map (http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts_info?database=release). For example, searching Unigene with W56561, an EST for a MAK-like kinase, the

following information is retrieved: Chr.14, D14S65-qTEL. The location of this gene on an "ideogram" of the cytogenetic map of chromosome 14 is also provided, showing that W56561 maps to the bottom of chromosome 14, between 14q31 and 14qTel. If Unigene has not mapped the EST, then the nucleic acid for the gene of interest is used as a query against databases, such as dbsts and htgs (described at http://www.ncbi.nlm.nih.gov/BLAST/blast_databases.html) containing sequences that have been mapped already. The nucleic acid sequence is searched using BLAST-2 at NCBI (http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast) and is used to query either dbsts or htgs. In addition to the Whitehead and GDB sites mentioned above, Stanford University maintains a useful site for chromosomal mapping from STS data (http://www-shgc.stanford.edu/RH/rhserverformnew.html). Matches in htgs are often resolved immediately because the genomic region hit is annotated in the htgs entry. If an exact match match is found (defined roughly as 99% identity over a region of about 100 base pairs or longer, excluding any repetitive sequence), then the mapped position of the entry in the database is assigned to the original kinase query. Once a cytogenetic region has been identified by one of these approaches, disease association is established by searching OMIM (see above for URL) with the cytogenetic location. OMIM maintains a searchable catalog of cytogenetic map locations organized by disease. A thorough search of available literature for the cytogenetic region is alo made using Medline (http://www.ncbi.nlm.nih.gov/PubMed/medline.html). References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123.

Results

The chromosomal location for 37 of the 110 novel protein kinases is shown on Table 1. Three of the novel protein kinases were mapped to regions associated with cancer amplicons, as shown on this table. The regions were also cross-checked with the Mendelian Inheritance in Man database, which tracks genetic information for many human diseases, including cancer. References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, et al., Am J Pathol, 1998, 152:1107-1123. Association of these mapped regions with other diseases is

documented in the Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/htbin-post/Omim).

EXAMPLE 3: Generation of Specific Immunoreagents

Materials and Methods

Peptide sequences to extra-catalytic regions of novel kinases are chosen which are not homologous to other known kinases based on a Smith Waterman homology search against the non-redundant protein database and predicted to be antigenic based on the DNAStar Protean program. These peptides are conjugated to KLH using Glutaraldehyde.

Rabbits are immunized with the KLH-peptide conjugates by four injections three weeks apart. The rabbits are bled ten and fourteen days following the third injection and bled out ten days after the fourth. The serum is checked against the peptide by ELISA.

Table 13. Peptides to be used as immunogens for raising antibodies

Clone Name	SEQ ID NO (aa)	Peptide Sequence	Amino Location
AA8256850	124	KSRDNSRDSSQSEND	339-353
		TEKLKRSQDLPREPLP	372-386
		RGWRPYDIHS	223-232
5R79-46-1	126	FEGPRRNKEVMYK	224-236
		KDDYNETVHKKTE	451-463
		GTHPKDRNVEKLQ	541-553
		EVSKYQEYTNELQET	643-657
AA256100	129	IDDTSNFDDFPESDI	405-419
		TEPDYKSKDWVFL	427-439
		EEKKLRRSQHARKET	61-75
AA210825	130	SNKDTLRKRHYWRLD	507-521
		RHTTRKSSTTLRE	488-500
		FQNNTTNRYYKEIPL	528-542
		GKHRKTGRDVAVK	668-680
		FPTKQESQLRNE	687-698

AA316804	132	ESHVHQEPSKRIPS	239-252
		HTKRKSSTMVKEGW	409-422
		PSDLDVERDEEAVK	375-388
		SPGQGKDHKDLSTSI	543-557
R47805	143	EPVGRWDQDYDRAVL	44-58
		KPKGPGGKRGHKRLI	325-339
		PTDVAQLPSRVPRDA	219-233
AA234451	167	DPFDWEKTGNDGSLT	293-307
		HPRPQEKDVWEE	374-385
		RENTDEVFPDEQLSD	340-354
		RSEITQPDRDIPLVR	427-441
AA460132	180	LKSYSTSSKKARPVL	222-236
		KKLDEVRLRGRKRSM	237-251
		ETEKTAQGLSNLAKT	131-145
N34132	183	SGRRRRPTKSKGSKS	1848-1862
		PGTAPSKPPLTKAPV	1474-1488
		VDSDTQPKAPGIDD	1365-1378
		AHSLDKTSHSSTTGL	1253-1267
5R69-17-2	187	GTTREKTDRVKST	178-190
		HSEAPELHGKIRSSN	138-152
		DETVTPPQFSIV	87-98
		QYDVKSEIYS	204-213
AA278842	206	TVDPEKSVRDQAFKA	515-529
		DSSTADRWDDEDWGS	637-651
		SVSEDPTQLEEVEKD	539-553
AA836348	232	NAPTKRPRSSTVTEA	323-337
		LDSEEDYYTPQKVDV	514-528
		GDKASYRQPKHVEKL	409-423

EXAMPLE 4. Expression analysis of Novel Mammalian Protein Kinases

GENE EXPRESSION ANALYSIS

Tissue Arrays

"cDNA libraries" derived from a variety of sources were immobilized onto nylon membranes and probed with 32P-labeled cDNA fragments derived from the gene(s) of interest.

Total RNA or mRNA was used as template in a reverse transcription reaction to generate single-stranded cDNAs (ss cDNA) that were tagged with specific sequences at each end. An oligo dT primer containing a specific sequence (CDS: AAGCAGTGGTAACAACGCAGAGTACT30VN (V=A,G,C N=A,G,C,T)) anneals at the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV RnaseH-) transcribes the antisense strand until it reaches the end of the RNA strand when it adds additional C residues. If a primer (SMII: AAGCAGTGGTAACAACGCAGAGTACGCGGG or ML2G: AAGTGGCAACAGAGATAACGCGTACGCGGG) ending with 3 Gs is added, it anneals to the added Cs and the MMLV recognizes the rest of the primer sequence as template and continues transcription. As a result, the synthesized cDNAs contain specific sequence tags at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same sequence (CDS and SMII) it is referred to as "symmetric." When the 5' end is tagged with a different sequence than the 3' end (CDS and ML2G) is referred to as "asymmetric" A double-stranded "cDNA library " is then generated by PCR amplification using the 3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT and ML2: AAGTGGCAACAGAGATAACGCGT) that anneal to the added sequence tags.

The amplified "cDNA libraries" were manually arrayed onto nylon membranes with a 384 pin replicator. The DNA was denatured by alkali treatment, neutralized and cross-linked by UV light. The arrays were pre-hybridized with Express Hyb (Clontech) and hybridized with 32P labeled probes generated by random hexamer priming of cDNA fragments corresponding to the genes of interest. After washing, the blots were exposed to phosphorimaging cassettes and the intensity of the signal was quantified. The amount of the DNA on the arrays was also quantified by treating non-denatured or denatured arrays with Syber Green I or Syber Green II respectively (1:100,000 in 50mM Tris, pH8.0) for 2 minutes. After washing with 50mM Tris, pH8.0, the fluorescent emission was detected

with a phosphorimager (Molecular Dynamics) and quantified. The amount of the arrayed DNA was used to normalize the hybridization signal and the corrected values are tabulated in Table 3.

Results

The results of the microarray expression analysis of the protein kinases presented in this application is shown in Table 3. Data presentation from left to right is as follows: "Tissue": tissue type of the cDNA; "Tumor sym", indicates that the tissue is derived from a tumor, "sym" refers to the fact that the 5' and 3' primers used to make the sample are the same; "Normal Sym", indicates normal tissue was used to make the sample, with symmetric primers as described above; "Tumor 1o", indicates that primary tumor tissue was used to make the cDNA; "Tumor cells", indicates that these cDNA samples were made from cultured tumor cells; "Normal", indicates that these samples are derived from normal tissue or cell lines; "Endos", indicates that these samples are derived from endothelium-related tissue sources; "p53" refers to the status, mutant or wild-type, of the p53 gene in the source samples. Normalized expression values are presented for each gene referred to by its SEQ ID# on the subsequent columns. Genes represented in expression Table 3 are: SEQ ID NO:3 (AA826850), SEQ ID NO:5 (TBK1), SEQ ID NO:6 (AA305176), SEQ ID NO:8 (AA256100), SEQ ID NO:9 (CAB43292), SEQ ID NO:11 (EPK2), SEQ ID NO:12 (PKNbeta), SEQ ID NO:14 (H19102), SEQ ID NO:16 (RSK4), SEQ ID NO:17 (AAD30182), SEQ ID NO:20 (SGK2), SEQ ID NO:22 (PTK9L), SEQ ID NO:26 (AA383293), SEQ ID NO:29 (DRAK2), SEQ ID NO:31 (DRAK1), SEQ ID NO:032 (AA015726), SEQ ID NO:40 (MAK-V), SEQ ID NO:044 (TRAD), SEQ ID NO:044 (TRAD), SEQ ID NO:45 (AA454060), SEQ ID NO:47 (AA234451), SEQ ID NO:48 (AA436054), SEQ ID NO:49 (AA626859), SEQ ID NO:51 (KIAA0904), SEQ ID NO:52 (AA789239), SEQ ID NO:54 (CCRK), SEQ ID NO:55 (CLK4), SEQ ID NO:56 (AA557536), SEQ ID NO:57 (W56561), SEQ ID NO:60 (AA579641), SEQ ID NO:63 (NEK7), SEQ ID NO:66 (CAMKKB), SEQ ID NO:68 (HIPK2), SEQ ID NO:72 (R19609), SEQ ID NO:73 (HRI), SEQ ID NO:78 (AA088547), SEQ ID NO:79 (AA449542), SEQ ID NO:082a (MLK4), SEQ ID NO:82 (MLK4b), SEQ ID NO:84 (RIP4), SEQ ID NO:88 (AA278842), SEQ ID NO:89 (AA195964), SEQ ID NO:90 (MSSK1), SEQ ID NO:93 (TSK4), SEQ ID NO:94 (AI025291), SEQ ID NO:95

(AA948538), SEQ ID NO:96 (AA905446), SEQ ID NO:97 (H85389), SEQ ID NO:100 (AA018361), SEQ ID NO:101 (AA311714), SEQ ID NO:110 (AA452647), SEQ ID NO:111 (AA310219), SEQ ID NO:112 (AI086865), SEQ ID NO:114 (MEKK6), and SEQ ID NO:116 (SuRTK106).

EXAMPLE 5. Kinase assays for Erk, JNK1 and p38 MAP kinases

293T cells were transiently transfected with HA- p38 or co-transfected with Flag-tagged wt MLK4A, kinase-dead MLK4A, wild-type MLK4B or kinase-dead MLK4B using Lipofectamine 2000 (Lifetech). Cells were lysed 36 hr post-transfection. Cell lysates normalized to contain equivalent amounts of HA-p38 were immunoprecipitated with anti-HA antibody (Mab HA-11, Babco). Immunoprecipitates were split in two portions, one portion was Western-blotted with anti- HA antibody and the other with a phospho-specific p38 antibody (Promega) to detect activated levels of p38. Activation of Erk1 and Jnk1 was measured similarly. (This example applies to AA232253 (SEQ ID NO:82, SEQ ID NO:201).)

Results:

In transient assays wild-type MLK4A and MLK4B (but not kinase-inactive MLK4A(K45M) or MLK4B(K45M)) activate Erk, JNK1 and p38 MAP kinases.

EXAMPLE 6. RAC1 guanine-exchange factor assay

293T cells were transiently transfected with HA-Rac1 or co-transfected with Flag-tagged Duet C, Duet E, Dbl and HA-Tiam-1. Cells were lysed 36 hour post-transfection. Cell lysates normalized to contain equivalent amounts of Rac1 were affinity precipitated with immobilized GST-PBD (p21-binding domain of Pak3). Bound proteins were Western blotted and probed with anti-HA antibody to detect levels of activated Rac1. ((This example applies to R199772 (Trad/Duet)(SEQ ID NO:44, SEQ ID NO:164).)

Results:

Duet C and Duet E both act as guanine nucleotide exchange factors on Rac1.

CONCLUSION

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

In particular, although some formulations described herein have been identified by the excipients added to the formulations, the invention is meant to also cover the final formulation formed by the combination of these excipients. Specifically, the invention includes formulations in which one to all of the added excipients undergo a reaction during formulation and are no longer present in the final formulation, or are present in modified forms.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush

group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

Other embodiments are within the following claims.

What is claimed is:

CLAIMS

1. An isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) is the complement of the nucleotide sequence of (a);

(c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide;

(d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(e) is the complement of the nucleotide sequence of (d);

(f) encodes a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229; SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, wherein said domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(g) is the complement of the nucleotide sequence of (f);

(h) encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID

NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, further comprising a vector or promoter effective to initiate transcription in a host cell.

4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

5. The nucleic acid molecule of claim 4, wherein said mammal is a human.

6. A nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

7. The probe of claim 6, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

8. A recombinant cell comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

9. The cell of claim 8, wherein said polypeptide is a fragment of a protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

10. An isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

12. The polypeptide of claim 10, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

13. The kinase polypeptide of claim 10, wherein said polypeptide is isolated, purified, or enriched from a mammal.

14. The kinase polypeptide of claim 13, wherein said mammal is a human.

15. The kinase polypeptide of claim 10, wherein said polypeptide is a AA144574, AA116841, AA256100, AA305176, AA210825, AA316804, AA980090, N42050, AA476563, AA626690, AA960957, H19102, AA045601, AA107515, AA109508 or AA887783 polypeptide.

16. The kinase polypeptide of claim 10, wherein said polypeptide is a H60215, AA197883, AA297313, W30246, AA172300, AA383293, AA542015, H01248, N23936, W44160, 2R22-5-11, 5R72-18-1, AA021445, AA207220, AA426580, AA544838, W90839, 5R79-54-1, AA839940, R19772 or 5R72-8-2 polypeptide.

17. The kinase polypeptide of claim 10, wherein said polypeptide is a AA234451 polypeptide.

18. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R65-16-1, AA061797, AA065538, AA124976, AA397553, AA435956, AA575635, AA626859, AA789239, AI086865, H17727, H29974, AA557536 or N28606 polypeptide.

19. The kinase polypeptide of claim 10, wherein said polypeptide is a AA631990 or W08549 polypeptide.

20. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R72-16-2, R19927 or R43524 polypeptide.

21. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R57-10-2 polypeptide.

22. The kinase polypeptide of claim 10, wherein said polypeptide is a AA232253 polypeptide.

23. The kinase polypeptide of claim 10, wherein said polypeptide is a AA430250, AA836348, R86668 or N34132 polypeptide.

24. The kinase polypeptide of claim 10, wherein said polypeptide is a AA098024or SuRTK106 polypeptide.

25. The kinase polypeptide of claim 10, wherein said polypeptide is a R47805, AA099102, AA589241, H85811, AA013524, AA452647, AA840598, AA088547, AA139478, AA826850, R87679, W65887, H97685, W20810, AA599286, AA425725, AA103218, AA711829, AA060026, AA399669, AA758539, AA883975, AA948538, AA018361, AA215311, AA311714, AA498104, 5R69-17-2, 5R69-23-3, 5R69-26-2, AA118352, AA396601, AA671275, AA278842, AA460132 or H05721 polypeptide.

26. An antibody or antibody fragment having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

27. The antibody or antibody fragment of claim 26, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

28. A hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

29. A method for identifying a substance that modulates kinase activity comprising:

(a) contacting a kinase polypeptide selected from the group consisting SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,

SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance;

(b) measuring the activity of said polypeptide; and

(c) determining whether said substance modulates the activity of said polypeptide.

30. A method for identifying a substance that modulates kinase activity in a cell comprising:

(a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID

NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) adding a test substance to said cell; and

(c) monitoring a change in cell phenotype or the interaction between said polypeptide and a natural binding partner.

31. A method for treating a disease or disorder by administering to a patient in need of such treatment a substance that modulates the activity of a kinase selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

32. The method of claim 31, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

33. The method of claim 31, wherein said substance modulates kinase activity *in vitro*.

34. The method of claim 33, wherein said substance is a kinase inhibitor.

35. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) contacting said sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding said polypeptide, fragments thereof, or the complements of said sequences and fragments; and

(b) detecting the presence or amount of the probe:target region hybrid as an indication of said disease.

36. The method of claim 35, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

37. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) comparing a nucleic acid target region encoding said kinase polypeptide in a sample, wherein said kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ

ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding said kinase polypeptide, or one or more fragments thereof; and

(b) detecting differences in sequence or amount between said target region and said control target region, as an indication of said disease or disorder.

38. The method of claim 37, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

Table 1

Gene Name	SP	Prov_Seq_ID_NA	Prov_Seq_ID_AA	SEQ_ID_#_na	SEQ_ID_#_aa	Family	Group	Length_NA	Length_AA	ORF_Start	ORF_end	ORF_Length	DNA Repeats	CHR localization
X69117_h BARK2_h	H	x	x	1	122	AGC	GRK	2067	688	1	2064	2064	x	22q11
AA144574_m BARK2_m	M	1	17	2	123	AGC	GRK	1368	378	2	1135	1134	x	NA
AA826850_h	H	140	176	3	124	AGC	Mo3C11.1_ce	1768	419	8	1264	1257	285-304	NA
AA960957_h	H	11	27	4	125	AGC	Mo3C11.1_ce	3224	414	65	1306	1242	x	4p16.1
5R79-46-1_h, TBK1_h	H	207	208	5	126	AGC	Mo3C11.1_ce	3013	729	93	2279	2187	x	NA
AA305176_h	H	4,2	18,20	6	127	AGC	NDR	1421	329	53	1039	987	x	10p11.2
AA118841_m	M	4,2	18,20	7	128	AGC	NDR	582	68	3	268	204	x	NA
AA256100_h	H	3	19	8	129	AGC	NDR	4983	464	86	1477	1392	x	12q11
AA210825_h	H	5	21	9	130	AGC	PKC	3263	978	117	3050	2934	x	19q13-q13.3
AA127299_h	H	203	204	10	131	AGC	PKC	315	105	1	315	315	x	NA
AA316804_h, EPK2	H	6	22	11	132	AGC	PKC	2673	890	1	2670	2670	x	2p21
N42050_h PKNbeta	H	8	24	12	133	AGC	PKC	2870	889	1	2667	2667	2221-2280	NA
AI021023_m PKNbeta_m	M	x	x	13	134	AGC	PKC	929	205	2	616	615	x	NA
H19102_h	H	12	28	14	135	AGC	S6K	1155	384	1	1152	1152	599-638	CHR17
AA478563_h RPS6KC1	H	9	25	15	136	AGC	S6K	1410	469	1	1407	1407	x	12q12-q13.1
AA526890_h RSK4	H	10	26	16	137	AGC	S6K	2238	745	1	2235	2235	x	Xq21.1
AA215680_h	H	227	228	17	138	AGC	S6K	1650	549	1	1647	1647	767-766	14q24.3
SGK_h	H	x	x	18	139	AGC	SGK	1296	431	1	1293	1293	656-683	6q21-q22
AA107515_m	M	x	x	19	140	AGC	SGK	2432	430	75	1364	1290	1604-1630	NA
AA109508_m	M	13	29	20	141	AGC	SGK	1346	244	2	733	732	x	NA
AA887763_h SGK3, SGKL	H	16	32	21	142	AGC	SGK	2250	446	36	1373	1338	x	NA
R47805_h PTK9L	H	131	167	22	143	Atypical	A6	1050	349	1	1047	1047	x	3p14.3
H60215_h	H	33	54	23	144	CAMK	AMPK	2310	440	420	1739	1320	x	1p31.1-1p32.3
SGK324_h	H	x	x	24	145	CAMK	CAMK	3240	692	7	2082	2076	208-227	NA
W30246_m SGK324_m	M	36	57	25	146	CAMK	CAMK	1248	297	1	891	891	x	NA
AA383293_h	H	38	59	26	147	CAMK	CAMK	2424	686	1	2058	2058	439-458	NA
AA197883_m	M	34	55	28	148	CAMK	CAMK	2421	806	1	2418	2418	x	NA
AA172300_h DRAK2	H	37	58	29	149	CAMK	DAPK	1626	373	262	1380	1119	x	2q31-2q24.3
W44150_m DRAK2_m	M	x	x	30	150	CAMK	DAPK	2671	372	171	1286	1116	x	NA
H01248_h, DRAK1_h	H	40	61	31	151	CAMK	DAPK	1245	414	1	1242	1242	91-110	7p11-q11
AA021445_h	H	45	66	32	152	CAMK	EMK	4321	1311	146	4078	3933	x	11q22.1-11q22.3
2R22-5-11_h	H	43	64	33	153	CAMK	EMK	2311	436	871	2178	1308	61-2281, 1258-12	NA
R31237_1_h, AAC33487	H	x	x	34	154	CAMK	EMK	2190	729	1	2187	2187	x	NA
W90839_m	M	49	70	35	155	CAMK	EMK	1594	520	1	1560	1560	x	NA
406786.5_h	H	x	x	36	156	CAMK	EMK	4139	1330	77	4066	3990	x	2q34-q37
AA544838_m 406786_m	M	48	69	37	157	CAMK	EMK	1350	230	3	692	690	1002-1022	NA
AA785735_h	H	x	x	38	158	CAMK	EMK	5163	926	155	2932	2778	x	NA
AA207220_h	H	46	67	39	159	CAMK	EMK	2291	629	103	1989	1887	x	NA
AA426580_h, MAK_V_h	H	47	68	40	160	CAMK	EMK	2145	714	1	2142	2142	x	21q11
Z36720_h	H	50	71	41	161	CAMK	MLCK	2625	874	1	2622	2622	x	NA
SGK088_h	H	x	x	42	162	CAMK	Trio	7710	2286	1	6858	6858	x	NA
AA542015_m SGK088_m	M	39	60	43	163	CAMK	Trio	1251	127	1	381	381	x	NA
R19772_h	H	52	73	44	164	CAMK	Trio	3864	1287	1	3861	3861	x	3q13.3-q21
5R72_8_2_h	H	53	74	45	165	CAMK	Unique	2586	514	406	1947	1542	x	11p15.1-11p15.2
SGK309_h	H	159	195	46	166	CKI	CKI	1620	508	97	1620	1524	843-862	NA
AA234451_h	H	75	76	47	167	CKI	CKI	2452	478	406	1839	1434	x	NA
AA435956_h	H	82	96	48	168	CMGC	CDK	1077	266	1	798	798	x	NA
AA626859_h	H	84	98	49	169	CMGC	CDK	911	247	2	742	741	84-119	NA
AA061797_m	M	x	x	50	170	CMGC	CDK	2615	296	2	889	888	x	NA
AA397553_h CRK7	H	81	95	51	171	CMGC	CDK	4473	1490	1	4470	4470	1219-1238	NA
AA789239_h	H	65	99	52	172	CMGC	CDK	1868	534	6	1607	1602	x	5q23-q23.3
AA124976_m	M	x	x	53	173	CMGC	CDK	1688	337	1	1011	1011	x	NA
AA575835_m CCRK_m	M	x	x	54	174	CMGC	CDK	1380	211	1	633	633	163-191	NA
AA631990_h CLK4	H	105	107	55	175	CMGC	CLK	2488	499	34	1530	1497	x	NA
AA557536_h	H	89	103	56	176	CMGC	RCK	1831	545	30	1664	1635	516-536	NA
N28606_h, MOK	H	90	104	57	177	CMGC	RCK	1260	419	1	1257	1257	x	14q32
AB023153_h, ICK	H	x	x	58	178	CMGC	RCK	1899	632	1	1896	1896	x	NA
AA839940_m	M	x	x	59	179	CMGC	RCK	1776	413	1	1239	1239	x	NA
AA460132_h	H	165	201	60	180	Microbial PK	YGR262_sc	1428	253	199	957	759	x	20q12 Amplicon
SGK034_h	H	x	x	61	181	Other	C26C2_ce	3304	462	1	1386	1386	x	NA
AA103218_m SGK034_m	M	147	183	62	182	Other	C26C2_ce	2326	281	2	844	843	x	NA
NEK7_h, N34132_h	H	122	126	63	183	Other	C26C2_ce	7328	1952	42	5897	5856	x	12p13.33

Table 1 (cont'd)

Gene Name	SP	Prov_Seq_ID_NA	Prov_Seq_ID_AA	SEQ_ID_#_na	SEQ_ID_#_aa	Family	Group	Length_NA	Length_AA	ORF_Start	ORF_end	ORF_Length	DNA Repeats	CHR localization
BCON3_h	H	x	x	64	184	Other	C26C2_ce	2164	536	113	1717	1608	248-267	NA
AA711829_m	M	148	184	65	185	Other	C26C2_ce	1568	378	1	1134	1134	x	NA
AA099102_h CaMKKB	H	132	168	66	186	Other	CAMKK	1767	588	1	1764	1764	65-84	12q23-q14
5R69_17_2_h	H	158	194	67	187	Other	CTR1	3387	241	1850	2572	723	499-521	NA
H85811_h	H	134	170	68	188	Other	DYRK	3993	1171	183	3695	3513	1326-1348	CHR7
AA02193_h DYRK3	H	x	x	69	189	Other	DYRK	2141	553	253	1911	1659	x	NA
AA589241_m DYRK3_m	M	133	169	70	190	Other	DYRK	741	168	3	506	504	x	NA
5R72_16_2_h, R19927_h	H	109	112	71	191	Other	EIFK	5163	1649	20	4966	4947	x	NA
R43524_h, HRI_h, R19609	H	111	114	73	192	Other	EIFK	1893	630	1	1890	1890	x	7p22-p22.3
17000057519457_h	H	x	x	74	193	Other	Endop	3055	253	219	977	759	2283-2365	NA
AA013524_m	M	135	171	75	194	Other	Endop	926	216	1	648	648	x	NA
17000139801197_h, IRAKM	H	x	x	76	195	Other	IRAK	1791	596	1	1788	1788	x	NA
AA840598_m IRAKM_m	M	137	173	77	196	Other	IRAK	2243	392	1	1175	1176	x	NA
AA088547_h	H	138	174	78	197	Other	IRE	2769	922	1	2766	2766	x	NA
HGP_6844468	H	x	x	79	198	Other	KYK2_dd	1857	322	179	1144	966	x	NA
AA449542_m	M	139	175	80	199	Other	KYK2_dd	1251	280	2	841	840	602-621	NA
5R57_10_2_m TESK2_m	M	115	116	81	200	Other	LIMK	140	41	2	124	123	x	NA
AA232253_h	H	117	118	82	201	Other	MLK	2403	800	1	2400	2400	x	NA
AI375137_h	H	209	210	83	202	Other	MLK	2508	835	1	2505	2505	2219-2238	NA
H97685_h	H	143	179	84	203	Other	RIP	2364	634	161	2062	1902	x	1q31
W20810_m	M	144	180	85	204	Other	RIP	1073	289	3	869	867	x	NA
AA744236_h	H	211	212	86	205	Other	SCY1_sc	2067	688	1	2064	2064	x	1q23
AI052250_h	H	225	226	87	206	Other	SCY1_sc	1739	505	174	1688	1515	x	NA
AA278842_h	H	164	200	88	207	Other	SCY1_sc	2668	808	105	2528	2424	1764-1783	11q12-q13 Amplicon
AA599288_h	H	145	181	89	208	Other	SLOB?	1949	649	1	1949	1949	x	NA
AA425725_h	H	146	182	90	209	Other	SRPK	1602	533	1	1599	1599	x	Xq28
SGK022_h	H	x	x	91	210	Other	STK22A	1038	268	184	987	804	x	NA
AA060026_m SGK022_m	M	149	185	92	211	Other	STK22A	1004	268	147	950	804	x	NA
AA399669_h	H	150	186	93	212	Other	STK22A	1537	292	372	1244	676	x	14p11-q11
AA758539_h	H	151	187	94	213	Other	STK22A	1322	358	101	1174	1074	x	NA
AA883975_h	H	153	189	95	214	Other	TSK	822	273	1	819	819	x	NA
AA905446_h	H	223	224	96	215	Other	TSK	1066	216	365	1012	648	x	NA
H29974_h	H	88	102	97	216	Other	UNC	1638	333	2	1000	999	x	NA
AA498104_m H29974_m	M	x	x	98	217	Other	UNC	1490	412	1	1236	1236	701-729	NA
AA215311_h	H	155	191	99	218	Other	UNC	2011	341	199	1221	1023	x	NA
AA018361_h	H	154	190	100	219	Other	UNC	2759	481	113	1555	1443	x	15q23
AA311714_h	H	156	192	101	220	Other	UNC	1876	565	136	1833	1695	x	NA
SGK384_h	H	x	x	102	221	Other	Unique	117	39	1	117	117	x	NA
AA210451_m SGK384_m	M	106	108	103	222	Other	Unique	2721	349	222	1268	1047	2251-2268	NA
SGK071_2_h	H	x	x	104	223	Other	Unique	2115	704	1	2112	2112	57-76, 318-337	NA
AA118352_m SGK071_m	M	161	197	105	224	Other	Unique	1729	540	3	1622	1620	x	NA
018653.9_h	H	162	198	106	225	Other	Unique	2461	540	1	1620	1620	240-259	NA
AA396601_m	M	x	x	107	226	Other	Unique	1886	365	3	1097	1095	x	NA
AA671275_h VRK3	H	163	199	108	227	Other	VRK	1425	474	1	1422	1422	x	19q13
S71575_m VRK3_m	M	x	x	109	228	Other	VRK	1009	234	3	704	702	937-957	NA
AA452647_h MPSK1	H	136	172	110	229	Other	YPL236_sc	918	305	1	915	915	x	3cen-3q21
H05721_h	H	166	202	111	230	Other	YQ09_ce	2688	581	95	1837	1743	x	1p32.3-31 Amplicon
AI088865_h	H	88	100	112	231	STE	NEK	2463	698	7	2100	2094	x	NA
AA836348_h	H	120	124	113	232	STE	NEK	2511	836	1	2508	2508	x	NA
R88668_h, MKK6	H	121	125	114	233	STE	STE11	3036	1011	1	3033	3033	x	1p32.3-p31.1
PAK6_h 5R95-20-11	H	219	220	115	234	STE	STE20-02	2160	719	1	2157	2157	x	20p12
SuRTK106_h 2R41-9-4_h	H	128,127	129, 130	116	235	TK	RTK-20	2460	495	1	1485	1485	x	12p12.3
AA098024_m	M	128,127	130	117	236	TK	RTK-20	1793	183	1	549	549	1362-1382	NA
SGK2alpha_h	H	x	x	118	237	AGC	SGK	1812	367	88	1188	1101	x	NA
H08950_h CCRK	H	87	101	120	238	CMGC	CDK	1359	452	1	1356	1356	x	9q21.1-q21.3
NM_007170_h TESK2	H	x	x	121	239	Other	LIMK	3016	555	396	2060	1665	x	NA

Table 2

SP	Patent Seq ID# na	Patent Seq ID# aa	Family	Group	nraa Pscore	Length aa	ID match aa	% Identity	% Similar	nraa Match ACC#	Description	Kinase Domain(s) start	Kinase Domain (s) end	Profile start	Profile end
H	1	122	AGC	GRK	2.7e-314	688	687	100	100	CAB45657.1	BARK2 [Homo sapiens]	191	453	1	261
M	2	123	AGC	GRK	1.30E-190	378	371	98	99	NP_037029.1	Adrenergic receptor kinase, beta 2 (G-protein-linked receptor kin	3	143	121	261
H	3	124	AGC	o3C11.1_ce	5.80E-106	419	282	71	86	CAB76471.1	Serine/threonine protein kinase [Homo sapiens]	26	286	1	261
H	4	125	AGC	o3C11.1_ce	1.40E-137	414	414	100	100	CAB76471.1	Serine/threonine protein kinase [Homo sapiens]	23	283	1	261
H	5	126	AGC	o3C11.1_ce	0	729	729	100	100	NP_037386.1	TANK-binding kinase 1 [Homo sapiens]	9	304	1	261
H	6	127	AGC	NDR	1.20E-09	329	73	46	66	BAA76817.1	KIAA0973 protein [Homo sapiens]	35	310	1	261
M	7	128	AGC	NDR	1.30E-19	88	42	49	71	AAF55594.1	CG7719 gene product [Drosophila melanogaster]	24	44	242	261
H	8	129	AGC	NDR	6.10E-181	464	463	100	100	BAA76809.1	KIAA0965 protein [Homo sapiens]	90	383	1	261
H	9	130	AGC	PKC	8.60E-160	978	615	67	80	NP_002733.1	Protein kinase C, mu [Homo sapiens]	651	907	1	261
H	10	131	AGC	PKC	1.10E-10	105	42	42	57	P05127	Protein kinase C, BETA-II TYPE (PKC-BETA-2) [Homo sapiens]	19	24	256	261
H	11	132	AGC	PKC	0	890	890	100	100	NP_005804.1	Protein kinase C, nu [Homo sapiens]	576	832	1	261
H	12	133	AGC	PKC	9.4e-319	889	889	100	100	NP_037487.1	PKNbeta [Homo sapiens]	559	818	1	261
M	13	134	AGC	PKC	1.20E-106	205	204	100	100	JC7083	Protein kinase N beta [Homo sapiens]	1	134	126	261
H	14	135	AGC	S6K	3.60E-12	384	94	38	55	AAC82495.1	Ribosomal protein S6 kinase 3 [Homo sapiens]	81	333	1	261
H	15	136	AGC	S6K	2.90E-257	469	469	100	100	NP_036556.1	Ribosomal protein S6 kinase, 52kD, polypeptide 1 [Homo sapien	225	459	1	261
H	16	137	AGC	S6K	7.00E-176	746	745	100	100	NP_055311.1	Ribosomal protein S6 kinase, 90kD, polypeptide 6 [Homo sapien	73 & 426	330 & 683	1	261
H	17	138	AGC	S6K	9.60E-222	549	549	100	100	AAD30182.1	Unknown [Homo sapiens]	153	539	1	261
H	18	139	AGC	SGK	9.20E-103	431	430	100	100	AAD41091.1	SGK [Homo sapiens]	98	355	1	261
M	19	140	AGC	SGK	2.90E-157	430	426	99	99	NP_035491.1	Serum/glucocorticoid regulated kinase [Mus musculus]	98	354	1	261
M	20	141	AGC	SGK	2.00E-76	244	244	100	100	AAF12757.2	Protein kinase [Homo sapiens]	1	169	24	261
H	21	142	AGC	SGK	4.10E-211	446	375	88	88	AAF27051.1	SGK-like protein SGKL [Homo sapiens]	182	369	1	261
H	22	143	Atypical	A6	5.60E-216	349	349	100	100	NP_009215.1	Protein tyrosine kinase 9-like (A6-related protein) [Homo sapien	10	17	253	261
H	23	144	CAMK	AMPK	1.40E-19	440	68	39	61	CAA04119.1	Phosphoprotein [Homo sapiens]	40	333	1	261
H	24	145	CAMK	CAMK	1.50E-165	699	466	65	77	O15075	DCAMKL1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1)	368	625	1	261
M	25	146	CAMK	CAMK	1.60E-62	297	199	67	83	AAF26675.1	CPG16 [Mus musculus]	59	297	1	261
H	26	147	CAMK	CAMK	2.60E-48	708	181	44	60	O15075	DCAMKL1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1)	416	673	1	261
M	28	148	CAMK	CAMK	2.60E-31	806	147	55	73	AAF26675.1	CPG16 [Mus musculus]	514	771	1	261
H	29	149	CAMK	DAPK	3.10E-121	372	372	100	100	NP_004217.1	Death-associated protein kinase-related 2	33	293	1	261
M	30	150	CAMK	DAPK	7.90E-93	372	340	91	95	NP_004217.1	Death-associated protein kinase-related 2	32	293	1	261
H	31	151	CAMK	DAPK	1.20E-113	414	414	100	100	NP_004751.1	Death-associated protein kinase-related 1	61	321	1	261
H	32	152	CAMK	EMK	5.90E-185	1311	1053	80	80	BAA76843.1	KIAA0999 protein [Homo sapiens]	8	259	1	261
H	33	153	CAMK	EMK	1.20E-45	436	153	51	70	T22427	Hypothetical protein F49C5.4 - [Caenorhabditis elegans]	74	325	1	261
H	33	153	CAMK	EMK	1.40E-32	436	122	46	65	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]				
H	34	154	CAMK	EMK	1.30E-184	729	729	100	100	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	56	307	1	261
M	35	155	CAMK	EMK	3.50E-126	462	462	100	100	AAC33487.1	R31237_1, partial CDS [Homo sapiens]	59	340	1	261
H	36	156	CAMK	EMK	0	1330	1235	100	100	BAA09484.1	KIAA0135 gene is related to pim-1 oncogene. [Homo sapiens]	999	1258	1	261
M	37	157	CAMK	EMK	5.10E-59	230	183	79	85	BAA09484.1	KIAA0135 gene, related to pim-1 oncogene. [Homo sapiens]	1	158	23	261
H	38	158	CAMK	EMK	3.00E-111	926	636	100	100	BAA34501.1	KIAA0781 protein [Homo sapiens]	20	271	1	261
H	39	159	CAMK	EMK	7.30E-80	629	367	57	69	NP_055655.1	KIAA0537 gene product [Homo sapiens]	53	304	1	261
H	40	160	CAMK	EMK	1.40E-244	714	714	100	100	NP_055401.1	Hormonally upregulated neu tumor-associated kinase [Homo sa	61	320	1	261
H	41	161	CAMK	MLCK	8.20E-76	874	211	63	80	AAA73168.1	Skeletal muscle myosin light chain kinase [Gallus gallus]	570	825	1	261
H	42	162	CAMK	Trio	0	2286	2227	100	100	BAA92535.1	KIAA1297 protein [Homo sapiens]	820 & 1086	873 & 1356	1	261
M	43	163	CAMK	Trio	7.80E-37	127	67	89	99	BAA92535.1	KIAA1297 protein [Homo sapiens]	3	78	186	261
H	44	164	CAMK	Trio	0	1287	1284	100	100	NP_008995.1	STK with Dbl- and pleckstrin homology domains [Homo sapiens	985	1239	1	261
H	45	165	CAMK	Unique	5.00E-20	514	114	41	63	P25323	MLCK [Dictyostelium discoideum]	116	381	1	261
H	46	166	CKI	CKI	3.30E-89	508	181	53	65	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	34	313	1	261
H	47	167	CKI	CKI	8.60E-98	478	188	57	68	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	21	471	1	261
H	48	168	CMGC	CDK	9.60E-39	266	138	62	79	NP_036527.1	PFTAIRE protein kinase 1 [Homo sapiens]	1	218	23	261
H	49	169	CMGC	CDK	7.10E-48	247	146	59	75	NP_004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sa	1	191	23	261

Table 2 (cont'd)

M	50	170	CMGC	CDK	2.90E-64	298	193	65	78	NP_004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sa	1	240	24	261
H	51	171	CMGC	CDK	1.10E-264	1490	1490	100	100	AAF36401.1	CDC2-related protein kinase 7 [Homo sapiens]	21	1020	1	261
H	52	172	CMGC	CDK	9.20E-101	534	377	82	82	AAF36509.1	NKIAMRE [Homo sapiens]	4	386	1	261
M	53	173	CMGC	CDK	1.40E-128	337	225	92	96	AAF34871.1	NKIATRE alpha [Rattus norvegicus]	1	28	235	261
M	54	174	CMGC	CDK	3.00E-68	211	159	79	84	NP_036251.1	Cell cycle related kinase [Homo sapiens]	1	163	134	261
H	55	175	CMGC	CLK	1.50E-242	499	436	91	93	NP_031740.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sa	177	493	1	261
H	56	176	CMGC	RCK	9.10E-89	544	343	57	64	AAD12719.1	Extracellular signal-regulated kinase 7; ERK7 [Rattus norvegicus	13	305	1	261
H	57	177	CMGC	RCK	2.30E-189	419	419	100	100	NP_055041.1	Renal tumor antigen [Homo sapiens]	4	285	1	261
H	58	178	CMGC	RCK	1.50E-180	632	632	100	100	AAF37278.1	Intestinal cell kinase [Homo sapiens]	4	284	1	261
M	59	179	CMGC	RCK	1.60E-79	413	198	60	77	P20689	MLCK [Rattus norvegicus]	109	364	1	261
H	60	180	Microbial PK	YGR262_sc	2.50E-45	253	102	46	67	AAF50799.1	CG10673 gene product [Drosophila melanogaster]	101	187	65	147
H	61	181	Other	C26C2_ce	2.30E-158	509	258	100	100	CAB70864.1	Hypothetical protein [Homo sapiens]	2	267	1	261
M	62	182	Other	C26C2_ce	1.80E-152	281	243	94	98	CAB70864.1	Hypothetical protein [Homo sapiens]	59	86	235	261
H	63	183	Other	C26C2_ce	6.70E-300	1952	1193	99	99	NP_055638.1	KIAA0344 gene product [Homo sapiens]	221	479	1	261
H	64	184	Other	C26C2_ce	1.10E-254	535	535	100	100	NP_037524.1	Nuclear receptor binding protein [Homo sapiens]	73	327	1	261
M	65	185	Other	C26C2_ce	2.50E-208	378	372	98	100	NP_037524.1	Nuclear receptor binding protein [Homo sapiens]	1	170	85	261
H	66	186	Other	CAMKK	3.80E-148	588	588	100	100	AAD31507.1	Ca2+/calmodulin-dependent protein kinase kinase beta [Homo s	165	446	1	261
H	67	187	Other	CTR1	9.90E-24	287	87	33	52	JQ1743	Hypothetical 33.6K protein - rabbit fibroma virus	24	285	1	261
H	68	188	Other	DYRK	0	1171	1137	97	99	AAD52566.1	Nuclear body associated kinase 1a [Mus musculus]	199	527	1	261
H	69	189	Other	DYRK	2.10E-280	553	553	100	100	NP_003573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	174	487	1	261
M	70	190	Other	DYRK	2.30E-95	168	149	90	98	NP_003573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	76	103	235	261
H	71	191	Other	EIFK	0	1649	1493	90	96	NP_038747.1	GCN2 eIF2alpha kinase [Mus musculus]	280 & 590	639 & 1001	1	261
H	73	192	Other	EIFK	1.50E-220	630	630	100	100	NP_055228.1	Heme-regulated initiation factor 2-alpha kinase [Homo sapiens]	167	583	1	261
H	74	193	Other	Endop	2.50E-45	253	102	46	67	AAF50799.1	CG10673 gene product [Drosophila melanogaster]	101	187	65	147
M	75	194	Other	Endop	3.70E-45	216	100	45	64	AAF50799.1	(AE003567) CG10673 gene product [Drosophila melanogaster]	116	150	116	147
H	76	195	Other	IRAK	0	596	596	100	100	NP_009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	165	443	1	261
M	77	196	Other	IRAK	1.20E-170	392	293	76	86	NP_009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	1	239	19	261
H	78	197	Other	IRE	1.5e-323	922	746	82	89	NP_036146.1	Ire1, inositol-requiring 1 gene [Mus musculus]	516	777	1	261
H	79	198	Other	KYK2_dd	8.70E-40	225	102	45	62	AAF48758.1	CG8173 gene product [Drosophila melanogaster]	32	318	1	261
M	80	199	Other	KYK2_dd	5.90E-32	280	109	32	50	AAF48758.1	CG8173 gene product [Drosophila melanogaster]	12	266	1	261
M	81	200	Other	LIMK	2.60E-17	41	37	92	95	NP_009101.1	testis-specific kinase 2 [Homo sapiens]	12	39	101	128
H	82	201	Other	MLK	2.50E-282	800	799	100	100	AAF63490.1	Mixed lineage kinase [Homo sapiens]	16	259	1	261
H	83	202	Other	MLK	8.60E-251	835	835	100	100	AAD28632.1	Putative protein-tyrosine kinase [Homo sapiens]	463	723	1	261
H	84	203	Other	RIP	2.20E-158	634	365	100	100	BAA32317.1	KIAA0472 protein [Homo sapiens]	357	620	1	261
M	85	204	Other	RIP	5.30E-158	289	288	100	100	AAF03133.1	Receptor interacting protein 3 [Mus musculus]	7	27	181	202
H	86	205	Other	SCY1_sc	0	688	688	100	100	CAB55300.1	Hypothetical protein [Homo sapiens]	57	83	50	78
H	87	206	Other	SCY1_sc	1.70E-209	505	354	98	98	BAA92598.1	KIAA1360 protein [Homo sapiens]	32	327	1	261
H	88	207	Other	SCY1_sc	2.20E-157	808	396	45	61	AAF56933.1	CG1973 gene product [Drosophila melanogaster]	65	131	47	116
H	89	208	Other	SLOB?	7.40E-196	649	649	100	100	BAA91097.1	Unnamed protein product [Homo sapiens]	230	305	81	143
H	90	209	Other	SRPK	5.80E-252	533	533	100	100	NP_055185.1	Serine/threonine kinase 23 [Homo sapiens]	79	531	1	261
H	91	210	Other	STK22A	3.80E-53	268	122	46	70	NP_033461.1	Serine/threonine kinase 22A (spermiogenesis associated) [Mus	10	265	1	261
M	92	211	Other	STK22	2.70E-52	268	127	48	68	NP_033462.1	serine/threonine kinase 22B (spermiogenesis associated)	10	265	1	261
H	93	212	Other	STK22A	4.60E-16	292	112	45	64	NP_033461.1	Serine/threonine kinase 22A (spermiogenesis associated)	25	280	1	261
H	94	213	Other	STK22A	5.10E-123	358	322	90	96	NP_033462.1	Serine/threonine kinase 22B (spermiogenesis associated) [Mus	12	272	1	261
H	95	214	Other	TSK	2.10E-33	273	122	46	62	NP_033461.1	Serine/threonine kinase 22A (spermiogenesis associated)	12	287	1	261
H	96	215	Other	TSK	2.50E-32	216	93	41	58	NP_033462.1	Serine/threonine kinase 22B (spermiogenesis associated)	1	213	7	261
H	97	216	Other	UNC	0.000062	333	57	38	56	AAD32787.1	Putative protein kinase [Arabidopsis thaliana]	1	329	1	261
M	98	217	Other	UNC	0.002492	412	53	37	52	BAA77341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	80	408	1	261
H	99	218	Other	UNC	0.001096	341	50	38	56	BAA77341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	8	340	1	261
H	100	219	Other	UNC	1.90E-68	480	247	100	100	T17265	Hypothetical protein DKFZp434C131.1 - human (fragment)	57	313	1	261
H	101	220	Other	UNC	1.60E-208	565	468	96	96	BAA91270.1	Unnamed protein product [Homo sapiens]	4	265	1	261
H	102	221	Other	Unique	6.70E-10	39	27	69	90	AAD00575.1	Serum-inducible kinase [Homo sapiens]	1	39	84	124

Table 2 (cont'd)

M	103	222	Other	Unique	0.000022	349	38	30	50	CAA18116.1	Serine/threonine protein kinase like protein [Arabidopsis thaliana	80	159	1	88
H	104	223	Other	Unique	0.000126	704	54	30	45	BAA86578.1	KIAA1264 protein [Homo sapiens]	1	246	25	261
M	105	224	Other	Unique	0.007385	640	25	42	61	AAF47916.1	Tie gene product [Drosophila melanogaster]	9	104	168	261
H	106	225	Other	Unique	0.31334	540	52	30	42	P10162	SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [Homo s	1	272	18	73
M	107	226	Other	Unique	0.022948	365	25	34	57	NP_006276.1	testis-specific kinase 1 [Homo sapiens]	68	96	42	71
H	108	227	Other	VRK	3.10E-263	474	474	100	100	BAA90769.1	Vaccinia related kinase 3 [Homo sapiens]	247	318	63	136
M	109	228	Other	VRK	1.20E-111	234	191	82	90	BAA90769.1	(AB031052) vaccinia related kinase 3 [Homo sapiens]	7	78	63	136
H	110	229	Other	YPL236_sc	7.40E-144	305	304	100	100	AAC28337.1	MPSK [Homo sapiens]	20	290	1	261
H	111	230	Other	YQ09_ce	5.10E-49	581	135	43	63	AAF46188.1	CG4523 gene product [Drosophila melanogaster]	156	507	1	261
H	112	231	STE	NEK	3.30E-30	698	122	48	67	P51954	NEK1 (NIMA-RELATED PROTEIN KINASE 1) [Mus musculus]	4	251	1	261
H	113	232	STE	NEK	2.70E-119	836	357	86	86	AAD31939.1	(AC007055) unknown [Homo sapiens]	52	308	1	261
H	114	233	STE	STE11	1.10E-291	1011	1011	100	100	NP_004663.1	mitogen-activated protein kinase kinase kinase 6 [Homo sapiens	376	629	6	261
H	115	234	STE	STE20-02	7.70E-177	719	719	100	100	BAA94194.1	(AB040812) protein kinase PAK5 [Homo sapiens]	449	700	1	261
H	116	235	TK	RTK-20	4.90E-24	495	77	38	56	AAA98465.1	(U40827) protein tyrosine kinase [Mus musculus]	187	453	1	261
M	117	236	TK	RTK-20	5.30E-18	183	53	39	57	NP_032036.1	fibroblast growth factor receptor 3 [Mus musculus]	8	143	123	261
H	118	237	AGC	SGK	6.30E-112	367	367	100	100	AAF12757.2	SGK2alpha protein kinase [Homo sapiens]	35	292	1	261
H	120	238	CMGC	CDK	2.80E-137	452	452	100	100	NP_036251.1	Cell cycle related kinase [Homo sapiens]	4	267	1	261
H	121	239	Other	LIMK	8.50E-233	555	555	100	100	NP_009101.1	Testis-specific kinase 2 [Homo sapiens]	62	293	5	261

Table 3

Tissue	Tumor-syn	Normal-syn	Tumor - fu	Tumor cells	Normal	Endo	p53	SEQ 003 A	SEQ 5 TBI	SEQ 008 A	SEQ 008 A	SEQ 9 CA	SEQ 11 EP	SEQ 12 PR	SEQ 14 NT	SEQ 16 RS
adrenal gland - h		1						7480	13881	583727	25948	34705	58908	11808	46820	13185
lymph node - h		2						8151	32253	1202404	118257	105718	55339	19807	94839	16254
bone marrow - h		3						4463	9236	1477586	35387	32237	33850	13151	82024	12108
mammary gland - h		4						984	376	108887	4031	4318	1984	1985	34739	2503
brain -h		5						9888	5023	238763	53822	21880	7881	7736	54253	7107
pancreas - h		6						5433	3574	334885	60925	32308	8821	11988	71540	12794
cerebellum - h		7						8350	19704	767223	84606	35862	16370	29260	83436	13345
pituitary gland - h		8						8542	7888	712184	80487	38568	19473	11010	87365	12166
fetal brain - h		9						15719	6046	867041	85401	30156	23343	13781	103271	8907
placenta - h		10						6763	15464	1232178	46305	45070	24271	13887	88342	10501
fetal kidney - h		11						4707	10839	837527	51059	67946	31171	19988	65084	10585
prostate, h		12						3477	1784	122058	60209	43912	11790	8464	74534	11164
fetal liver- h		13						3307	6294	1548111	28108	35129	17029	10418	68677	9440
salivary gl. - h		14						2725	3888	429781	37947	37758	11433	13806	60783	14403
fetal lung - h		15						6315	8461	1305487	79578	58484	31911	24594	82518	15835
skeletal muscle - h		16						9480	5785	187882	61853	13319	10888	11874	57531	8285
heart - h		17						3012	1915	227934	27479	20873	6357	11717	43881	7763
small intestine - h		18						3820	6581	635316	28567	28580	11720	12220	42979	11051
kidney - h		19						3588	8455	412001	41491	24182	7829	8806	48325	12082
spinal cord - h		20						5186	2798	234008	21586	12872	12298	4848	54755	8758
liver - h		21						3763	4479	338987	34583	18281	11566	8365	40332	8300
Spleen - h		22						3384	1519	208606	48111	29875	10798	8109	44868	8581
lung - h		23						4121	1821	488827	35613	25347	10830	4418	37827	7084
stomach -h		24						2854	419	312882	33851	12206	5878	3009	18018	5109
testis - h		25						6542	15362	1255953	88041	19148	117943	8866	44850	11194
thymus -h		27						7856	4906	1874082	122988	80846	46509	31139	85252	13780
HPAEC		28				28		7304	0	58068	34171	26274	3819	14479	67087	9110
thyroid gland - h		29						3870	1073	194311	42836	25881	9827	9143	43670	8007
RPTEC		30				30		24571	1923	80360	21213	3357	3387	15054	42340	7144
trachea - h		31						6734	3082	807783	88848	49813	15268	16042	78868	11767
HMEC		32						7791	1356	138806	24824	15301	4715	11713	65184	3838
uterus - h		33						5386	4649	534257	34433	33931	14725	15085	86678	8840
HCAEC		34						7878	0	82241	26246	12125	1768	29455	51717	8203
Pancreas - h		35						11088	519	41843	19592	15818	6140	6513	46443	7564
lymph node - h		36						8132	731	47839	15791	20735	8420	3812	64078	7285
Skeletal muscle - h		37						5506	77	0	11060	6411	6294	2070	30349	3459
fetal liver- h		38						8850	2171	146493	18355	15506	6458	2447	58121	9104
Heart - h		39						7091	745	8019	15303	8552	2515	3820	47872	7275
thymus,h		40						8718	2472	87220	40613	17473	10184	1502	70722	18210
Duodenum - h		41						2879	0	28026	9776	14880	4049	8070	42191	6580
Fetal brain - h		42						12385	3365	21478	20505	18311	15818	3563	84860	9323
Salivary gl. - h		43						4456	0	6914	17344	12177	4150	3293	35172	8065
testis - h		44						8962	23888	33514	19562	14858	17832	4369	57084	8767
HT219-normal					365			115	357	8191	3368	2191	1738	134	12858	1034
HT213-normal					363			0	427	8712	1918	0	144	1080	8245	803
HT157-normal					361			0	15	35470	2726	735	12030	854	16328	4100
Bev-13					356	356		8530	1886	563114	40109	10880	30146	4692	82144	17604
Bev-12					354	354		11250	1285	58750	69854	8439	12012	3467	59087	13420
cerebellum - h					344			0	242	31891	2939	1746	2851	1243	27729	4240
brain -h					342			0	565	20541	2850	0	3454	2223	31402	4429
RPTEC					334	334		1977	0	29114	24733	2279	333	6057	71003	20777
lymph node - h					332			706	0	1941	7347	7055	14451	1180	30788	8636
h adult SMC 10/21/02_#17					330			605	0	6314	8587	1044	0	540	47380	9864
Fetal brain - h					328			7190	318	151277	69029	10433	9006	2972	70908	18134
HT388-normal					327			638	0	217335	6223	320	8848	632	60974	7284
thymus,h					326			6784	80	258220	54119	10538	7917	2366	70826	13384
HT149 - normal					321			187	81	801	2827	0	198	1743	41371	8508
HE-PM 3d untreated					320			3252	0	88128	12132	3837	4353	3048	61910	10734
uterus - h					318			4613	4034	653304	38332	19858	31221	6216	66463	15656
trachea - h					316			4883	258	118883	24238	13380	10150	4750	46848	11180
thyroid gland - h					314			2530	845	856481	34488	13185	38383	6319	44846	13837
salivary gl. - h					311			881	447	181154	19056	6484	8878	1955	51587	11348
prostate, h					308			45	842	103824	14523	6434	8183	1052	47808	10249
pituitary gland - h					307			1228	0	110830	16053	2008	4827	819	34764	6532
pancreas - h					305			193	807	101847	8652	2836	7486	1847	44917	10318
mammary gland - h					303			1134	700	1072119	24205	8728	22380	3908	68451	12912
bladder - h					302			14712	0	38751	25857	8608	7386	3929	72421	11980
testis - h					298			4347	11127	777026	53008	20343	35776	5832	83198	23280
liver - h					297			2935	1344	481051	20812	18344	10059	3549	63754	17381
Spleen - h					296			56	1587	219030	20791	9704	11809	2088	53225	10529
spinal cord - h					294			2252	1632	328128	25847	14237	15258	3701	62962	13872
small intestine - h					292			155	115	380879	12005	3217	6860	1320	41632	4784
skeletal muscle - h					290			1375	1482	417579	27541	13818	20044	5272	60372	13025
bone marrow - h					279			0	918	34347	2111	3118	3421	1687	50657	10424
adrenal gland - h					277			0	2174	88342	4719	2578	8223	862	84753	8058
HPAEC					275	275		501	123	4987	8845	1414	652	1062	37188	7713
HT382-normal					268			0	50	79406	4467	0	4488	861	38846	3881
HT383-normal					266			253	680	12358	4938	878	11869	308	44114	7870
Bev-11					239	239		1719	4286	206065	19772	1587	13430	4370	73567	13425
Bev-8					235	235		41	561	52163	6331	1048	7759	6820	50453	7306
HT372-normal					234			787	0	34038	18387	5368	8133	2350	78267	14120
Bev-7					233	233		0	1939	63364	7278	2074	9250	2888	71554	9109
Bev-6					231	231		391	2454	48140	7845	5702	6877	2380	52712	9473
Bev-2					229	229		468	1684	74813	8508	788	7032	3425	43446	6479
Bev-1					227	227		826	4854	83881	6235	1903	4847	1048	41858	8080
bladder - h					222			329	458	6047	2850	2386	3425	171	33431	5059
Heart - h					215			682	0	6149	9086	2384	7814	1837	48468	8442
stomach -h					214			466	1512	138794	14038	3792	13118	1751	58881	10281
fetal liver- h					213			864	547	8475	6415	1846	1036	478	38867	6120
placenta - h					212			622	1977	218837	6781	2164	9108	1232	43929	9805
HCAEC					211	211		143	0	5183	8957	184	569	1143	34737	8333
fetal brain - h					210			687	3137	52807	8488	7857	14801	1515	70127	12888
HMEC					208			264	102	5034	8400	0	214	885	48678	6198
Duodenum - h					205			1	0	4305	8029	620	1551	579	38258	8176
Skeletal muscle - h					203			623	0	5083	6853	674	1211	1041	34158	5114
Pancreas - h					201			415	16	56167	5487	3004	4308	891	33307	6559
testis - h					198			730	154	3162	2304	2527	3485	347	26853	4123
Salivary gl. - h					197			436	16	37617	4851	2308	5218	762	38068	4117
HEPM 3d TGFB1 detergent-DNase					196			82	0	4577	3408	236	1291	374	21318	2326
thymus -h					193			2683	0	247405	21041	4884	10787	3458	33113	8284
WI-38 72h					179			0	0	6881	2190	0	380	0	21246	1771
lymph node - h					61			314	273	34816	18701	4009	4334	2288	27301	4256
lung - h					58			787	1251	348147	9218	10510	18808	2388	79635	9151
kidney - h					57			0	334	46381	8870	3152	7038	4	68806	7384
heart - h					55			0	1134	38762	3229	3702	4377	442	37503	3584
fetal lung - h					53			0	1323	24481	1809	232	1176	1297	12636	1580
fetal liver- h					51			235	37	43001	3182	510	4042	297	21581	2372
fetal kidney - h					49			277	641	37881	3680	2842	11886	3196	31744	4737
HELA-2h-031800				79				1376	744	108312	5953	2313	5206	1472	38080	6294
HELA-4h-031800				81				486	2343	171123	4142	2131	8136	6196	67302	7191
HELA-6h-031800				83				635	1081	88381	3757	1680	4822	1615	63322	5752
HELA-0h-031800				86				646	85	201388	5429	1801	8703	1222	28774	4729
HELA-8h-031800				88				1271	184	182436	8381	4751	8408	2346	55350	11016
HELA-9h-031800				90				303	416	75136	7198	1647	8801	1836	55168	7319
HELA-10h-031800				92				819	804	88535	8048	4308	19174	5137	52933	8050
HELA-11h-031800				94				0	8	33279	4209	312	4843	1654	42482	5981
HELA-12h-031800				96				0	367	43634	9207	1105	6047	885	34825	5882
NCI-H322M				146				1456	246	44456	3419	38703	29485	2702	15600	3126
NCI-H460				148				1834	168	13845	3671	3859	21487	685	22032	3340
NCI-H522				150				913	254	33841	2579	3237	8637	616	28184	1818
SNB-19				152				1115	0	13025	1124	8980	6003	0	16076	2527
SNB-75				154				1156	0	22559	3786	8636	8150	1642	27275	4196
SF-268				156				231	0	4801	2766	3218	8806	447	18225	3162
SF-295				158				0	342	10878	2136	892	579	848	8339	1613
CCRF-CEM				160				1001	255	18120	317	5242	2231	418	16835	1684
DU-145				162				206	405	7942	1480	2626	2384	119	14306	1866
HCT 116				164				721	0	21002	1198	6856	2690	3879	13034	1853

Table 3 (cont'd)

Tissue	Tumor-gyn	Normal-gyn	Tumor - lu	Tumor cells	Normal	Endo	p53	SEQ 603 A	SEQ 5 TB	SEQ 604 A	SEQ 606 A	SEQ 9 CA	SEQ 11 EP	SEQ 12 PK	SEQ 14 M	SEQ 16 RS
								13671	0	188824	24041	16731	12712	9676	48043	6344
Hs 578T	156							13420	1292	37520	28262	9797	5704	8670	48543	5189
MCF7/ADR-RES	153							15337	1095	930087	82916	21779	15850	10792	63848	9415
MCF7	151							6452	586	204414	17174	10734	18348	2544	63303	4830
M14	149							11456	0	153616	13887	10437	42807	4588	38000	8237
UACC-257	147							3456	123	58725	21571	11116	27584	1929	27441	4561
UACC-62	145							4479	0	350627	13751	7222	23647	2124	28861	5824
SK-MEL-28	144							6387	0	247414	15130	8047	23533	4196	88230	8343
UO-31	143							5444	680	430888	19485	4434	30762	7048	23301	8242
SK-MEL-5	142							6433	377	43470	12308	4008	4525	2784	30992	3132
KM-12	141							2946	331	331483	10906	13817	13874	7005	30577	5799
SK-MEL-2	140							1187	8	352056	14372	8250	17403	6476	54739	10741
HCT-15	139							6598	0	403468	18670	8670	21327	8334	45080	7827
Malme-3M	138							6349	0	384009	16785	8568	17491	4863	57736	10848
COLO 205	137							4208	204	1678684	23713	10725	23814	5598	38018	7615
LOX IMVI	136							11829	0	622856	18564	5852	18514	7213	38849	5702
SW-620	135							3536	1542	230533	21155	7632	9482	4091	43207	8844
TK-10	134							3482	0	184816	13980	7388	8546	4065	37409	6317
HCT 116	133							3284	0	388284	17720	4982	13644	5047	34175	4877
786-0	132							6670	2297	388088	17568	5751	10030	3671	82382	8455
HCC-2998	131							9682	177	84811	18458	10358	8438	4863	38080	6785
ACHN	130							12090	0	48624	14186	4679	6473	3508	35262	6853
PC-3	129							9833	278	488833	21616	7110	11086	3324	40444	5886
RXF 393	128							10828	138	30590	12131	3150	3840	3261	37777	3307
DU-145	127							3046	722	712846	12748	8898	13345	4297	35257	8467
CAKI-1	126							3585	257	420391	13247	3820	10151	2543	37850	4327
SR	125							9123	0	64349	18090	41974	17229	4374	39104	6250
A498	124							2278	0	277936	16389	9419	28798	1191	50465	5058
RPMI 8226	123							6263	217	303677	17182	14350	29787	6796	32578	5287
SN12C	122							11442	0	137022	8869	5329	22423	4164	38440	4509
HL-60	121							4384	0	440040	12769	10231	15496	2806	28309	4478
MOLT-4	120							3930	368	1080525	16534	5752	41980	4117	25375	8836
OVCAR-5	119							2180	798	804733	14187	8845	24825	9040	54213	9030
K-562	118							2856	3587	4865335	18528	8049	112397	5681	42598	3203
OVCAR-4	117							4910	0	3588707	21767	9518	81643	9563	36120	4575
CCRF-CEM	116							3371	0	551858	10974	7064	21828	5119	52017	8813
OVCAR-3	115							4819	0	882870	13041	4718	18083	2804	34865	6113
SF-539	114							2174	389	345780	13736	5656	11035	3280	19576	4413
HOP-62	113							11905	216	88583	16107	8440	7184	2565	40830	7962
SF-295	112							17217	598	378850	27272	12358	18817	5358	47439	8328
A549/ATCC	111							3084	1353	230341	18800	6661	11824	2278	30245	3718
SF-268	110							4147	0	1138384	19715	19185	32962	3153	44511	6645
NCI-H522	109							6539	373	230300	18786	8508	12058	6746	84076	8280
U251	108							6777	0	452383	13088	8898	18003	4436	28806	5244
NCI-H460	107							2579	630	27892	8839	323	8216	2822	41104	4518
SNB-75	106							6471	871	888327	19449	14479	18523	3322	49837	6532
NCI-H322M	105							7360	0	218881	17548	7858	12434	3103	90554	5744
SNB-19	104							32859	310	108338	20806	10728	24197	3054	81587	8960
NCI-H226	103							9457	0	302769	15647	7470	11071	2287	33178	2984
SK-OV-3	102							9814	371	108502	13285	8342	15724	2809	38481	3518
NCI-H23	101							19803	708	313545	14157	9518	8579	2981	41809	3318
IGROV1	100							5229	1110	368878	18812	9432	21798	2010	25017	3634
EKVX	99							17781	614	98774	10361	4170	8064	3120	31129	4019
OVCAR-8	98							7808	0	317848	22815	4246	38600	3282	33300	3960
HOP-92	97							11086	0	177631	18183	8067	4047	3528	32090	4127
h fibroblasts 3/31/92 #12	48							4478	137	8072	14410	12090	3096	588	30837	5335
h adult SMC 10/21/92 #17	47							13002	240	155425	22184	6858	14419	3871	29128	5742
h keratinocytes 2/25/92 #10	46							8000	0	560454	15245	18288	19157	3439	22053	6471
TCOP	26						wt	1491	6421	44805	11719	0	0	0	0	0
A549 - 1							wt	138	4212	28336	8707	0	0	0	0	0
A549 - 3							wt	278	6323	38473	10836	0	0	0	0	0
A549 - 4							wt	488	2872	28688	10727	0	0	0	0	0
A549 - 5							wt	148	162	15733	8798	0	0	0	0	0
A549 - 7							mutant	848	1343	68034	18784	0	0	0	0	0
EKVX - 1							mutant	1400	43880	79380	25018	0	0	0	0	0
EKVX - 4							mutant	835	934	22897	12511	0	0	0	0	0
EKVX - 3							mutant	0	[illegible]	60803	7740	0	0	0	0	0
EKVX - 5							mutant	732	1578	20802	11042	0	0	0	0	0
EKVX - 7							wt	840	718	80119	10888	0	0	0	0	0
MCF-7 - 1							wt	607	6245	68350	7883	0	0	0	0	0
MCF-7 - 3							wt	839	1156	140711	14817	0	0	0	0	0
MCF-7 - 4							wt	224	1050	81148	11019	0	0	0	0	0
MCF-7 - 5							wt	0	1337	10567	8726	0	0	0	0	0
MCF-7 - 7							mutant	0	3885	91125	18486	0	0	0	0	0
ADR-RES - 1							mutant	425	525	27534	8082	0	0	0	0	0
ADR-RES - 3							mutant	0	961	15870	4448	0	0	0	0	0
ADR-RES - 4							mutant	288	472	35086	7549	0	0	0	0	0
ADR-RES - 5							mutant	860	7302	12823	13082	0	0	0	0	0
ADR-RES - 7							wt	819	8	41827	24067	0	0	0	0	0
WI 38 - 1							wt	508	217	40870	18323	0	0	0	0	0
WI 38 - 3							wt	647	751	32710	9317	0	0	0	0	0
WI 38 - 4							wt	1151	3721	17081	11387	0	0	0	0	0
WI 38 - 5							wt	216	4617	84191	12288	0	0	0	0	0
WI 38 - 7							HPV E6	532	12621	16493	13319	0	0	0	0	0
HeLa - 1							HPV E6	400	843	51837	17033	0	0	0	0	0
HeLa - 3							HPV E6	802	3311	46208	7885	0	0	0	0	0
HeLa - 4							HPV E6	213	1168	40254	16027	0	0	0	0	0
HeLa - 5							HPV E6	0	1049	37166	8575	0	0	0	0	0
HeLa - 7							mutant	844	0	68067	14723	0	0	0	0	0
H1299 - 1							mutant	336	0	88284	14722	0	0	0	0	0
H1299 - 3							mutant	338	2070	78788	25363	0	0	0	0	0
H1299 - 4							mutant	204	1806	33235	10427	0	0	0	0	0
H1299 - 5							mutant	440	0	41846	10384	0	0	0	0	0
H1299 - 7							wt	194	4270	37307	8382	0	0	0	0	0
A549 - 2							mutant	638	2003	23382	15628	0	0	0	0	0
EKVX - 2							wt	408	8587	38039	8134	0	0	0	0	0
HCT-116 - 1							wt	1123	3756	40630	21130	0	0	0	0	0
HCT-116 - 2							mutant	861	1388	43251	13827	0	0	0	0	0
HT29 - 2							wt	0	1849	19007	13005	0	0	0	0	0
SF539 - 1							wt	112	2474	46281	13141	0	0	0	0	0
SF539 - 2							mutant	662	317	42852	13335	0	0	0	0	0
SF-268-1							mutant	819	550	74505	12538	0	0	0	0	0
SF-268-2							wt	332	68	70236	13108	0	0	0	0	0
OVCAR-4 - 1							wt	342	1643	101777	10427	0	0	0	0	0
OVCAR-4 - 2							mutant	228	581	19836	14267	0	0	0	0	0
OVCAR-5 - 1							mutant	10	10	8110	8476	0	0	0	0	0
OVCAR-5 - 2							wt	281	1433	11062	7683	0	0	0	0	0
MCF-7 - 2							mutant	0	731	31787	18443	0	0	0	0	0
ADR-RES - 2							HPV E6	518	0	112434	14374	0	0	0	0	0
HeLa - 2							mutant	326	0	68775	9762	0	0	0	0	0
SW480 - 1							mutant	1091	7826	68139	12357	0	0	0	0	0
SW480 - 2							mutant	6823	2573	57384	15081	0	0	0	0	0
H1299 - 2							mutant	882	18707	8647	15486	0	0	0	0	0
C33A - 1							mutant	884	1155	43084	11732	0	0	0	0	0
C33A - 2							mutant	810	86	151505	10872	0	0	0	0	0
U2OS - 1							mutant	721	0	140871	22177	0	0	0	0	0
U2OS - 2							wt	287	882	29884	10011	0	0	0	0	0
[illegible] - 1							wt	863	883	35277	11670	0	0	0	0	0
[illegible] - 2							wt	415	2478	38744	25528	0	0	0	0	0
WI 38 - 2								574	265	8294	116430	0	0	0	0	0
MMhd - 1								1123	3267	38128	16855	0	0	0	0	0
MMhd - 2								885	886	34711	31829	0	0	0	0	0
MMhd - 3								1936	0	12352	28485	0	0	0	0	0
MMhd - 4								730	0	8477	277573	0	0	0	0	0
MMhd - 5								672	9430	13002	31583	0	0	0	0	0
MMhd - 6								1350	1837	14384	24789	0	0	0	0	0
MMhd - 8								654	0	15325	11036	0	0	0	0	0
MMhd - 9																

Table 3 (cont'd)

Tissue	Tumor-eyes	Normal-eyes	Tumor - hi	Tumor cells	Normal	Endos	p53	SEQ 883 A	SEQ 8 TRI	SEQ 886 A	SEQ 888 A	SEQ 8 CA	SEQ 11 EP	SEQ 12 PK	SEQ 14 HT	SEQ 16 RS
DaPung-7								4081	4153	130751	48007	0	0	0	0	0
DaPung-8								1843	0	123284	31808	0	0	0	0	0
DaPung-9								1704	352	23137	22383	0	0	0	0	0
DaPung-11								2364	2918	58836	34353	0	0	0	0	0
DaPung-12								1621	0	143418	14764	0	0	0	0	0
DaPung-10								1137	11437	88719	25013	0	0	0	0	0
DaPung-1								1808	0	178675	67121	0	0	0	0	0
DaPung-2								778	282	80117	44171	0	0	0	0	0
DaPung-3								1038	6089	86419	23252	0	0	0	0	0
DaPung-4								44	3575	48050	13488	0	0	0	0	0
DaPung-5								447	217	37705	9858	0	0	0	0	0
DaPung-6								1754	0	104257	34508	0	0	0	0	0
A549-8							wt	141	1853	30854	11740	0	0	0	0	0
EKVX-8							mutant	281	6488	74722	34175	0	0	0	0	0
HCT-116-7							wt	458	0	45374	15408	0	0	0	0	0
HCT-116-8							wt	308	846	86048	23678	0	0	0	0	0
HT29-1							mutant	292	3581	22154	18810	0	0	0	0	0
HT29-7							mutant	78	3147	6867	8481	0	0	0	0	0
HT29-8							mutant	181	467	80732	18019	0	0	0	0	0
SF539-7							wt	7388	375	15224	8477	0	0	0	0	0
SF539-8							wt	0	0	57678	8738	0	0	0	0	0
SF-268-7							mutant	507	446	33057	13176	0	0	0	0	0
SF-268-8							mutant	902	0	39102	8841	0	0	0	0	0
OVCAR4-7							wt	881	1305	72107	15862	0	0	0	0	0
OVCAR4-8							wt	1388	527	105549	21781	0	0	0	0	0
OVCAR5-7							mutant	0	338	52988	10750	0	0	0	0	0
OVCAR5-8							mutant	158	0	17818	10867	0	0	0	0	0
MCF-7-8							wt	855	740	24190	11163	0	0	0	0	0
ADR-RES-8							mutant	822	3013	12558	17722	0	0	0	0	0
HeLa-8							HPV E6	0	2243	23863	8106	0	0	0	0	0
SW480-7							mutant	727	1081	24521	12811	0	0	0	0	0
SW480-8							mutant	226	7328	43102	9808	0	0	0	0	0
H1299-8							mutant	102	2363	53883	10761	0	0	0	0	0
C33A-7							mutant	372	3128	11403	8774	0	0	0	0	0
C33A-8							mutant	0	1813	38317	18670	0	0	0	0	0
U2OS-7							mutant	20	2184	72682	14777	0	0	0	0	0
U2OS-8							mutant	87	0	156867	8029	0	0	0	0	0
Hs68-7							wt	538	4024	28229	10808	0	0	0	0	0
Hs68-8							wt	502	4497	24757	14258	0	0	0	0	0
WI 38-8							wt	232	87	8256	7519	0	0	0	0	0
458 medulla RNA								8548	0	615446	28823	15276	21829	3328	37686	7008
CRL1572 3/17/88								110	0	3070	1153	867	2901	1237	25504	2088
Bev-4						84		348	1576	68918	7421	4938	12083	23363	99610	5229
HT368								1340	605	67915	9767	4864	6347	916	32554	7686
HT378								457	545	15808	8158	4064	4910	729	37558	5769
HT385								3179	0	88246	34038	7565	18311	2526	78812	7937
HT308								0	300	86198	8834	704	7808	2308	21782	8807
Bev-3						173		40	505	9532	3582	193	2025	795	38821	2784
Bev-5						175		9	420	8094	1236	1058	683	751	18850	1689
Bev-6						177		325	0	9381	5220	859	1788	715	39076	4356
h keratinocytes 2/25/82 #10								1003	0	14465	12819	1856	1118	1942	80327	6863
Bev-10						237		881	0	83681	8288	1542	8225	2251	45162	7011
HTB10								136	0	18813	8510	5896	15018	1115	86288	14731
h fibroblasts 3/31/82 #12								515	0	27263	8050	253	3038	1099	44374	8168
prostate, h								384	37	2733	6219	1565	387	34	29035	5417
MNNG-OS poly A+								486	0	280879	11883	2186	10484	1829	24678	4588
SA-OS (Moreily) poly A+								1201	0	21774	11088	2632	1808	1585	27097	4279
MK poly A+								1683	354	75322	17840	3824	3415	2424	32134	7106
HCT-116-3							wt	420	2054	84554	8849	0	0	0	0	0
HCT-116-4							wt	983	0	58778	8562	0	0	0	0	0
HCT-116-5							wt	258	377	34555	13803	0	0	0	0	0
HCT-116-6							wt	0	348	93380	12786	0	0	0	0	0
A549-8							wt	0	4346	3330	7326	0	0	0	0	0
HT29-3							mutant	302	3771	40888	8815	0	0	0	0	0
EKVX-8							mutant	238	0	82583	8837	0	0	0	0	0
HT29-4							mutant	27	0	88030	8240	0	0	0	0	0
HT29-5							mutant	448	1209	25013	18176	0	0	0	0	0
HT29-6							mutant	309	0	84835	10000	0	0	0	0	0
OVCAR4-3							wt	581	1208	80523	11477	0	0	0	0	0
OVCAR4-4							wt	379	467	83478	8801	0	0	0	0	0
OVCAR4-5							wt	45	3826	84009	14824	0	0	0	0	0
OVCAR4-6							wt	0	522	29881	8741	0	0	0	0	0
SF539-3							wt	381	0	53862	13881	0	0	0	0	0
SF539-4							wt	408	0	34234	19917	0	0	0	0	0
SF539-5							wt	288	1459	16387	12242	0	0	0	0	0
SF539-6							wt	0	817	27807	14984	0	0	0	0	0
OVCAR5-3							mutant	848	2513	53162	8772	0	0	0	0	0
OVCAR5-4							mutant	0	3088	46680	10488	0	0	0	0	0
OVCAR5-6							mutant	512	444	6783	7292	0	0	0	0	0
ADR-RES-6							mutant	215	922	19634	7377	0	0	0	0	0
MCF-7-6							wt	711	3112	80711	12210	0	0	0	0	0
HeLa-6							HPV E6	0	0	82588	16798	0	0	0	0	0
H1299-6							mutant	313	358	21098	11967	0	0	0	0	0
SW480-3							mutant	829	228	50568	8787	0	0	0	0	0
SW480-4							mutant	84	3044	76488	17095	0	0	0	0	0
SW480-5							mutant	922	0	58510	28236	0	0	0	0	0
SW480-6							mutant	0	240	50818	23858	0	0	0	0	0
C33A-3							mutant	858	0	88006	21184	0	0	0	0	0
C33A-4							mutant	298	0	42319	25174	0	0	0	0	0
C33A-5							mutant	428	211	77746	11333	0	0	0	0	0
C33A-6							mutant	144	875	18216	9454	0	0	0	0	0
Hs68-6							wt	353	0	9305	7627	0	0	0	0	0
U2OS-3							mutant	385	85	217525	20512	0	0	0	0	0
U2OS-4							mutant	817	2742	145703	12520	0	0	0	0	0
U2OS-5							mutant	835	1376	81555	17428	0	0	0	0	0
U2OS-6							mutant	454	828	110718	12778	0	0	0	0	0
WI 38-6							wt	26	4047	8098	8925	0	0	0	0	0
Hs68-3							wt	232	4744	57189	10844	0	0	0	0	0
Hs68-4							wt	1338	1334	67073	17844	0	0	0	0	0
SF-268-3							mutant	1761	740	80050	27637	0	0	0	0	0
SF-268-4							mutant	1145	8482	19567	21808	0	0	0	0	0
SF-268-5							mutant	821	1850	40558	20121	0	0	0	0	0
SF-268-6							mutant	574	1800	30521	12423	0	0	0	0	0
DaPung-13								1771	1829	127530	48046	0	0	0	0	0
Mitchell-20								1817	6046	256833	60802	0	0	0	0	0
Mitchell-21								1349	67	74348	63037	0	0	0	0	0
Mitchell-22								1278	2514	120280	25262	0	0	0	0	0
OVCAR5-5							mutant	1053	0	81886	27874	0	0	0	0	0
Mitchell-10								1387	15	19166	73812	0	0	0	0	0
Mitchell-11								813	0	98458	97514	0	0	0	0	0
Mitchell-12								1081	0	150032	98862	0	0	0	0	0
Mitchell-13								2111	0	248801	27331	0	0	0	0	0
Mitchell-14								2946	0	58283	28880	0	0	0	0	0
Mitchell-15								739	0	184082	16747	0	0	0	0	0
Mitchell-16								519	0	58748	13836	0	0	0	0	0
Mitchell-17								676	0	40277	10300	0	0	0	0	0
Mitchell-18								469	567	148758	19832	0	0	0	0	0
Mitchell-19								844	4	300523	9470	0	0	0	0	0

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - tis	Tumor cells	Normal	Endo	p53	SEQ 17 AA	SEQ 20 SQ	SEQ 22 PT	SEQ 29 AA	SEQ 29 DR	SEQ 31 DR	SEQ 832 A	SEQ 44 MA	SEQ 844 T
adrenal gland - h		1						46820	1342	157762	6931	11409	3483	86050	589	4349
lymph node - h		2						84639	9084	373107	14301	80824	15382	135195	338	2571
bone marrow - h		3						82024	345	117789	11387	51933	8446	7358	0	294
mammary gland - h		4						24735	0	18847	1710	2723	266	5276	154	306
brain - h		5						54253	1876	136461	6478	829	1184	7030	3150	2311
pancreas - h		6						71546	2036	48628	7425	7287	2972	31495	4955	1246
cerebellum - h		7						83436	104	298725	10723	2744	2858	135678	8036	274
pituitary gland - h		8						87365	232	110587	15543	7314	2404	74670	3058	3472
fetal brain - h		9						103271	0	187682	27024	3638	1150	63217	7424	8836
placenta - h		10						80342	684	105483	8213	8436	6595	128884	1306	4165
fetal kidney - h		11						65064	9826	152978	10980	12224	2363	55346	8050	4517
prostate, h		12						74834	1446	84243	10864	17733	1143	24080	878	88
fetal liver - h		13						68677	3153	86695	11342	15732	2418	38084	278	2130
salivary gl. - h		14						80783	0	122833	3600	18787	1080	12202	0	233
fetal lung - h		15						82518	1478	187088	8127	18042	4178	67488	1544	3405
skeletal muscle - h		16						57531	171	575843	2744	1837	505	88874	1877	2017
heart - h		17						43881	0	298349	865	4856	2245	31338	1102	2174
small intestine - h		18						42979	1357	80561	3801	14338	2921	21878	832	1837
kidney - h		19						48325	6757	77677	1795	3202	1358	38578	2144	1494
spinal cord - h		20						84756	1315	83517	21224	5273	1063	21487	787	716
liver - h		21						46332	3539	53838	4414	2272	1224	34138	176	413
Spleen - h		22						44068	0	129408	2530	30444	4982	17845	0	822
lung - h		23						37827	577	103801	816	25798	5316	33798	0	452
stomach - h		24						18018	863	37850	1810	8805	1908	11833	865	331
testis - h		25						44850	88	88083	38895	13224	4542	387139	1806	1333
thymus - h		27						83252	83	422519	10160	38850	8722	120548	1733	217
HPAEC						28		67087	0	2134	3084	2437	1015	0	728	0
thyroid gland - h		29						43870	542	181029	8252	4819	828	37702	8	755
RPTEC						30		42348	0	3012	6372	4367	356	418	8	0
trachea - h		31						78566	303	144782	8232	30484	3321	42087	602	2353
HMEC		32						65184	850	21473	3421	0	2672	7056	397	0
uterus - h		33						60678	354	142065	5371	8756	1003	37845	2648	3831
HCAEC		34						51717	373	22708	2128	118	560	198	342	0
Pancreas - h		35						46443	0	0	4314	13335	0	2588	0	1082
lymph node - h		36						84078	0	0	5859	63785	2110	2825	208	0
Skeletal muscle - h		37						30348	418	28839	4136	26	319	2005	812	0
fetal liver - h		38						56121	849	0	2487	9159	1008	745	947	256
Heart - h		39						47872	0	2818	3406	1134	0	4306	492	0
thymus, h		40						70722	0	0	3341	57019	1486	2672	220	0
Duodenum - h		41						42191	145	0	4363	4470	580	2529	101	3081
Fetal brain - h		42						86080	570	0	6154	4108	205	1081	384	386
Salivary gl. - h		43						35172	48	827	1319	17131	0	1205	0	0
testis - h		44						57084	129	294	2689	13574	402	3483	328	0
HT218-normal					365			12858	0	0	2058	9	97	0	356	0
HT213-normal					363			8345	77	0	346	222	347	327	584	0
HT157-normal					361			16328	0	0	248	163	0	842	0	0
Bow-13					356	356		82144	1084	0	23735	8795	7232	5309	1480	12
Bow-12					354	354		50687	58	0	42866	4027	1119	422	476	0
cerebellum - h					344			27729	0	0	230	838	50	8	0	71
brain -h					342			31402	290	0	0	98	78	8	0	0
RPTEC					334	334		71803	0	0	8004	8509	61	479	113	0
lymph node - h					332			30798	277	335	2891	52857	253	367	0	0
h. adult SMC 10/21/92 #17					330			47360	237	0	788	41	0	223	54	0
Fetal brain - h					328			70808	0	8377	29085	10509	83	2749	1212	0
HT388-normal					327			88874	0	388	0	10808	356	202	1110	0
thymus,h					326			70826	0	834	42378	281101	721	750	528	115
HT148 - normal					321			41371	416	0	0	0	43	168	325	0
HEPM 3d untreated					320			81910	0	10739	6705	2982	225	3880	232	0
uterus - h					318			88453	444	3041	24906	188533	8035	4242	1297	188
trachea - h					316			46848	674	0	23803	129836	7113	2740	893	440
thyroid gland - h					314			44846	0	1464	18881	64886	5240	1886	0	506
salivary gl. - h					311			84587	0	0	2684	38362	1045	347	0	0
prostate, h					309			47809	625	0	280	23416	666	176	635	0
pituitary gland - h					307			34784	119	0	1582	19211	875	376	869	157
pancreas - h					305			44817	0	0	631	13638	1321	520	128	586
mammary gland - h					303			86451	1188	0	8443	102882	7874	407	323	0
bladder - h					302			72421	667	3702	6722	10739	184	4728	1088	58
testis - h					298			83188	444	0	35822	80342	8342	2816	1714	0
liver - h					297			63754	0	1047	34117	8023	1482	3474	1158	81
Spleen - h					296			63225	0	138	2172	73586	6138	806	0	0
spinal cord - h					294			62982	464	0	23722	28430	3183	1843	1158	155
small intestine - h					292			41632	38	0	2123	14056	2505	868	0	133
skeletal muscle - h					290			80372	0	19	20791	62231	3687	2424	525	886
bone marrow - h					278			50567	27	0	0	27722	358	0	0	0
adrenal gland - h					277			84753	27	0	2306	8860	58	0	0	355
HPAEC					275	275		37189	0	0	0	1157	0	432	0	0
HT382-normal					268			38846	504	0	0	20068	0	741	586	0
HT382-normal					266			44114	0	1370	0	3833	0	308	0	605
Bow-11					239	239		73567	1154	0	1180	10288	1984	14	218	144
Bow-8					235	235		50463	281	525	108	2291	857	0	0	0
HT372-normal					234			78267	0	1188	2607	13756	0	0	0	0
Bow-7					233	233		71564	374	0	1052	1379	755	0	801	0
Bow-6					231	231		52712	0	307	0	1671	1227	0	73	196
Bow-2					229	229		45448	0	581	212	2318	740	0	575	0
Bow-1					227	227		41888	0	0	783	1630	942	0	0	0
bladder - h					222			33431	805	0	1298	6282	57	0	86	0
Heart - h					215			48488	0	226	744	1154	0	0	139	0
stomach -h					214			58801	0	767	68	63831	3007	323	579	0
fetal liver- h					213			39067	483	0	2248	383	43	339	131	0
placenta - h					212			43029	0	0	0	11419	2776	0	387	0
HCAEC					211	211		34737	280	30	1627	0	0	0	0	43
fetal brain - h					210			70127	0	0	23	8838	226	0	448	0
HMEC					208			48676	155	87	1209	2433	28	1108	0	0
Duodenum - h					205			38290	0	0	0	7386	35	322	336	120
Skeletal muscle - h					203			34158	0	0	982	34	0	0	323	285
Pancreas - h					201			33307	0	148	0	13233	0	685	0	0
testis - h					199			26853	0	0	178	8880	0	0	0	0
Salivary gl. - h					197			30858	0	8020	586	19657	0	2026	83	0
HEPM 3d TGFB1 detergent+DNase					195			21318	328	546	1731	270	58	34	198	0
thymus -h					193			33113	338	0	14228	86431	8113	752	505	0
WI-38 72h					179			21245	0	0	0	75	0	888	0	0
lymph node - h					61			27301	0	0	257	38127	2067	218	53	0
lung - h					59			78635	580	0	2724	108553	7184	840	484	0
kidney - h					57			68006	0	0	0	7821	768	449	126	247
heart - h					55			37503	0	88	107	10848	438	0	0	0
fetal lung - h					53			12835	0	0	779	2307	229	52	0	0
fetal liver- h					51			21581	48	0	382	7618	515	749	0	0
fetal kidney - h					48			31744	244	37	341	12404	168	141	200	329
HELA-2h-031800				79				38800	536	0	144	0	800	507	419	0
HELA-4h-031800				81				67302	0	0	79	462	1366	94	0	0
HELA-8h-031800				83				67322	0	0	0	0	156	0	714	0
HELA-0h-031800				86				28774	86	0	1042	0	827	530	0	0
HELA-6h-031800				88				56350	0	0	3037	894	291	298	195	0
HELA-8h-031800				90				85168	0	0	884	1247	1197	385	1438	0
HELA-10h-031800				92				62803	0	0	0	1258	2798	0	196	0
HELA-11h-031800				94				43462	0	0	0	836	982	428	0	0
HELA-12h-031800				98				34825	98	0	0	298	1008	0	313	0
NCI-H322M				146				15800	857	0	0	3944	3313	295	605	980
NCI-H460				148				22032	0	1157	0	719	1753	401	97	282
NCI-H522				150				20164	72	0	0	530	701	0	183	357
SNB-19				152				18878	0	211	251	386	3491	846	0	57
SNB-75				154				27275	0	786	0	15	4401	114	8838	175
SF-268				156				18225	0	383	232	155	882	0	0	0
SF-295				158				9338	114	0	107	110	389	24	743	141
CCRF-CEM				160				18835	380	0	334	408	254	0	29	0
DU-145				162				14305	133	0	60	317	923	291	0	778
HCT 116				164				13034	0	351	670	422	642	0	676	0

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - 1o	Tumor cells	Normal	Endoe	p53	SEQ 17 AA	SEQ 28 BC	SEQ 22 PT	SEQ 26 AA	SEQ 29 DE	SEQ 31 DE	SEQ 832 A	SEQ 48 MA	SEQ 844 T
Calu-1				195				25841	1	0	727	671	4112	0	0	0
786-0				194				43253	1415	1044	2482	2283	8374	108	0	88
T-47D				109				52705	0	4822	838	771	1518	1109	0	124
Ken-3				171				30045	47	219	800	0	86	0	0	0
CRL 1441 RNA 8/30				181				11952	0	486	1471	342	339	32	157	176
791T untreated + DHmo				183				21315	0	0	0	0	0	691	120	0
KB poly A+				194				23582	194	0	1630	2000	1064	365	0	0
HOS poly A+				196				38104	0	0	1156	3112	1682	145	46	30
ACHN				198				23818	0	1874	1888	823	874	750	371	126
UACC-62				200				19193	130	88	1284	812	846	0	659	0
MCF-7/ADR-RES				202				12681	314	0	714	406	215	178	0	435
UTOS (Mandy) poly a+				204				8408	0	0	1294	672	149	0	887	0
WISH (Collagen) poly A+				205				12580	0	0	14	0	82	0	309	0
458 nodule mRNA				206				83548	0	1041	3508	14082	411	0	411	0
CCL 137 RNA 3/21/88				218				21190	0	683	0	631	47	0	498	0
WI-38 72h 0.5%FBS, 24h 10% FBS				219				38088	0	0	0	3727	0	143	176	134
CRL 1441 + TPA (24h) 8/30				220				14725	0	133	0	0	366	862	0	0
Ken-1				221				28116	84	8	1488	338	447	157	381	0
Ken-2				223				32546	60	0	383	0	235	0	0	0
Ken-4				225				37538	43	804	154	0	22	0	887	0
HOP-62				241				22249	0	0	58	726	740	63	0	0
MOLT-4				242				18708	0	13383	142	22	3864	838	0	50
SKVX				243				22457	387	303	1836	637	2757	371	0	0
HL-60				244				33149	0	0	0	0	4255	2803	0	0
NCI-H23				245				29842	880	901	308	387	858	1115	1154	1434
RPMI 8226				246				34425	0	0	309	367	1614	134	222	60
A549/ATCC				247				30516	0	0	885	0	0	153	612	401
SR				248				19506	0	1351	0	354	733	0	897	62
OVCAR-3				249				27443	30	200	663	852	1417	284	3825	286
HCT-15				250				34819	0	5278	813	1806	2385	1074	208	0
OVCAR-4				251				10333	478	1077	0	157	587	0	718	0
UO-31				252				13456	0	415	0	242	757	0	0	116
OVCAR-5				253				60297	0	3782	1757	584	7064	635	1034	271
SN12C				254				38550	119	3368	0	204	483	0	0	0
OVCAR-8				255				18487	158	573	882	512	215	819	104	0
LOX IMVI				256				43485	0	18804	0	784	8133	0	279	889
IGROV1				257				36126	171	290	740	373	1340	390	231	208
SK-MEL-2				258				34735	737	289	1017	0	536	377	73	0
SK-OV-3				259				17172	282	0	0	312	584	0	157	115
SK-MEL-5				260				13827	212	806	0	141	339	0	54	0
SF-539				261				38531	856	1771	824	856	3488	0	858	408
SK-MEL-28				262				39495	0	337	617	1130	2525	0	252	0
K-562				263				30125	188	11139	0	179	2889	588	55	336
UACC-257				264				25143	184	0	606	210	617	97	612	0
M14				265				10129	48	0	0	178	34	279	0	0
MCF7				267				68835	0	2860	480	807	1109	2558	448	543
MDA-MB-435				269				26815	0	679	819	40	503	5	0	0
HT29				270				39490	0	0	550	7537	0	418	1472	278
MDA-N				271				37574	727	7083	0	0	492	2143	424	625
Y79 poly A+				273				102505	972	2309	0	822	608	534	1356	0
KHOS poly A+				288				38003	44	0	9854	8283	4347	3083	147	0
HTB38 24h TPA RNA 8/23				300				47107	0	0	550	3518	0	511	387	0
HELA-EXP-031898				313				19309	0	0	0	0	31	298	42	0
HTB38 0h RNA				322				62088	109	0	7168	17280	2781	1134	503	0
HT347				323				40870	186	787	295	18626	0	1252	13	0
458 nodule RNA				325				64258	0	0	18772	5011	0	840	383	0
NCI-H226				326				23074	0	184	757	0	334	408	129	860
HOP-62				327				19884	0	187	1038	1027	2365	1532	731	0
MDA-MB-231				328				35092	0	8843	45452	11567	18823	5581	1838	1619
U251				329				33858	0	19509	13847	7782	63808	10227	1071	5180
PT cells poly A+				340				11007	71	105	0	0	1453	0	0	48
PC-3				341				23466	138	283	3488	8270	813	386	0	282
HCC-2998				342				17789	0	601	1731	774	355	873	29	422
SW 620				345				15302	0	819	1383	606	203	481	1336	849
HT192				346				42850	87	0	2871	17368	2232	1465	0	73
COLO 205				347				12548	0	0	2265	0	100	0	757	0
HT219				348				29025	0	0	383	8440	0	0	0	0
304-12				349				21718	0	1585	2179	779	390	0	531	349
HT151				350				55838	898	8470	2432	8252	43	408	511	279
A498				351				23833	0	183	4815	0	152	803	828	0
HT363				352				83325	483	0	8775	15803	2060	0	0	0
RXF 393				353				23448	0	0	1811	337	2050	212	425	0
TK-10				355				42915	208	8535	22002	8342	8829	3400	23	578
Malme-3M				357				74434	651	84082	18863	11058	31229	6343	1280	2753
Hs 578T				358				23716	71	2207	1608	824	1418	425	372	0
HT213			50					41730	0	909	282	12170	288	0	0	0
HT288			52					34634	610	0	3488	38848	289	0	0	0
HT139			54					37801	506	713	1971	0	0	104	55	143
HT155			56					37780	0	0	784	12374	28	0	581	65
HT163			58					38017	0	0	354	4844	0	408	141	0
HT170			60					58864	781	0	7384	55230	87	807	820	0
HT172			62					31378	8	0	871	3857	0	0	638	357
HT138			63					41851	0	345	0	17086	0	171	0	0
HT178			64					37107	0	0	296	1881	78	0	443	45
HT154			65					22270	0	0	0	11739	0	866	0	193
HT189			66					28571	8	0	801	3611	683	73	2343	77
HT180			67					20113	0	0	2803	1192	2544	0	1630	0
HT143			68					27825	267	0	1324	35	358	725	704	0
[illegible]			69					20412	0	475	366	0	0	0	0	257
HT198			70					19084	135	0	435	6171	0	0	558	19
HT145			71					27515	675	0	7947	23627	0	0	231	348
HT227			72					30808	0	0	3488	278	423	0	537	31
HT302			73					37705	0	0	1987	71933	761	0	200	0
HT314			74					38827	475	0	131	18809	313	0	0	0
HT317			76					68238	816	0	6815	82566	2803	0	429	0
Nodular melanoma 6/25 11/8			77					30458	0	0	142	119	0	256	0	0
HT323			78					81848	187	538	0	12817	182	0	0	0
HT327			80					43118	150	0	786	7845	97	1631	849	0
HT335			82					47065	0	179	0	3179	9	330	169	40
HT146			85					13508	209	0	0	2507	0	183	36	90
HT346			87					51446	631	0	182	16307	0	126	725	99
HT311			170					37227	266	0	454	9866	89	0	0	114
HT356			185					38862	0	0	0	6577	1908	558	780	0
HT140			187					18306	0	0	0	452	0	0	307	78
HT281			189					35781	0	0	0	28196	194	0	1358	0
HT372			191					43132	0	0	30	1744	427	0	319	305
TCGP			207					38117	0	158	1	0	0	0	0	53
HT160			216					18433	205	283	1107	1329	0	0	344	0
HT307			217					17447	84	0	352	1273	353	0	0	142
HT368			224					38703	0	0	8188	19488	17	799	0	61
HT370			226					30028	0	0	215	10361	8	0	0	0
HT371			228					40577	8	1	0	8937	258	3	253	287
HT377			230					45558	428	187	0	12382	0	0	334	0
HT382			236					44406	0	0	1948	8161	0	327	427	0
neuroblastoma RNA			281					18068	368	0	0	63	0	0	0	0
HT334			298					68856	803	0	3020	25038	0	0	0	0
HT338			301					48347	335	0	3584	15153	145	473	221	0
HT382			315					17927	253	0	695	1637	0	303	0	0
HT384			317					30800	449	115	2363	40458	0	704	714	534
HT312			319					37806	0	0	633	1822	865	164	379	0
HT192			323					25856	0	522	175	0	208	130	149	0
HT306			358					34087	98	0	2208	17868	0	486	215	0
HT157			380					67210	0	0	12307	18780	385	233	0	0
T-47D	163							28111	54	34135	2506	413	91	7891	768	0
MDA-N	161							28304	0	218095	2539	259	0	18184	98	740
MDA-MB-435	159							34704	859	136649	2347	2104	326	15625	104	365
MDA-MB-231	157							43092	712	15181	24031	4452	1312	23542	140	412

Table 3 (cont'd)

Tissue	Tumor-syn	Normal-syn	Tumor - fo	Tumor cells	Normal	Endos	p53	SEQ 44 T	SEQ 45 AA	SEQ 47 AA	SEQ 48 AA	SEQ 49 AA	SEQ 51 KI	SEQ 52 AA	SEQ 54 CC	SEQ 55 CL
DaPung-7								85383	578	729	0	0	0	0	0	0
DaPung-8								29480	348	374	0	0	0	0	0	0
DaPung-9								44303	796	158	0	0	0	0	0	0
DaPung-11								34867	0	628	0	0	0	0	0	0
DaPung-12								95343	0	495	0	0	0	0	0	0
DaPung-10								20110	284	211	0	0	0	0	0	0
DaPung-1								7684	864	23	0	0	0	0	0	0
DaPung-2								3139	381	38	0	0	0	0	0	0
DaPung-3								888	1703	253	0	0	0	0	0	0
DaPung-4								28852	324	0	0	0	0	0	0	0
DaPung-5								40688	0	51	0	0	0	0	0	0
DaPung-6								32008	20	0	0	0	0	0	0	0
A549 - 8							wt	1956	23	90	0	0	0	0	0	0
EKVX - 8							mutant	859	212	0	0	0	0	0	0	0
HCT-116 - 7							wt	0	722	0	0	0	0	0	0	0
HCT-116 - 8							wt	771	122	55	0	0	0	0	0	0
HT29 - 1							mutant	310	0	144	0	0	0	0	0	0
HT29 - 7							mutant	0	0	25	0	0	0	0	0	0
HT29 - 8							mutant	0	0	51	0	0	0	0	0	0
SF539 - 7							wt	1307	937	38	0	0	0	0	0	0
SF539 - 8							wt	3338	7	130	0	0	0	0	0	0
SF-268-7							mutant	17078	832	0	0	0	0	0	0	0
SF-268-8							mutant	15222	32	118	0	0	0	0	0	0
OVCAR-4 - 7							wt	1233	28	0	0	0	0	0	0	0
OVCAR-4 - 8							wt	12764	4	179	0	0	0	0	0	0
OVCAR-5 - 7							mutant	4732	0	0	0	0	0	0	0	0
OVCAR-5 - 8							mutant	3132	0	4	0	0	0	0	0	0
MCF-7 - 8							wt	3375	440	0	0	0	0	0	0	0
ADR-RES - 8							mutant	838	0	0	0	0	0	0	0	0
HeLa - 8							HPV E6	1097	88	0	0	0	0	0	0	0
SW480 - 7							mutant	1922	717	22	0	0	0	0	0	0
SW480 - 8							mutant	412	4	72	0	0	0	0	0	0
H1299 - 8							mutant	8	162	10	0	0	0	0	0	0
C33A - 7							mutant	8	235	4	0	0	0	0	0	0
C33A - 8							mutant	444	0	0	0	0	0	0	0	0
U2OS - 7							mutant	28619	148	84	0	0	0	0	0	0
U2OS - 8							mutant	4758	418	0	0	0	0	0	0	0
Hs68 - 7							wt	1393	0	0	0	0	0	0	0	0
Hs68 - 8							wt	512	324	0	0	0	0	0	0	0
WI 38 - 8							wt	1504	41	0	0	0	0	0	0	0
458 medulla RNA								0	0	0	70	5790	2685	308	588	9888
CRL1572 3/17/00								340	0	0	134	1830	255	6	517	691
Bov-4						84		642	0	0	188	5574	0	88	0	12425
HT388								0	0	0	801	4678	0	0	7	16708
HT378								0	0	34	0	4412	215	0	8	2038
HT385								10732	0	0	0	5567	8257	81	154	8810
HT308								0	0	8	0	8143	168	0	0	24582
Bov-3						173		53	0	7	0	3031	498	328	297	1815
Bov-5						175		0	0	58	34	1425	843	284	0	93
Bov-9						177		0	0	7	17	2354	228	0	0	1298
h keratinocytes 2/25/02 #10								0	0	93	13	3675	0	112	0	198
Bov-10						237		0	0	19	123	4065	150	40	281	3522
HTB18								0	0	0	0	7531	0	421	650	1625
h fibroblasts 3/01/02 #12								0	0	39	23	4648	0	0	206	883
prostate, h								0	0	0	91	2883	0	0	0	5850
MHNG-OS poly A+								918	0	0	0	2857	291	94	0	2243
SA-OS (Mandy) poly A+								0	0	0	98	1148	0	176	0	1566
MK poly A+								0	0	67	0	2620	0	257	0	5073
HCT-116 - 3							wt	398	22	3	0	0	0	0	0	0
HCT-116 - 4							wt	438	1211	0	0	0	0	0	0	0
HCT-116 - 5							wt	127	304	26	0	0	0	0	0	0
HCT-116 - 6							wt	1178	0	0	0	0	0	0	0	0
A549 - 6							wt	0	0	4	0	0	0	0	0	0
HT29 - 3							mutant	19858	0	247	0	0	0	0	0	0
EKVX - 6							mutant	881	0	0	0	0	0	0	0	0
HT29 - 4							mutant	0	17	28	0	0	0	0	0	0
HT29 - 5							mutant	1078	0	244	0	0	0	0	0	0
HT29 - 6							mutant	0	0	62	0	0	0	0	0	0
OVCAR-4 - 3							wt	5253	108	30	0	0	0	0	0	0
OVCAR-4 - 4							wt	0	0	0	0	0	0	0	0	0
OVCAR-4 - 5							wt	2869	271	0	0	0	0	0	0	0
OVCAR-4 - 6							wt	0	0	32	0	0	0	0	0	0
SF539 - 3							wt	4462	146	140	0	0	0	0	0	0
SF539 - 4							wt	3258	281	32	0	0	0	0	0	0
SF539 - 5							wt	891	0	38	0	0	0	0	0	0
SF539 - 6							wt	1280	312	0	0	0	0	0	0	0
OVCAR-5 - 3							mutant	2388	0	118	0	0	0	0	0	0
OVCAR-5 - 4							mutant	0	0	37	0	0	0	0	0	0
OVCAR-5 - 6							mutant	241	0	0	0	0	0	0	0	0
ADR-RES - 6							mutant	80	6	129	0	0	0	0	0	0
MCF-7 - 6							wt	629	646	80	0	0	0	0	0	0
HeLa - 6							HPV E6	1297	1571	0	0	0	0	0	0	0
H1299 - 6							mutant	0	269	0	0	0	0	0	0	0
SW480 - 3							mutant	0	303	138	0	0	0	0	0	0
SW480 - 4							mutant	1137	629	67	0	0	0	0	0	0
SW480 - 5							mutant	3274	0	39	0	0	0	0	0	0
SW480 - 6							mutant	885	725	0	0	0	0	0	0	0
C33A - 3							mutant	180	0	90	0	0	0	0	0	0
C33A - 4							mutant	4870	0	0	0	0	0	0	0	0
C33A - 5							mutant	0	678	98	0	0	0	0	0	0
C33A - 6							mutant	3886	0	0	0	0	0	0	0	0
Hs68 - 6							wt	0	0	58	0	0	0	0	0	0
U2OS - 3							mutant	79697	293	0	0	0	0	0	0	0
U2OS - 4							mutant	4629	0	0	0	0	0	0	0	0
U2OS - 5							mutant	7931	149	17	0	0	0	0	0	0
U2OS - 6							mutant	0	0	49	0	0	0	0	0	0
WI 38 - 6							wt	2111	0	242	0	0	0	0	0	0
Hs68 - 3							wt	2882	0	57	0	0	0	0	0	0
Hs68 - 4							wt	53108	1252	248	0	0	0	0	0	0
SF-268-3							mutant	123828	0	0	0	0	0	0	0	0
SF-268-4							mutant	70351	1540	0	0	0	0	0	0	0
SF-268-5							mutant	32299	292	0	0	0	0	0	0	0
SF-268-6							mutant	0	2127	0	0	0	0	0	0	0
DaPung-13								43164	628	750	0	0	0	0	0	0
Mitchell - 20								5819	5543	71	0	0	0	0	0	0
Mitchell - 21								6250	3048	128	0	0	0	0	0	0
Mitchell - 22								7053	8567	388	0	0	0	0	0	0
OVCAR-5 - 5							mutant	2910	793	112	0	0	0	0	0	0
Mitchell - 10								2788	1330	113	0	0	0	0	0	0
Mitchell - 11								2188	781	45	0	0	0	0	0	0
Mitchell - 12								6365	61	288	0	0	0	0	0	0
Mitchell - 13								4834	133	1023	0	0	0	0	0	0
Mitchell - 14								4037	0	891	0	0	0	0	0	0
Mitchell - 15								8840	0	1013	0	0	0	0	0	0
Mitchell - 16								3877	3	0	0	0	0	0	0	0
Mitchell - 17								1275	0	165	0	0	0	0	0	0
Mitchell - 18								1210	3480	665	0	0	0	0	0	0
Mitchell - 19								3	0	0	0	0	0	0	0	0

Table 3 (cont'd)

Tissue	Tumor-syn	Normal-syn	Tumor - ts	Tumor cells	Normal	Endos	p53	SEQ 36 AA	SEQ 37 WT	SEQ 60 AA	SEQ 63 NE	SEQ 65 CA	SEQ 63 HR	SEQ 118 R	SEQ 73 HR	SEQ 78 AA
adrenal gland - h		1						1179	45305	13724	16216	11737	18736	4758	34187	161827
lymph node - h		2						1862	70208	24586	33524	13883	27463	7405	31327	144030
bone marrow - h		3						67	80493	12341	24328	20126	21479	3888	86136	183884
mammary gland - h		4						102	6988	308	309	3138	2988	984	4197	30763
brain - h		5						1567	23741	2587	8670	113657	27944	3679	13512	88724
pancreas - h		6						2734	38449	11763	2583	14282	19704	3837	27524	88825
cerebellum - h		7						2187	88557	2723	29667	401142	55813	7267	38350	150166
pituitary gland - h		8						2771	86387	14885	10920	5342	28061	5844	23798	126706
fetal brain - h		9						2182	88083	14224	9117	115506	32985	5260	23245	130701
placenta - h		10						7654	29116	15082	6421	27503	31523	4144	29454	118927
fetal kidney - h		11						3080	45761	9882	12231	27386	42058	4885	38782	202584
prostate - h		12						2873	25467	15030	5177	8510	18409	4446	8670	180508
fetal liver - h		13						1982	31433	13743	10943	16727	34911	2114	47817	95705
salivary gl. - h		14						1275	20868	9416	1858	19056	11078	2253	23301	188079
fetal lung - h		15						4579	80513	8398	8440	27133	27718	2082	32855	175336
skeletal muscle - h		16						3544	34674	86	5882	6833	12917	1781	8575	128486
heart - h		17						1236	18128	3837	3249	17179	16473	2254	8412	108323
small intestine - h		18						2013	18561	17258	1848	8510	17382	1878	15805	254853
kidney - h		19						1538	23780	8208	10080	7388	38848	2088	17836	150384
spinal cord - h		20						2970	15071	6250	8086	3857	29454	1989	7081	130873
liver - h		21						4785	15711	8344	2177	3843	30372	2313	10324	110984
Spleen - h		22						1065	28778	16388	2832	3727	20754	2087	4881	114231
lung - h		23						464	22182	6232	6714	4273	28712	2193	6428	125806
stomach - h		24						1619	10425	12130	1652	4031	20888	2181	6584	387434
testis - h		25						8482	103115	8233	18184	8398	18158	4776	28107	122629
thymus - h		27						1876	57984	40345	18139	17350	19038	4763	33850	115427
HPAEC		28				28		294	14425	0	806	4198	12372	3412	0	83109
thyroid gland - h		29						2584	29474	3465	2102	11250	11291	3114	13897	88705
RPTEC		30				30		508	12784	748	1729	1861	15158	3649	13263	88954
trachea - h		31						5137	74825	8278	5113	34729	22943	3380	21166	714306
HMEC		32						18853	21362	29857	3353	0	25487	2897	8475	78553
uterus - h		33						1208	41825	3525	6626	34917	19418	3493	15360	68624
HCAEC		34						0	18916	752	8	435	17803	1992	4218	72012
Pancreas - h		35						554	11765	0	3362	290	8341	2332	6068	128381
lymph node - h		36						1745	12072	6582	2849	638	7798	3831	3205	77767
Skeletal muscle - h		37						621	3817	0	1071	2029	4538	905	2324	38353
fetal liver - h		38						0	9143	382	6911	1095	14308	2211	50874	76358
Heart - h		39						836	6677	0	8788	908	4578	886	1733	58107
thymus h		40						1510	11513	1144	6800	53	9098	2118	8482	94284
Duodenum - h		41						827	6294	630	102	405	4145	1544	5179	35243
Fetal brain - h		42						1670	16310	0	5643	551	9086	3845	9281	124700
Salivary gl. - h		43						1306	4830	0	2304	0	4275	1481	3676	81426
testis - h		44						1658	17351	0	4560	0	13191	2101	10038	120863
HT218-normal					365			0	7137	125	79	130	156	1614	501	20873
HT213-normal					363			0	8044	0	131	0	743	1102	0	24983
HT157-normal					361			451	3420	0	8	22	171	1861	336	30438
Bov-13					356	356		298	91127	404	1118	5137	10567	14131	14920	172796
Bov-12					354	354		1760	128846	0	21	3012	8067	7821	2525	85002
cerebellum - h					344			0	4508	72	83	228	428	2304	1811	30731
brain - h					342			0	1387	715	175	0	129	2380	443	32872
RPTEC					334	334		1346	21042	10083	0	357	701	4284	274	185421
lymph node - h					332			153	12413	0	1318	7	1558	3869	0	65390
h adult SMC 10/21/02 #17					330			0	8643	0	0	94	34	2890	0	43498
Fetal brain - h					328			256	64197	537	825	1683	12083	8886	3760	95415
HT300-normal					327			1215	4588	0	87	1	1603	1982	7794	38102
thymus h					326			463	78773	0	287	5123	4823	8846	1169	88548
HT148 - normal					321			0	2317	57	0	1	1318	2550	152	37683
HEPM 3d untreated					320			1317	22630	0	846	214	5813	4217	2089	66214
uterus - h					318			0	65419	1050	1252	1531	16860	11203	30226	123875
trachea - h					316			0	40355	806	1959	2194	12222	8263	140783	104866
thyroid gland - h					314			1	42987	0	1846	151	10332	6871	86901	114788
salivary gl. - h					311			0	6858	0	0	0	2738	2519	4532	101244
prostate, h					308			0	6480	0	233	129	1622	3462	3068	70453
pituitary gland - h					307			858	14108	0	114	235	1127	2486	2133	38846
pancreas - h					305			6	8503	0	45	0	2836	2581	3386	66363
mammary gland - h					303			104	26315	680	487	220	8827	4345	18318	98789
bladder - h					302			1973	19158	0	3240	507	9250	4498	7821	65038
testis - h					298			1747	103581	7298	489	1502	19319	7297	29073	140418
liver - h					297			2987	40917	2131	330	1808	8744	6235	13181	101949
Spleen - h					296			808	9815	0	137	117	2898	3770	5858	81130
spinal cord - h					294			205	48295	1484	52	1208	10727	7977	11556	112019
small intestine - h					292			188	7475	318	0	70	1941	2923	8383	64002
skeletal muscle - h					290			2187	53059	1405	547	843	11138	8446	29427	184587
bone marrow - h					279			0	785	1572	0	0	0	1603	1806	30233
adrenal gland - h					277			0	6188	56	375	0	405	2158	675	24322
HPAEC					275	275		182	3675	56	0	0	504	2487	0	38020
HT382-normal					268			0	3036	229	114	257	0	3137	407	53419
HT382-normal					266			2212	3888	0	162	163	1078	3510	2147	71286
Bov-11					238	238		623	8248	0	0	0	7268	4208	18005	157428
Bov-8					235	235		0	3824	0	0	0	2750	2873	1723	61030
HT373-normal					234			0	14411	412	420	0	17	3430	803	80887
Bov-7					233	233		3431	3138	40	116	227	1502	2686	4367	60074
Bov-6					231	231		778	4003	0	57	0	1458	2754	3814	31581
Bov-2					229	229		197	5734	0	0	33	1082	2889	2380	48128
Bov-1					227	227		1082	3874	0	145	196	1528	2485	8847	40717
bladder - h					222			258	4008	0	17	322	0	2880	363	44379
Heart - h					215			0	1810	0	0	28	6343	3087	1770	107307
stomach -h					214			0	4816	0	0	0	3148	3365	5834	81804
fetal liver- h					213			0	2868	0	0	328	456	2202	490	41586
placenta - h					212			138	3720	0	0	153	3470	2561	7793	58882
HCAEC					211	211		135	2157	0	0	117	0	2312	1	45376
fetal brain - h					210			0	6854	0	386	230	879	3280	4176	62140
HMEC					208			779	3894	0	4	198	0	2108	0	37886
Duodenum - h					205			319	2084	43	13	0	483	1652	238	40848
Skeletal muscle - h					203			333	3298	60	0	29	3	2208	124	43570
Pancreas - h					201			0	3195	383	98	0	188	2439	364	43068
testis - h					199			385	9731	0	160	338	0	2248	390	44576
Salivary gl. - h					197			0	5746	885	132	411	2172	2792	2052	53185
HEPM 3d TGFB1 detergent+DMase					195			584	3763	0	0	32	538	1518	62	35673
thymus -h					193			0	28305	348	366	25	254	1356	2652	47888
WI-38 72h					179			0	3118	0	204	0	841	1363	72	22161
lymph node - h					61			8	4438	0	0	0	2063	938	879	36753
lung - h					59			0	18888	803	158	88	3840	3001	5587	125162
kidney - h					57			0	3419	0	567	0	2379	2158	3845	68857
heart - h					55			1173	7101	0	0	622	1020	2135	1868	47950
fetal lung - h					53			273	3213	0	0	0	0	777	622	35486
fetal liver- h					51			0	3097	0	188	176	0	1157	8005	35043
fetal kidney - h					49			390	3589	0	63	0	805	2196	5247	65106
HELA-2h-031800				79				608	7753	0	67	819	1798	2759	21226	73028
HELA-4h-031800				81				5076	2581	0	186	0	791	2338	8863	73885
HELA-6h-031800				83				301	2784	0	59	203	1776	2285	6212	75474
HELA-0h-031800				86				1863	2781	854	162	90	2720	1297	4070	33775
HELA-8h-031800				88				94	12582	253	0	81	0	1843	4366	70122
HELA-9h-031800				90				232	3278	0	185	82	983	1744	3048	61476
HELA-10h-031800				92				1224	8588	0	98	90	1344	1761	7822	88408
HELA-11h-031800				94				476	938	0	195	192	0	1726	2548	44168
HELA-12h-031800				96				328	647	0	0	0	831	1409	1929	78433
NCI-H322M				146				706	6767	0	3283	283	807	4168	47498	20844
NCI-H460				148				362	5027	0	703	80	432	3194	13322	29260
NCI-H522				150				0	3419	8	225	0	378	1671	2808	24405
SNB-19				152				258	3181	0	373	0	1514	2329	30387	24696
SNB-75				154				488	6471	0	753	40	2908	3295	17171	28081
SF-268				156				0	2778	432	235	0	1122	1851	8488	18046
SF-295				158				0	0	0	67	436	732	656	2043	12380
CCRF-CEM				160				365	1885	0	0	186	921	667	303	15083
DU-145				162				0	2190	0	144	40	1288	1957	13460	18145
HCT 116				164				0	4548	0	248	0	471	1324	10125	12384

Table 3 (cont'd)

Tissue	Tumor-avg	Normal-avg	Tumor - to	Tumor cells	Normal	Endom	p53	SEQ 17 AA	SEQ 19 SC	SEQ 22 PT	SEQ 26 AA	SEQ 29 DR	SEQ 31 DR	SEQ 832 A	SEQ 48 MA	SEQ 844 T
Hs 578T	155							48043	143	111614	7206	2356	887	9345	0	389
MCF-7/ADR-RES	153							48543	0	70411	771	387	0	15559	0	859
MCF7	151							53969	834	30004	11924	2950	218	13820	0	0
M14	149							63303	371	22226	15025	2725	257	4104	975	73
UACC-257	147							38000	1060	72538	4016	111	8	32383	0	311
UACC-62	145							27441	0	7806	302	806	74	8800	306	251
SK-MEL-28	144							20851	71	10349	1402	2016	634	4087	176	254
UO-31	143							66230	0	12483	3316	644	1206	1827	1065	0
SK-MEL-5	142							28301	0	137878	1862	110	260	18800	490	134
KM12	141							30682	297	6923	2025	5	65	1287	0	329
SK-MEL-2	140							30577	0	59294	3528	827	495	19563	0	189
HCT-15	139							64738	445	25382	2769	1572	387	8866	642	0
Malme-3M	138							46080	1406	86409	4322	243	294	12794	226	451
COLO 205	137							67736	433	10862	2580	486	0	5756	0	174
LOX IMVI	136							20010	0	101759	1512	680	562	25226	348	628
SW-620	135							38849	437	29579	750	203	198	9408	376	168
TK-10	134							43207	68	18876	1719	683	282	7085	72	48
HCT 116	133							37409	345	18776	1178	0	458	3812	721	68
786-0	132							30175	0	27523	0	534	157	6539	887	14
HCC-2998	131							62382	734	17250	0	159	239	3861	0	541
ACHN	130							30060	329	81730	1353	617	303	10449	25	228
PC-3	129							35282	33	50087	1005	106	457	8256	619	0
RXF 393	128							40444	385	82951	3148	2477	2041	26824	478	0
DU-145	127							37777	0	8182	5153	140	400	15854	0	0
Caki-1	126							35257	331	91153	6431	85	527	22288	886	190
SR	125							37858	0	80238	7587	1172	661	26808	156	0
A498	124							39104	0	106712	4214	0	1665	2925	473	686
RPMI 8226	123							50465	737	8134	2800	2182	625	13014	0	0
SN12C	122							32578	85	44277	536	1473	150	23839	0	537
HL-60	121							36440	886	2018	0	325	771	707	68	380
MOLT-4	120							20309	782	17795	681	532	1023	4039	0	0
OVCAR-5	119							25375	0	42226	1986	337	1595	6852	569	77
K-562	118							54213	582	18149	2128	382	222	5444	0	0
OVCAR-4	117							42568	1300	108842	5320	2238	2583	8251	1228	1110
CCRF-CEM	116							38120	576	100622	2761	831	470	41560	0	0
OVCAR-3	115							52017	548	47691	1242	959	303	10048	2443	0
SF-539	114							34865	86	14022	2825	0	350	19293	0	252
HOP-62	113							19578	0	64830	1645	1198	665	7726	0	100
SF-295	112							40830	257	17908	700	708	1184	5386	417	637
A549/ATCC	111							47430	0	78728	1610	498	303	17019	1514	572
SF-268	110							30345	64	56487	972	185	76	13647	482	568
NCI-H522	109							44511	0	61026	565	813	276	8039	0	94
U251	108							54078	433	46750	573	124	718	17877	886	0
NCI-H460	107							28866	356	75179	438	405	803	17568	808	152
SNB-75	106							41104	0	17012	403	456	369	4792	884	316
NCI-H322M	105							49837	89	10250	3058	4822	461	20339	746	0
SNB-19	104							80554	442	13825	1417	451	2044	32854	156	625
NCI-H226	103							61587	833	9072	2208	1331	606	18328	743	69
SK-OV-3	102							33170	0	18508	3841	522	200	19891	343	61
NCI-H23	101							38481	0	5616	4702	140	203	29589	0	481
IGROV1	100							41869	442	11790	3691	229	303	11318	0	0
EKVX	99							25017	0	14573	1822	0	642	34177	0	0
OVCAR-8	98							31129	0	7825	48	101	187	8382	11	0
HOP-92	97							33300	0	18562	1074	306	466	12792	492	103
h fibroblasts 3/21/02 #12	48							33080	0	8173	1558	5770	341	401	200	184
h adult SMC 10/21/02 #17	47							30837	188	0	2185	0	130	0	983	127
h keratinocytes 3/25/02 #10	46							29129	66	23401	1117	0	92	10270	344	0
TCGP	26							22053	700	19106	7310	99	120	6277	1704	111
A549 - 1							wt	0	0	0	349	1138	4308	413	571	0
A549 - 3							wt	0	0	0	631	124	4678	538	1003	0
A549 - 4							wt	0	0	0	0	1294	7989	0	880	0
A549 - 6							wt	0	0	0	0	456	6066	143	0	0
A549 - 7							wt	0	0	0	0	913	6874	767	0	0
EKVX - 1							mutant	0	0	0	1340	3420	6820	475	2339	0
EKVX - 4							mutant	0	0	0	2098	4210	10861	330	180	0
EKVX - 3							mutant	0	0	0	1909	0	4861	0	705	0
EKVX - 5							mutant	0	0	0	284	1113	9667	137	0	0
EKVX - 7							mutant	0	0	0	0	37	7463	867	0	0
MCF-7 - 1							wt	0	0	0	453	801	110	3344	155	0
MCF-7 - 3							wt	0	0	0	96	1048	2987	0	482	0
MCF-7 - 4							wt	0	0	0	976	827	1029	218	1386	0
MCF-7 - 6							wt	0	0	0	1191	2031	4029	0	988	0
MCF-7 - 7							wt	0	0	0	0	500	430	607	629	0
ADR-RES - 1							mutant	0	0	0	0	2736	2797	4898	2088	0
ADR-RES - 3							mutant	0	0	0	1149	3462	4030	1066	0	0
ADR-RES - 4							mutant	0	0	0	112	0	2817	637	801	0
ADR-RES - 6							mutant	0	0	0	403	2399	852	0	0	0
ADR-RES - 7							mutant	0	0	0	2011	2098	1855	988	488	0
WI 38 - 1							wt	0	0	0	0	7798	3848	589	1631	0
WI 38 - 3							wt	0	0	0	865	6896	6250	197	0	0
WI 38 - 4							wt	0	0	0	1631	3006	5488	0	1593	0
WI 38 - 5							wt	0	0	0	1300	7877	3292	563	587	0
WI 38 - 7							wt	0	0	0	1486	3377	5828	312	0	0
HeLa - 1							HPV E6	0	0	0	693	0	1919	0	60	0
HeLa - 3							HPV E6	0	0	0	842	849	4257	548	0	0
HeLa - 4							HPV E6	0	0	0	250	281	9659	335	850	0
HeLa - 5							HPV E6	0	0	0	1177	1708	4044	1280	173	0
HeLa - 7							HPV E6	0	0	0	1543	274	4788	0	0	0
H1299 - 1							mutant	0	0	0	114	2065	2347	0	337	0
H1299 - 3							mutant	0	0	0	0	431	2212	542	546	0
H1299 - 4							mutant	0	0	0	267	123	4874	421	612	0
H1299 - 5							mutant	0	0	0	0	1456	2278	28	0	0
H1299 - 7							mutant	0	0	0	458	1853	1187	10	0	0
A549 - 2							wt	0	0	0	334	756	2012	286	604	0
EKVX - 2							mutant	0	0	0	1435	820	20773	0	0	0
HCT-116 - 1							wt	0	0	0	1196	330	6040	1648	296	0
HCT-116 - 2							wt	0	0	0	2980	2835	6294	149	811	0
HT29 - 2							mutant	0	0	0	1014	2541	1846	486	0	0
SF539 - 1							wt	0	0	0	313	2130	1019	0	547	0
SF539 - 2							wt	0	0	0	819	8447	744	780	179	0
SF-268-1							mutant	0	0	0	2143	3277	4430	835	0	0
SF-268-2							mutant	0	0	0	326	5072	4867	2865	1246	0
OVCAR-4 - 1							wt	0	0	0	1444	2283	19120	251	662	0
OVCAR-4 - 2							wt	0	0	0	0	1826	13774	409	441	0
OVCAR-5 - 1							mutant	0	0	0	1743	6553	3468	483	339	0
OVCAR-5 - 2							mutant	0	0	0	1268	3797	1735	635	0	0
MCF-7 - 2							wt	0	0	0	769	3092	0	288	0	0
ADR-RES - 2							mutant	0	0	0	776	1983	945	0	44	0
HeLa - 2							HPV E6	0	0	0	941	1918	8717	1522	0	0
SW480 - 1							mutant	0	0	0	428	1570	6813	1196	1923	0
SW480 - 2							mutant	0	0	0	1209	703	2907	0	4409	0
H1299 - 2							mutant	0	0	0	283	0	2016	1014	540	0
C33A - 1							mutant	0	0	0	205	4364	0	121	448	0
C33A - 2							mutant	0	0	0	804	1162	880	200	373	0
U2OS - 1							mutant	0	0	0	2046	7970	7073	653	3787	0
U2OS - 2							mutant	0	0	0	8100	11204	3320	1903	3826	0
Hs68 - 1							wt	0	0	0	1432	4561	6728	0	609	0
Hs68 - 2							wt	0	0	0	0	1983	2935	263	0	0
WI 38 - 2							wt	0	0	0	2505	8887	5771	442	19	0
[illegible] - 1								0	0	0	1158	3116	0	344	0	0
[illegible] - 2								0	0	0	4465	2081	0	408	0	0
[illegible] - 3								0	0	0	6420	11049	13408	0	1371	0
[illegible] - 4								0	0	0	5850	41855	4026	0	1037	0
[illegible] - 5								0	0	0	4520	3681	0	282	0	0
[illegible] - 6								0	0	0	1708	340	318	143	0	0
[illegible] - 8								0	0	0	3347	131	0	1175	118	0
[illegible] - 9								0	0	0	48	21772	273	603	0	0

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - fx	Tumor cells	Normal	Endos	p53	SEQ 17 AA	SEQ 38 SC	SEQ 22 PT	SEQ 35 AA	SEQ 29 DR	SEQ 31 DR	SEQ 632 A	SEQ 40 HA	SEQ 844 T
DaPong-7								0	0	0	21884	8478	31596	2723	1224	0
DaPong-8								0	0	0	10065	8543	17854	1800	1078	0
DaPong-9								0	0	0	9122	1586	25773	1318	884	0
DaPong-11								0	0	0	7501	9218	14351	1457	860	0
DaPong-12								0	0	0	3437	3288	16748	1029	0	0
DaPong-10								0	0	0	6482	290	19429	311	210	0
DaPong-1								0	0	0	3941	12536	8787	932	17852	0
DaPong-2								0	0	0	3679	10380	6327	148	68825	0
DaPong-3								0	0	0	4784	2946	2782	3207	4773	0
DaPong-4								0	0	0	1944	4731	97	4214	903	0
DaPong-5								0	0	0	1179	2029	327	1817	2183	0
DaPong-6								0	0	0	12057	6346	0	2638	1453	0
A549 - 8							wt	0	0	0	6	1464	9852	0	427	0
EKVX - 8							mutant	0	0	0	1933	2153	6498	580	17	0
HCT-116 - 7							wt	0	0	0	742	2507	3043	5498	619	0
HCT-116 - 8							wt	0	0	0	814	8117	2307	761	0	0
HT29 - 1							mutant	0	0	0	420	3056	3122	801	0	0
HT29 - 7							mutant	0	0	0	444	150	8	0	151	0
HT29 - 8							mutant	0	0	0	1051	2806	2178	0	1146	0
SF539 - 7							wt	0	0	0	0	6143	2843	1075	208	0
SF539 - 8							wt	0	0	0	65	10346	2922	862	0	0
SF-268-7							mutant	0	0	0	771	8891	2712	1198	1054	0
SF-268-8							mutant	0	0	0	1168	8034	4822	384	0	0
OVCAR-4 - 7							wt	0	0	0	0	1284	8363	0	0	0
OVCAR-4 - 8							wt	0	0	0	2050	2109	13808	685	3736	0
OVCAR-5 - 7							mutant	0	0	0	0	857	21830	0	0	0
OVCAR-5 - 8							mutant	0	0	0	88	2053	7100	2583	0	0
MCF-7 - 8							wt	0	0	0	0	3538	1521	0	180	0
ADR-RES - 8							mutant	0	0	0	465	672	3321	0	0	0
HeLa - 8							HPV E6	0	0	0	1829	225	4785	1418	0	0
SW480 - 7							mutant	0	0	0	248	841	4842	0	1427	0
SW480 - 8							mutant	0	0	0	0	870	4328	0	1186	0
H1299 - 8							mutant	0	0	0	1405	4781	2495	298	49	0
C33A - 7							mutant	0	0	0	0	2082	2718	1002	837	0
C33A - 8							mutant	0	0	0	0	6683	451	865	0	0
U2OS - 7							mutant	0	0	0	2235	4049	3018	977	1215	0
U2OS - 8							mutant	0	0	0	31	4880	8016	0	0	0
HeLa - 7							wt	0	0	0	1026	348	3165	144	0	0
HeLa - 8							wt	0	0	0	1446	1183	3374	1982	0	0
WI 38 - 8							wt	0	0	0	1470	0	3574	0	455	0
458 muscle RNA								37880	0	4415	210	290	1447	6182	0	0
CRL1572 3/17/98								25584	578	736	643	4685	27	570	16	58
Bov-4						84		59810	0	0	1007	3021	1652	0	336	0
HT368								32554	0	0	7687	21100	2573	29	0	301
HT378								37558	9	386	662	2800	5874	0	0	0
HT385								76812	0	0	14370	8858	1358	316	0	0
HT308								21762	851	0	0	32309	1103	185	873	574
Bov-3						173		30821	38	0	0	1954	1010	78	178	0
Bov-5						175		19850	0	0	0	311	60	0	171	10
Bov-8						177		38076	0	142	383	0	643	0	418	110
h keratinocytes 3/25/92 #10								80327	0	0	3049	556	49	0	1798	0
Bov-10						237		45182	257	0	245	733	2244	400	105	0
HTB10								66288	0	0	1379	3583	0	0	0	0
h fibroblasts 3/31/92 #12								44374	88	0	0	4810	70	0	251	0
prostate, h								29035	7	0	0	5762	14	0	0	0
MNNG-OS poly A+								24870	236	1075	3582	3701	1721	1048	0	0
SA-OS (Mundy) poly A+								27087	0	0	10788	8881	674	0	0	0
MK poly A+								32124	0	281	12809	10417	478	1982	863	403
HCT-116 - 3							wt	0	0	0	11	1768	4484	297	24	0
HCT-116 - 4							wt	0	0	0	0	3318	7870	113	0	0
HCT-116 - 5							wt	0	0	0	1789	1850	3247	0	0	0
HCT-116 - 6							wt	0	0	0	598	2678	7618	267	246	0
A549 - 6							wt	0	0	0	0	2201	52	0	302	0
HT29 - 3							mutant	0	0	0	148	4634	7875	1143	813	0
EKVX - 6							mutant	0	0	0	0	1949	2376	0	435	0
HT29 - 4							mutant	0	0	0	1239	323	3234	181	0	0
HT29 - 5							mutant	0	0	0	1070	3886	3867	0	383	0
HT29 - 6							mutant	0	0	0	0	2080	8879	800	0	0
OVCAR-4 - 3							wt	0	0	0	1203	1613	11856	870	1055	0
OVCAR-4 - 4							wt	0	0	0	0	708	8721	0	669	0
OVCAR-4 - 5							wt	0	0	0	859	3034	13758	1750	3049	0
OVCAR-4 - 6							wt	0	0	0	813	10879	2575	211	284	0
SF539 - 3							wt	0	0	0	1208	4103	1672	138	746	0
SF539 - 4							wt	0	0	0	0	1860	3256	0	108	0
SF539 - 5							wt	0	0	0	846	1282	2380	414	0	0
SF539 - 6							wt	0	0	0	580	5480	0	540	808	0
OVCAR-5 - 3							mutant	0	0	0	1847	6497	7120	0	111	0
OVCAR-5 - 4							mutant	0	0	0	0	3700	2419	28	400	0
OVCAR-5 - 6							mutant	0	0	0	236	308	1633	13	0	0
ADR-RES - 6							mutant	0	0	0	636	2829	2267	433	0	0
MCF-7 - 6							wt	0	0	0	0	1854	2830	84	718	0
HeLa - 6							HPV E6	0	0	0	1327	1684	4791	129	182	0
H1299 - 6							mutant	0	0	0	309	0	372	0	0	0
SW480 - 3							mutant	0	0	0	0	850	3500	580	2508	0
SW480 - 4							mutant	0	0	0	0	377	3879	562	1084	0
SW480 - 5							mutant	0	0	0	2315	1275	4248	380	14325	0
SW480 - 6							mutant	0	0	0	1702	1928	4535	50	1577	0
C33A - 3							mutant	0	0	0	0	0	1963	0	298	0
C33A - 4							mutant	0	0	0	72	775	451	0	808	0
C33A - 5							mutant	0	0	0	0	5487	8	0	0	0
C33A - 6							mutant	0	0	0	0	80	21373	0	0	0
HeLa - 6							wt	0	0	0	578	41	5477	3651	284	0
U2OS - 3							mutant	0	0	0	1438	11036	8821	10000	5193	0
U2OS - 4							mutant	0	0	0	1198	6140	5864	1818	2083	0
U2OS - 5							mutant	0	0	0	1756	6156	2586	0	3200	0
U2OS - 6							mutant	0	0	0	606	17687	518	802	210	0
WI 38 - 6							wt	0	0	0	1829	2318	2946	398	0	0
HeLa - 3							wt	0	0	0	2401	8487	7121	105	529	0
HeLa - 4							wt	0	0	0	2760	6182	20860	1817	0	0
SF-268-3							mutant	0	0	0	1194	5180	6451	0	0	0
SF-268-4							mutant	0	0	0	1417	2882	4751	1674	22	0
SF-268-5							mutant	0	0	0	1835	3820	3241	0	0	0
SF-268-6							mutant	0	0	0	1614	4390	84	402	0	0
DaPong-13								0	0	0	5019	12553	12086	2259	8086	0
Mikhail - 20								0	0	0	4071	10817	12559	2867	7190	0
Mikhail - 21								0	0	0	2819	4867	7808	580	3387	0
Mikhail - 22								0	0	0	3863	3314	2833	7314	651	0
OVCAR-5 - 5							mutant	0	0	0	4563	8671	4413	260	2940	0
Mikhail - 10								0	0	0	3874	538	476	163	4383	0
Mikhail - 11								0	0	0	2320	0	12	305	4583	0
Mikhail - 12								0	0	0	1877	2702	1025	812	17009	0
Mikhail - 13								0	0	0	1770	11411	1191	2922	251	0
Mikhail - 14								0	0	0	3018	0	0	3030	61	0
Mikhail - 15								0	0	0	1208	13215	645	747	4238	0
Mikhail - 16								0	0	0	1737	602	4336	438	980	0
Mikhail - 17								0	0	0	2243	98	0	673	433	0
Mikhail - 18								0	0	0	2479	6986	4281	1120	582	0
Mikhail - 19								0	0	0	1954	12880	4413	653	1020	0

Table 3 (cont'd)

Tissue	Tumor-eye	Normal-eye	Tumor - lo	Tumor cells	Normal	Endo	p53	SEQ 944 T	SEQ 45 AA	SEQ 47 AA	SEQ 48 AA	SEQ 49 AA	SEQ 51 KI	SEQ 52 AA	SEQ 54 CC	SEQ 55 CL
adrenal gland - h		1						10634	0	205	168	7815	2253	1782	20262	37091
lymph node - h		2						2518	0	267	584	8574	7108	2170	7791	70790
bone marrow - h		3						1986	0	237	0	5663	3816	1381	1112	45217
mammary gland - h		4						441	0	8	8	2785	1143	280	0	3258
brain - h		5						4861	0	188	230	6495	809	867	11958	31129
pancreas - h		6						368	0	0	344	7076	3342	888	8722	44206
cerebellum - h		7						8688	0	70	0	7603	2836	3189	13785	85353
pituitary gland - h		8						10870	0	60	231	8525	6597	932	32295	38020
fetal brain - h		9						52140	0	257	88	7743	5614	3007	25437	47438
placenta - h		10						4424	0	61	67	8183	2360	2312	41080	35806
fetal kidney - h		11						2337	0	223	0	8334	8430	1375	30344	73605
prostate - h		12						2083	0	174	0	7873	3767	334	5551	21151
fetal liver - h		13						2978	0	110	180	6859	1682	810	4385	47110
salivary gl. - h		14						0	0	130	0	8005	3418	1128	5531	28823
fetal lung - h		15						8850	0	319	348	10713	8378	1758	20842	64757
skeletal muscle - h		16						32808	0	8	0	5708	1942	1180	2008	14517
heart - h		17						8442	0	98	181	8123	472	1022	2810	14767
small intestine - h		18						2779	0	96	144	7037	2985	443	4172	22398
kidney - h		19						0	0	181	225	6344	2082	761	7039	31845
spinal cord - h		20						0	0	139	0	8879	2846	658	1254	14331
liver - h		21						8348	0	8	0	4814	0	833	0	15760
Spleen - h		22						2363	0	0	198	5447	3308	631	997	18480
lung - h		23						3011	0	105	177	3866	2134	673	3438	34017
stomach - h		24						2692	0	175	0	3808	812	281	1343	17807
testis - h		25						20445	0	1160	200	6830	8251	11684	321778	49537
thymus - h		27						1202	0	47	23	8191	4825	1638	11408	85005
HPAEC		28				28		306	0	0	35	8358	0	0	0	8076
thyroid gland - h		29						806	0	158	0	5306	1800	556	8454	27800
RPTEC		30				30		188	0	19	88	4184	10744	84	0	8483
trachea - h		31						3411	0	79	0	8363	4192	1597	8586	34958
HMEC		32						0	0	33	188	4408	144	19	383	8798
colon - h		33						3081	0	62	307	7257	7343	1366	7384	36340
HCAEC		34						194	0	26	70	5751	6835	219	681	4988
Pancreas - h		35						570	0	0	0	6208	0	0	17	21419
lymph node - h		36						1518	0	196	0	5373	20884	112	9807	25025
Skeletal muscle - h		37						309	0	14	0	3413	0	31	0	2243
fetal liver - h		38						8035	0	0	0	6981	5072	134	0	23681
Heart - h		39						998	0	17	35	4065	10604	4	0	2701
thymus - h		40						100	0	0	97	4633	8751	0	0	28458
Duodenum - h		41						92	0	0	0	3050	0	0	0	2975
Fetal brain - h		42						11823	0	0	0	5869	8204	145	0	18626
Salivary gl. - h		43						0	0	0	407	5511	1477	0	0	16266
testis - h		44						1732	0	27	53	7444	19542	115	12733	22783
HT216-normal					365			671	0	0	0	301	0	0	0	
HT213-normal					363			0	0	0	0	295	0	32	0	482
HT157-normal					361			2198	0	0	47	1307	387	21	0	8462
Bev-13					356	356		5100	0	0	403	8850	2807	248	0	6825
Bev-12					354	354		8027	0	40	0	6406	346	316	330	2534
cerebellum - h					344			0	0	71	0	1862	487	88	380	8738
brain - h					342			0	0	0	0	1829	1178	0	208	7347
RPTEC					334	334		0	0	0	200	8040	117	0	0	0
lymph node - h					332			2714	0	0	0	4034	0	521	0	27615
h adult SMC 10/21/92 #17					330			0	0	0	328	4482	0	87	0	551
Fetal brain - h					328			3525	0	250	10	7086	29	603	4350	15417
HT388-normal					327			0	0	118	176	4857	0	0	42	408
thymus - h					326			2917	0	0	250	6583	0	625	547	78037
HT149 - normal					321			249	0	0	0	3458	0	0	0	7102
HEPM 3d untreated					320			1442	0	0	0	3821	0	0	0	3657
uterus - h					318			3628	0	213	0	6338	8643	0	0	66984
trachea - h					316			1424	0	29	184	6057	2227	167	5551	22075
thyroid gland - h					314			3800	0	229	175	3272	443	380	5468	68839
salivary gl. - h					311			0	0	64	0	5060	610	27	0	17721
prostate - h					308			236	0	0	0	5456	708	0	0	11078
pituitary gland - h					307			0	0	0	370	3428	0	66	205	5805
pancreas - h					305			0	0	34	250	6133	2283	58	822	22076
mammary gland - h					303			3840	0	262	33	5370	4075	0	0	37185
Bladder - h					302			1375	0	370	104	8051	1673	145	1017	7898
testis - h					298			8010	0	233	64	8600	12917	844	2097	97619
liver - h					297			3854	0	8	414	4872	0	44	1593	30392
Spleen - h					296			248	0	114	0	3615	3035	0	462	38430
spinal cord - h					294			0	0	84	0	5831	2045	304	843	36978
small intestine - h					292			221	0	86	0	2932	657	176	134	18375
skeletal muscle - h					290			13803	0	245	0	6290	631	58	824	48825
bone marrow - h					278			0	0	88	338	6448	196	0	395	8531
adrenal gland - h					277			189	0	0	0	4734	1192	6	1346	10127
HPAEC					275	275		0	0	41	181	3704	674	83	0	0
HT380-normal					268			0	0	7	0	3583	242	348	0	6225
HT362-normal					266			1297	0	0	118	3680	303	94	474	11174
Bev-11					239	239		0	0	180	0	7854	7092	0	1621	13792
Bev-8					235	235		83	0	154	8	4088	680	0	52	9082
HT372-normal					234			0	0	0	0	6155	542	568	0	2467
Bev-7					233	233		675	0	47	0	4956	0	0	0	6731
Bev-6					231	231		0	0	130	168	4138	2231	118	417	1492
Bev-2					229	229		0	0	80	169	3519	4880	152	0	6169
Bev-1					227	227		0	0	107	0	4155	717	0	0	4163
bladder - h					222			0	0	14	3	2450	0	83	0	8054
Heart - h					215			16777	0	0	124	5047	0	0	454	12723
stomach - h					214			1488	0	41	143	6036	1880	0	138	33040
fetal liver - h					213			0	0	90	78	3033	0	133	0	12002
placenta - h					212			1298	0	0	77	8011	1804	156	77	19058
HCAEC					211	211		107	0	0	0	5208	241	0	0	640
fetal brain - h					210			4482	0	173	0	5800	4194	160	691	18685
HMEC					208			38	0	11	0	2824	3235	38	586	316
Duodenum - h					205			5184	0	0	132	4247	0	0	0	3834
Skeletal muscle - h					203			1310	0	0	0	2630	0	110	0	278
Pancreas - h					201			752	0	29	0	3179	108	0	0	4188
testis - h					199			208	0	15	0	2830	6	20	0	12550
Salivary gl. - h					197			180	0	15	0	2207	18730	52	4298	22443
HEPM 3d TGFB1 ...					196			0	0	44	0	1367	174	62	23	1813
thymus - h					193			118	0	23	0	3008	565	77	0	24671
WI-38 72h					179			0	0	0	0	1150	0	0	480	70
lymph node - h					81			0	0	6	88	3620	855	0	0	8800
lung - h					59			1425	0	0	0	7982	1000	0	0	25022
kidney - h					57			685	0	0	0	4677	2940	74	388	22336
heart - h					55			242	0	64	0	3084	247	79	0	8323
fetal lung - h					53			0	0	0	0	1718	142	0	537	410
fetal liver - h					51			174	0	22	242	2821	381	0	197	7087
fetal kidney - h					49			0	0	96	0	3883	2158	0	91	12023
HELA-2h-031800				79				0	0	0	70	4570	826	0	0	37510
HELA-4h-031800				81				0	0	82	2280	4853	257	0	21	3414
HELA-6h-031800				83				143	0	48	0	6886	4607	0	200	1575
HELA-7h-031800				86				686	0	39	0	3814	0	0	237	9984
HELA-8h-031800				88				290	0	0	380	7318	835	0	0	3846
HELA-9h-031800				90				0	0	183	0	8783	707	663	0	6370
HELA-10h-031800				92				53	0	70	52	6402	731	43	0	28215
HELA-11h-031800				94				405	0	0	0	6657	0	239	0	1053
HELA-12h-031800				96				1639	0	98	0	4356	4121	72	0	1789
NCI-H322M				146				86	0	0	0	3197	579	0	5223	6625
NCI-H460				148				22	0	0	153	2164	60	143	1732	435
NCI-H522				150				0	0	30	0	1847	1853	194	708	2447
SNB-19				152				2072	0	0	347	2204	0	343	3370	2928
SNB-75				154				980	0	0	0	3623	1190	0	6096	5502
SF-268				156				0	0	42	247	1822	0	0	758	1822
SF-295				158				0	0	42	578	646	0	539	1114	0
CCRF-CEM				160				0	0	82	140	1720	1178	0	0	231
DU-145				162				0	0	43	0	1622	217	233	1036	1640
HCT 116				164				13264	0	0	0	1244	0	153	1606	4064

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - tu	Tumor cells	Normal	Endo	p53	SEQ 844 T	SEQ 45 AA	SEQ 47 AA	SEQ 48 AA	SEQ 49 AA	SEQ 51 IG	SEQ 52 AA	SEQ 54 CC	SEQ 55 CL
CaMa1				155				0	0	47	88	4012	0	184	258	5443
786-0				158				4017	0	0	912	7868	46	0	21543	20865
T-47D				169				0	0	70	212	4456	73	295	6531	7187
Ken-3				171				0	0	0	25	1645	278	6	0	261
CRL1441 RNA 8/30				181				0	0	0	682	1300	120	383	152	0
7811 untreated + DMxxx				183				0	0	31	6	867	0	1	212	410
KB poly A+				184				0	0	0	135	1853	24	52	211	7891
HOS poly A+				195				282	0	43	0	2437	0	84	84	3781
ACHN				196				0	0	0	6	2832	209	171	8142	3184
UACC-62				200				385	0	39	131	1268	0	0	1277	1373
MCF-7/ADR-RES				202				0	0	36	6	1357	700	0	1430	1020
UTOS (Mucoid) poly A+				204				0	0	171	22	0	0	0	0	8433
WISH (Collagen) poly A+				206				0	0	0	8	742	843	44	42	1191
466 module mRNA				208				5841	0	0	8	7137	0	0	0	8852
CCL137 RNA 3/21/88				218				0	0	80	141	1184	3	100	0	827
WI-38 72h 0.5%FBS, 24h 10% FBS				219				0	0	0	0	2120	0	77	0	882
CRL1441 + TPA (24h) 8/30				220				0	0	0	224	885	83	0	0	0
Ken-1				221				688	0	0	16	1572	0	0	0	1257
Ken-2				223				0	0	0	0	2235	330	85	0	1961
Ken-4				225				736	0	172	0	2728	0	0	0	1331
HOP-92				241				126	0	0	3	1124	372	0	0	1758
MOLT-4				242				1229	0	0	0	4186	1258	0	2452	5150
EKVX				243				884	0	0	129	2740	130	217	2610	7440
HL-60				244				0	0	0	0	3652	507	614	1498	10317
NCI-H23				245				237	0	30	183	3528	1613	221	3362	6328
RPMI 8226				246				0	0	88	413	2687	7116	182	0	738
A549/ATCC				247				0	0	98	0	2959	0	0	0	1084
SR				248				0	0	0	0	2108	1910	33	281	2209
OVCAR-3				249				0	0	17	267	2481	0	45	153	544
HCT-15				250				1042	0	0	82	4008	1567	283	848	13841
OVCAR-4				251				63	0	83	13	557	0	7	880	847
UO-31				252				347	0	0	86	814	0	0	483	1047
OVCAR-5				253				0	0	89	722	6152	0	362	4788	6832
SN12C				254				811	0	0	0	3554	2301	0	10456	8666
OVCAR-8				255				322	0	0	13	3581	872	0	2102	1742
LOX IMVI				256				0	0	77	343	8201	4980	283	2950	8100
IGROV1				257				884	0	0	84	3889	571	3	2367	3537
SK-MEL-2				258				0	0	115	0	2345	491	338	1374	2004
SK-OV-3				259				0	0	0	0	1166	0	164	1459	1437
SK-MEL-5				260				0	0	0	472	1328	198	0	198	1486
SF-539				261				1273	0	108	458	6873	2291	0	7414	2589
SK-MEL-28				262				857	0	6	0	3780	861	0	2858	2053
X-867				263				157	0	86	31	8148	4336	216	2537	1782
UACC-257				264				606	0	0	0	2881	0	42	0	1280
M14				265				0	0	74	0	877	151	181	0	1458
MCF7				267				5520	0	0	26	8238	0	0	17404	29802
MDA-MB-435				268				0	0	60	227	1824	0	0	744	1343
HT279				270				1743	0	0	0	1565	2580	67	0	2984
MDA-N				271				0	0	17	0	4127	0	293	1252	2025
Y79 poly A+				273				8005	0	137	0	7232	1809	43	858	18372
XOXOS poly A+				288				2709	0	18	260	3265	32	284	579	8284
HT836 24h TPA RNA 8/23				309				0	0	10	0	2952	546	171	86	6576
HELA-EXP-031800				313				0	0	19	49	2177	949	24	0	10940
HT1536 8h RNA				322				639	0	0	189	4154	606	428	773	4214
HT347				323				442	0	5	0	2448	3812	0	169	58352
458 module RNA				324				2290	0	55	0	3454	0	11	761	1101
NCI-H226				336				0	0	0	38	2566	0	100	0	1149
HOP-62				337				0	0	0	357	3132	301	181	5222	2879
MDA-MB-231				338				7980	0	22	0	8113	4565	0	8554	26831
U251				339				10346	0	86	0	11559	18310	202	141693	38706
PT cells poly A+				340				0	0	0	0	1865	0	0	2461	2005
PC-3				341				0	0	0	227	3670	708	83	584	818
HCC-2998				343				31	0	0	0	2169	0	138	0	1570
SW-620				345				0	0	72	83	2072	0	106	36	0
HT192				346				679	0	60	25	4300	508	0	3475	19731
COLO 205				347				0	0	28	45	703	888	0	0	0
HT218				348				4211	0	0	0	1703	0	0	0	1056
KM-12				349				0	0	44	137	1724	842	102	0	1130
HT151				350				0	0	30	202	3787	1503	299	0	8776
A498				351				7848	0	0	184	1948	0	200	0	0
HT383				352				295	0	0	0	6001	0	0	0	18131
RXF 393				353				0	0	114	0	2570	0	0	0	775
TK-10				356				5344	0	0	0	7058	2225	0	3098	17089
Malme-3M				357				2845	0	0	0	28180	16670	313	37531	7453
Hs 578T				358				0	0	0	0	1858	0	0	996	1109
HT213			50					0	0	162	0	19822	1275	37	0	4385
HT208			52					195	0	197	0	6482	437	0	429	48848
HT139			54					0	0	0	31	3241	0	0	0	2708
HT155			56					0	0	114	0	3081	0	0	0	12179
HT163			58					337	0	35	28	3238	588	0	0	348
HT170			60					0	0	28	0	8032	0	0	0	12650
HT172			62					0	0	5	0	4071	0	94	104	2202
HT138			63					1302	0	0	0	3571	121	0	0	25749
HT178			64					0	0	0	291	5024	0	0	0	2901
HT154			65					1835	0	0	0	8175	1983	0	0	1773
HT140			66					0	0	73	0	4846	0	0	0	2924
HT168			67					0	0	0	0	884	24	45	243	1369
HT189			68					0	0	28	5	4352	0	440	0	3840
HT143			69					5	0	0	1176	2024	0	57	0	986
HT190			70					2869	0	61	0	4240	876	150	634	4445
HT145			71					360	0	0	0	5818	0	0	0	3695
HT227			72					0	0	30	114	4036	0	0	0	4727
HT302			73					420	0	0	133	8415	97	32	419	8164
HT314			74					429	0	0	0	4709	6214	0	0	5832
HT317			76					543	0	27	0	9318	2871	0	0	20250
Medulloblastoma #425 11/8			77					295	0	33	320	3198	575	220	287	2212
HT323			78					60	0	110	0	6528	2804	197	0	6220
HT327			80					0	0	128	0	3771	1776	60	14	2370
HT335			82					0	0	71	0	4430	11073	0	422	17130
HT146			85					432	0	120	0	1141	0	419	0	364
HT348			87					0	0	0	0	5314	18455	0	304	21360
HT311			170					368	0	28	0	3141	4853	256	0	5243
HT388			185					0	0	186	0	3280	0	229	0	3166
HT140			187					0	0	0	0	812	0	0	0	305
HT281			189					0	0	244	0	2857	1134	0	0	947
HT372			191					0	0	65	342	3358	203	247	0	451
TCGP			207					0	0	0	212	2836	494	0	611	1517
HT180			218					131	0	0	0	801	0	202	429	2230
HT307			217					0	0	115	0	1315	0	0	0	4418
HT369			224					0	0	45	15	3538	0	50	827	3309
HT370			226					1627	0	22	0	2562	44	134	644	11856
HT371			228					0	0	58	27	4211	0	0	281	8810
HT377			230					405	0	23	0	3752	779	292	0	18006
HT382			236					240	0	28	0	3820	408	0	627	7060
neuroblastoma RNA			281					0	0	0	887	0	0	0	0	0
HT334			298					0	0	32	0	4472	0	0	0	33016
HT338			301					0	0	0	3	2010	0	202	0	8382
HT392			315					544	0	0	71	2188	0	0	0	2010
HT394			317					0	0	0	102	2127	10712	3	9	9879
HT312			319					2077	0	0	108	2504	65	0	60	8512
HT162			325					0	0	10	0	1411	0	193	0	0
HT386			354					0	0	0	0	5212	295	0	182	4313
HT157			360					785	0	5	330	3318	426	0	374	12146
T-47D	163							510	0	0	0	4107	384	253	18835	8109
MDA-N	161							228	0	49	0	4806	0	336	132869	7574
MDA-MB-435	159							1148	0	68	130	5389	818	809	74036	5480
MDA-MB-231	157							3004	0	0	103	4223	381	200	141	8901

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - fx	Tumor cells	Normal	Endo	p53	SEQ 644 T	SEQ 45 AA	SEQ 47 AA	SEQ 48 AA	SEQ 49 AA	SEQ 51 NA	SEQ 52 AA	SEQ 54 CC	SEQ 55 CL
Hs 578T	155							4159	0	64	0	4775	0	670	1535	18385
MCF-7/ADR-RES	153							0	0	0	188	3752	0	110	1847	4538
MCF7	151							3033	0	181	0	7051	0	1002	0	27225
M14	148							0	0	150	0	3887	1881	802	0	8825
UACC-257	147							0	0	0	0	6335	586	0	813	14836
UACC-62	145							0	0	47	45	3306	319	64	1253	4501
SK-MEL-28	144							885	0	191	0	4298	130	22	96	6386
UO-31	143							755	0	0	0	6134	1914	426	0	5096
SK-MEL-5	142							806	0	14	0	4762	579	464	1913	6211
KM-12	141							1080	0	0	29	3880	299	437	868	1796
SK-MEL-2	140							0	0	4	0	3863	388	177	1587	12058
HCT-15	139							0	0	0	0	6167	0	386	370	16881
Malme-3M	138							1858	0	0	0	4947	25	311	1067	6770
COLO 205	137							2152	0	222	338	5649	0	0	0	5236
LOX IMVI	136							6430	0	0	131	5835	885	93	0	11410
SW-620	135							1038	0	37	0	3684	1187	384	858	3486
TK-10	134							1885	0	0	18	3828	1883	344	895	11184
HCT 116	133							519	0	107	104	3803	1058	150	0	4867
786-0	132							2701	0	7	118	3530	0	370	374	8085
HCC-2998	131							1371	0	0	0	6332	787	261	770	2845
ACHN	130							0	0	0	104	4598	627	102	820	8037
PC-3	129							0	0	0	0	3859	818	250	246	5809
RXF 393	128							3345	0	11	212	3357	0	368	982	19587
DU-145	127							456	0	0	83	2437	231	91	0	2441
Caki-1	126							0	0	132	180	4822	0	285	487	7704
SR	125							1045	0	2	0	3578	0	0	629	7915
A498	124							2368	0	126	305	4481	0	732	4011	12101
RPMI 8226	123							0	0	0	84	3852	1414	102	8477	5650
SN12C	122							0	0	0	258	4346	1762	359	1146	10454
HL-60	121							0	0	0	144	3536	0	203	0	7486
MOLT-4	120							581	0	24	0	3217	559	83	3283	4857
OVCAR-5	119							575	0	56	30	4828	0	85	4365	7868
K-562	118							0	0	0	0	7270	0	372	2107	2543
OVCAR-4	117							1705	0	0	0	8408	2352	302	4352	12924
CCRF-CEM	116							518	0	70	0	3041	150	1813	852	14584
OVCAR-3	115							2335	0	86	0	3837	0	180	281	5529
SF-539	114							841	0	2	0	3003	813	0	183	4097
HOP-62	113							527	0	0	186	3830	208	25	911	14232
SF-295	112							678	0	0	210	8431	2145	397	1058	10018
A549/ATCC	111							1174	0	0	193	8631	1777	654	1209	11839
SF-268	110							863	0	0	112	2881	432	102	1883	5008
NCI-H522	109							0	0	21	0	5351	1071	403	863	6165
U251	108							1687	0	0	474	4687	640	331	1215	7924
NCI-H460	107							294	0	221	41	4589	651	345	0	8432
SNB-75	106							883	0	76	3	2867	633	300	0	1015
NCI-H322M	105							0	0	0	28	2880	134	348	0	8695
SNB-19	104							20	0	83	0	3171	1079	491	2088	4580
NCI-H226	103							4486	0	19	0	7057	1881	244	1819	7164
SK-OV-3	102							842	0	58	0	3732	2018	625	0	11044
NCI-H23	101							200	0	142	0	3780	1389	492	1750	6447
IGROV1	100							0	0	0	0	4198	1010	788	0	4586
EKVX	99							783	0	14	187	3052	0	445	38	8847
OVCAR-8	98							0	0	72	285	3056	79	46	1511	2451
HOP-92	97							0	0	0	108	3660	1247	54	446	4634
h fibroblasts 3/31/92 #12	48							1168	0	123	0	3077	1635	88	1338	2848
h adult SMC 10/21/92 #17	47							2238	0	112	0	4184	0	86	742	4832
h keratinocytes 3/25/92 #10	46							1043	0	0	329	3112	734	278	0	2214
TCGP	28							0	0	115	0	3362	7036	256	211570	3115
A549 - 1							wt	487	48	37	0	0	0	0	0	0
A549 - 3							wt	317	106	0	0	0	0	0	0	0
A549 - 4							wt	0	28	153	0	0	0	0	0	0
A549 - 5							wt	321	109	62	0	0	0	0	0	0
A549 - 7							wt	0	238	48	0	0	0	0	0	0
EKVX - 1							mutant	5881	2138	285	0	0	0	0	0	0
EKVX - 4							mutant	2147	641	0	0	0	0	0	0	0
EKVX - 3							mutant	2885	0	480	0	0	0	0	0	0
EKVX - 5							mutant	1030	0	0	0	0	0	0	0	0
EKVX - 7							mutant	0	1823	0	0	0	0	0	0	0
MCF-7 - 1							wt	0	0	0	0	0	0	0	0	0
MCF-7 - 3							wt	403	0	46	0	0	0	0	0	0
MCF-7 - 4							wt	150	0	115	0	0	0	0	0	0
MCF-7 - 5							wt	3124	0	0	0	0	0	0	0	0
MCF-7 - 7							wt	848	0	0	0	0	0	0	0	0
ADR-RES - 1							mutant	0	1818	135	0	0	0	0	0	0
ADR-RES - 3							mutant	30924	0	290	0	0	0	0	0	0
ADR-RES - 4							mutant	4757	279	108	0	0	0	0	0	0
ADR-RES - 6							mutant	635	572	84	0	0	0	0	0	0
ADR-RES - 7							mutant	748	381	11	0	0	0	0	0	0
WI 38 - 1							wt	2518	51	178	0	0	0	0	0	0
WI 38 - 3							wt	1849	0	80	0	0	0	0	0	0
WI 38 - 4							wt	0	0	0	0	0	0	0	0	0
WI 38 - 5							wt	3008	0	37	0	0	0	0	0	0
WI 38 - 7							wt	812	0	43	0	0	0	0	0	0
HeLa - 1							HPV E6	0	385	7	0	0	0	0	0	0
HeLa - 3							HPV E6	652	0	30	0	0	0	0	0	0
HeLa - 4							HPV E6	848	0	115	0	0	0	0	0	0
HeLa - 5							HPV E6	2547	788	172	0	0	0	0	0	0
HeLa - 7							HPV E6	429	850	7	0	0	0	0	0	0
H1299 - 1							mutant	0	0	27	0	0	0	0	0	0
H1299 - 3							mutant	1148	0	193	0	0	0	0	0	0
H1299 - 4							mutant	1155	0	36	0	0	0	0	0	0
H1299 - 5							mutant	819	83	106	0	0	0	0	0	0
H1299 - 7							mutant	0	0	71	0	0	0	0	0	0
A549 - 2							wt	751	381	0	0	0	0	0	0	0
EKVX - 2							mutant	21741	2830	206	0	0	0	0	0	0
HCT-116 - 1							wt	649	0	206	0	0	0	0	0	0
HCT-116 - 2							wt	8208	882	430	0	0	0	0	0	0
HT29 - 2							mutant	407	255	66	0	0	0	0	0	0
SF539 - 1							wt	1107	281	0	0	0	0	0	0	0
SF539 - 2							wt	623	202	71	0	0	0	0	0	0
SF-268-1							mutant	9784	184	139	0	0	0	0	0	0
SF-268-2							mutant	11614	4311	265	0	0	0	0	0	0
OVCAR-4 - 1							wt	2880	701	0	0	0	0	0	0	0
OVCAR-4 - 2							wt	0	0	0	0	0	0	0	0	0
OVCAR-5 - 1							mutant	705	0	0	0	0	0	0	0	0
OVCAR-5 - 2							mutant	387	448	0	0	0	0	0	0	0
MCF-7 - 2							wt	2184	0	43	0	0	0	0	0	0
ADR-RES - 2							mutant	418	747	86	0	0	0	0	0	0
HeLa - 2							HPV E6	2741	0	53	0	0	0	0	0	0
SW480 - 1							mutant	883	1075	209	0	0	0	0	0	0
SW480 - 2							mutant	613	718	50	0	0	0	0	0	0
H1299 - 2							mutant	322	571	8	0	0	0	0	0	0
C33A - 1							mutant	318	0	57	0	0	0	0	0	0
C33A - 2							mutant	6480	0	75	0	0	0	0	0	0
U2OS - 1							mutant	8301	1141	0	0	0	0	0	0	0
U2OS - 2							mutant	3542	1288	0	0	0	0	0	0	0
Hs68 - 1							wt	2218	164	46	0	0	0	0	0	0
Hs68 - 2							wt	4302	734	18	0	0	0	0	0	0
WI 38 - 2							wt	0	631	21	0	0	0	0	0	0
Mithel - 1								813	0	72	0	0	0	0	0	0
Mithel - 2								310	0	2768	0	0	0	0	0	0
Mithel - 3								60334	0	0	0	0	0	0	0	0
Mithel - 4								64782	808	0	0	0	0	0	0	0
Mithel - 5								6016	0	0	0	0	0	0	0	0
Mithel - 6								8098	738	311	0	0	0	0	0	0
Mithel - 8								2854	0	37	0	0	0	0	0	0
Mithel - 9								2068	0	0	0	0	0	0	0	0

Table 3 (cont'd)

Tissue	Tumor-cyst	Normal-cyst	Tumor - tis	Tumor cells	Normal	Endoc	p53	SEQ 56 AA	SEQ 57 W	SEQ 60 AA	SEQ 63 NE	SEQ 66 CA	SEQ 68 HI	SEQ 116 R	SEQ 73 HI	SEQ 75 A
Caki-1				166				863	4675	157	1028	872	1529	1954	17265	29405
786-0				168				533	8526	227	878	272	8850	5204	82251	95578
T-47D				169				6805	8618	0	1074	352	580	2801	19722	38831
Ken-3				171				0	1853	0	234	13	137	1787	138	37872
CRL 1441 RNA 8/30				181				276	3104	0	24	0	0	1858	0	13078
781T untreated + DHmm				183				197	1800	0	62	0	0	843	230	14562
KB poly A+				194				0	6034	0	108	0	1498	1616	668	31818
HOS poly A+				196				297	3205	8277	0	0	528	2915	868	62778
ACHN				198				0	6583	0	358	0	1156	4807	14587	28142
UACC-62				200				1482	8083	0	212	0	475	2225	2825	17274
MCF-7/ADR-RES				202				185	2228	765	0	11	381	1444	2582	14807
UTOS (bloody) poly A+				204				0	7612	0	104	0	0	1028	617	9607
WISH (Collagen) poly A+				206				150	0	0	84	189	893	579	725	11442
458 medulla mRNA				208				0	18176	0	623	53	0	2362	2915	60583
CCL137 RNA 3/21/88				218				219	1868	0	298	0	381	1447	915	23844
WI-38 72h 0.5%FBS, 24h 10% FBS				219				271	3187	1198	0	34	403	2280	0	41474
CRL 1441 + TPA (24h) 8/30				220				0	5682	0	31	683	0	1066	63	98180
Ken-1				221				2280	2513	0	6	0	453	2919	154	45286
Ken-2				223				705	2806	0	115	0	302	2129	41	41277
Ken-4				225				521	4040	0	31	0	1303	2242	89	38345
HOP-62				241				0	2362	0	218	0	87	1773	13338	19084
MOLT-4				242				646	6364	702	493	461	2626	3182	30419	23872
EKVX				243				0	13083	0	328	73	3139	6467	108714	30253
HL-60				244				0	14211	606	23	4311	2402	3669	15908	30367
NCI-H23				245				850	13052	572	2945	167	3423	6364	85508	46201
RPMI 8226				246				0	1320	400	179	0	354	2272	18378	20669
A549/ATCC				247				80	3450	0	619	394	681	1981	2385	18871
SR				248				0	1814	383	0	23	344	2097	60201	17287
OVCAR-3				249				0	7307	0	214	120	1070	2434	7704	20878
HCT-15				250				0	10765	590	1456	0	3530	4642	106630	27562
OVCAR-4				251				223	314	1330	0	189	473	805	1401	7613
UO-31				252				372	3404	0	0	6	143	547	1109	6300
OVCAR-5				253				2585	9439	1911	625	52	1738	3048	12208	24504
SN12C				254				0	5112	504	176	108	3335	2875	26805	16317
OVCAR-8				255				0	3508	868	733	0	1122	1350	35633	14140
LOX IMVI				256				823	17298	405	608	81	6603	5263	30147	30646
IGROV1				257				1194	8352	758	716	88	2032	3644	20934	31704
SK-MEL-2				258				0	5305	0	19	0	0	863	4982	15816
SK-OV-3				259				85	3527	0	200	0	1050	3782	8318	17004
SK-MEL-5				260				135	3911	0	49	103	1340	1148	3811	13542
SF-539				261				3832	12225	0	864	150	7673	6550	62279	61506
SK-MEL-28				262				0	7037	0	384	0	1713	1581	9611	34907
K-562				263				867	8200	1949	1685	99	8059	4578	196694	61730
UACC-257				264				0	6275	0	408	0	1590	2368	3496	29095
M14				265				0	2838	0	0	214	804	918	1178	17725
MCF7				267				829	16845	820	986	604	4688	8019	79777	80830
MDA-MB-435				268				144	6376	477	643	0	868	1857	1148	24187
HT270				270				14	4493	0	0	0	881	2525	281	41491
MDA-N				271				276	7085	0	354	92	1290	1836	5866	18806
Y79 poly A+				273				0	6894	0	379	0	3785	6025	24854	77881
KHOS poly A+				290				0	20758	17445	371	238	6785	4275	38066	78881
HTB38 24h TPA RNA 8/23				300				783	3881	0	1456	0	2298	2492	221	31917
HELA-EXP-031890				313				834	1812	0	247	0	1590	2048	4161	30794
HTB38 0h RNA				322				1461	24464	0	0	989	3512	6180	3044	81684
HT347				323				404	4586	0	0	0	2938	3484	15822	40401
458 medulla RNA				324				1327	40573	0	0	748	890	4386	476	69088
NCI-H226				336				672	6101	721	345	0	1515	2111	2329	37119
HOP-62				337				0	15366	0	908	78	2608	1717	38496	71036
MDA-MB-231				338				1105	65815	1217	9728	1217	25352	13718	259035	103178
U251				339				132	80374	1171	18256	382	76758	33680	2025349	111822
PT cells poly A+				340				483	1482	0	467	0	1987	2005	45862	18256
PC-3				341				177	13879	62	362	2330	6703	8884	40554	71885
HCC-2998				343				92	8206	0	652	889	1782	2289	23873	21576
SW-620				345				25	7776	0	621	200	1251	2046	10731	24715
HT192				346				1001	7290	408	182	0	1412	5254	2082	65025
COLO 205				347				162	8047	0	306	0	0	689	1304	8915
HT218				348				440	4819	0	77	158	0	1385	391	30049
KM12				349				49	11952	0	406	0	891	1115	34049	17488
HT151				350				138	6054	0	0	0	723	3737	497	45600
A498				351				797	20305	0	401	1584	1030	2626	4743	30376
HT383				352				728	15335	57	0	0	2602	4435	5637	60853
RXF 393				353				0	8872	0	114	73	348	2720	7230	24306
TK-10				355				738	78686	684	3780	1673	23029	12524	129780	71952
Malme-3M				357				2111	93276	13897	38206	2444	66479	34072	201421	150808
Hs 578T				359				0	9184	0	68	82	2391	2875	6581	48092
HT213			50					0	6740	47	0	0	878	1700	28	57671
HT288			52					179	8067	0	0	272	783	2581	7541	84143
HT130			54					821	6343	0	4	635	0	1926	276	65037
HT155			56					0	6880	0	281	632	2304	2131	2121	61017
HT163			58					1082	1302	364	0	253	281	1594	340	81243
HT170			60					37	15071	0	252	0	1862	4234	15427	83038
HT172			62					0	2376	0	0	17	284	975	0	46345
HT138			63					0	2623	0	0	43	787	1070	4034	45881
HT178			64					31	3185	0	0	145	348	974	800	51853
HT154			65					0	1277	2384	0	44	108	1138	0	52719
HT188			66					278	2507	0	58	0	862	885	197	43129
HT160			67					427	4940	0	0	229	289	456	1230	28200
HT189			68					69	4098	288	122	0	346	1043	3366	79481
HT143			69					2067	346	0	0	0	161	828	42	38405
HT199			70					0	6719	984	58	0	0	1854	0	69009
HT145			71					1053	3301	639	0	74	3282	1833	230	58087
HT227			72					0	5705	0	83	183	2486	1928	257	65548
HT302			73					0	18129	0	438	112	0	2801	685	84861
HT214			74					0	10943	138	0	41	279	1786	1198	51087
HT317			76					275	25782	0	2002	651	98	6151	6403	100831
Medulloblastoma 8425 11/8			77					0	3161	0	128	250	0	3011	615	99514
HT323			78					0	7907	0	1120	58	335	3764	1841	107547
HT327			80					224	8360	0	267	41	934	1737	888	53009
HT336			82					0	7044	112	1	201	2495	2254	813	70437
HT146			85					2097	790	546	142	0	0	898	981	12152
HT348			87					2368	8054	1312	369	203	3809	1570	2273	40849
HT311			170					1002	3027	0	0	0	609	3081	1158	57188
HT308			185					2942	11424	803	258	0	0	1950	614	31322
HT140			187					0	2198	0	317	70	484	1007	0	19444
HT281			189					0	7338	0	37	0	0	1916	0	41150
HT372			191					641	2808	0	130	104	0	1932	708	89062
TCGP			207					196	3446	0	114	33	139	1578	0	18184
HT160			216					0	1990	383	0	107	749	937	0	34541
HT307			217					0	3175	0	0	210	1003	1067	731	21629
HT309			224					0	12133	0	125	177	558	2374	876	40414
HT370			226					64	2565	0	0	180	1017	1956	0	27470
HT371			228					867	4002	0	0	0	1523	2322	1349	34833
HT377			230					0	3241	0	56	0	684	1678	443	25063
HT382			236					116	5719	518	0	0	3205	2839	1024	43216
neuroblastoma RNA			281					0	10149	0	0	295	155	803	0	9483
HT334			299					0	20876	0	850	0	5887	8479	14342	67294
HT338			301					139	13101	313	0	0	899	2548	2090	34682
HT392			315					48	4032	0	0	48	1315	1461	6518	38163
HT394			317					1373	6204	1881	249	21	1009	2951	11044	48292
HT312			319					270	3848	0	5567	0	840	2695	0	35234
HT162			325					357	2017	0	306	0	0	1241	965	22972
HT386			354					553	5137	0	0	6	1105	2121	3677	68581
HT157			360					0	19080	0	21	0	4818	4833	1407	140477
T-47D	163							3006	30724	5671	1575	2021	6944	1536	13760	45303
MDA-N	161							1387	29169	1029	1361	6862	17212	1169	8794	36475
MDA-MB-435	159							847	17967	3441	2565	5842	17246	1815	13089	33644
MDA-MB-231	157							576	50640	2818	2248	1727	42196	2891	10358	68995

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - fe	Tumor cells	Normal	Endos	p53	SEQ 56 AA	SEQ 57 W	SEQ 58 AA	SEQ 63 NE	SEQ 64 CA	SEQ 64 HH	SEQ 110 R	SEQ 73 HR	SEQ 78 AA
Hs 578T	155							0	41445	847	1806	3442	20751	2567	8386	55674
MCF-7/ADR-RES	153							2256	18577	3382	2918	488	22338	1862	3882	64013
MCF7	151							3886	38808	180	1500	2844	11886	3485	22510	81756
M14	149							778	16702	0	704	437	8271	3880	4071	68408
UACC-257	147							158	14876	1834	7208	183	8007	2195	17873	61725
UACC-62	145							800	8415	0	2946	4	6453	1568	4231	41268
SK-MEL-28	144							40	12812	4856	577	770	5176	1071	2980	58831
UO-31	143							448	8850	1716	634	98	14005	2232	3834	105691
SK-MEL-5	142							1182	27302	1994	1944	2909	13116	1215	8555	42911
KM12	141							325	5737	5512	104	0	1651	1317	64	48588
SK-MEL-2	140							1967	14486	3221	795	1827	7349	1575	7479	62671
HCT-15	139							740	12275	771	857	808	4827	2857	7421	71198
Malme-3M	138							1725	28340	2545	2981	2553	10072	2038	7321	42597
COLO 205	137							3484	9860	2705	438	1949	13401	1681	2407	98313
LOX IMVI	136							303	37237	202	3101	4339	32433	882	8051	33734
SW-620	135							630	8511	0	1807	1939	10151	1195	2788	38388
TK-10	134							845	8427	1317	1508	1062	23888	1771	11381	42220
HCT 116	133							1015	7308	0	148	413	11794	2013	1498	38586
786-0	132							886	8319	827	1162	947	28089	1670	7153	41600
HCC-2998	131							1700	9389	0	397	1115	8212	1984	3255	74506
ACHN	130							610	9938	1426	1253	845	21377	1468	7925	49258
PC-3	129							577	10302	0	33	809	14268	1450	3151	45670
RXF 393	128							1087	12023	1508	4327	377	20896	1884	13035	43831
DU-145	127							1200	8043	100	126	178	4862	2174	3858	46338
Caki-1	126							981	13976	861	2888	334	4806	1933	15823	42979
SR	125							0	9754	0	1096	357	1794	2308	4070	44877
A498	124							9313	18049	351	295	0	14129	2475	10968	49807
RPMI 8226	123							0	5461	0	1	112	580	3030	6708	65176
SN12C	122							0	17323	0	2502	134	6784	2447	10677	75056
HL-60	121							393	4211	641	118	240	1354	2057	2980	56854
MOLT-4	120							226	4406	2178	551	811	5501	1313	7213	70188
OVCAR-5	119							839	10544	8273	2442	877	12121	968	32826	40584
K-562	118							1044	4812	2234	380	598	6276	1771	8526	56039
OVCAR-4	117							2174	13967	4166	240	1640	14315	1408	21344	44825
CCRF-CEM	116							1509	31473	868	4834	891	4841	1458	7738	56657
OVCAR-3	115							555	6082	2368	1091	179	3448	1421	25044	42501
SF-539	114							1113	7238	0	668	834	10017	1247	4855	41075
HOP-62	113							0	6296	2082	8258	887	16786	698	24991	25387
SF-295	112							200	7764	204	1051	2778	8791	878	16864	47319
A549/ATCC	111							1371	14738	0	3249	2645	18298	1303	66894	51984
SF-268	110							1333	11509	0	2309	1054	18314	1000	8620	32506
NCI-H522	109							335	10129	1948	3365	1263	17062	2084	15285	42496
U251	108							1614	8600	2187	374	1811	29319	2225	10568	53640
NCI-H460	107							1091	11864	2329	8708	870	15224	1506	32438	40200
SNB-75	106							252	7303	127	539	25	20030	1080	1580	40388
NCI-H322M	105							3883	13987	3336	3512	473	11090	2186	20863	68284
SNB-19	104							0	7540	1418	888	329	14888	2884	9129	52719
NCI-H226	103							822	19491	1502	2982	372	7883	4474	13486	103492
SK-OV-3	102							0	10957	871	740	482	6154	2758	8202	51778
NCI-H23	101							872	12336	1798	6027	716	1791	3129	30387	54491
IGROV1	100							672	10901	3057	295	865	3356	3272	7830	55870
EKVX	99							0	8485	898	3398	217	4005	2078	21182	42470
OVCAR-8	98							347	7233	2437	897	574	8534	1949	4824	48858
HOP-92	97							474	12057	2367	2697	792	12382	2385	31301	30830
h fibroblasts 3/31/92 #12	48							1505	4800	0	3536	215	24750	1814	6365	82900
h adult SMC 10/21/92 #17	47							37	3414	0	477	60	26787	1464	16148	75029
h keratinocytes 2/25/92 #10	46							4753	10827	0	2520	7014	16844	1176	5161	73676
TCOP	28							889	12493	55	30916	791	8829	2429	9414	61036
A549 - 1							wt	0	2806	867	13218	0	1576	331	14898	19283
A549 - 3							wt	0	3582	0	363	0	317	314	3847	10191
A549 - 4							wt	0	3769	0	1896	0	523	157	11425	16682
A549 - 5							wt	0	4433	0	2173	0	486	242	15448	13087
A549 - 7							wt	0	3415	0	879	0	1083	281	12240	20201
EKVX - 1							mutant	0	7819	219	10405	0	2358	802	27454	14000
EKVX - 4							mutant	0	6808	0	7440	0	2883	1003	78154	19451
EKVX - 3							mutant	0	4185	0	6533	0	1342	397	7118	16820
EKVX - 5							mutant	0	2062	442	1504	0	2086	781	19082	27288
EKVX - 7							mutant	0	3306	1404	40	0	1233	1385	5245	36816
MCF-7 - 1							wt	0	3465	0	3855	0	306	207	11222	19811
MCF-7 - 3							wt	0	4324	0	2219	0	177	321	15876	14247
MCF-7 - 4							wt	0	2871	982	297	0	707	191	16884	15080
MCF-7 - 5							wt	0	4849	0	312	0	0	60	24367	14480
MCF-7 - 7							wt	0	2815	0	341	0	388	118	9134	14350
ADR-RES - 1							mutant	0	13125	0	4485	0	1135	860	48482	43329
ADR-RES - 3							mutant	0	7896	206	1643	0	583	715	8378	15627
ADR-RES - 4							mutant	0	3613	612	79	0	1047	635	10884	22984
ADR-RES - 6							mutant	0	1814	0	5874	0	572	116	18216	11986
ADR-RES - 7							mutant	0	5007	0	1519	0	635	310	4944	17865
WI 38 - 1							wt	0	19054	0	1743	0	480	818	23088	31030
WI 38 - 3							wt	0	8068	317	2832	0	2774	777	23708	13274
WI 38 - 4							wt	0	6701	0	184	0	2280	795	25508	14200
WI 38 - 5							wt	0	8553	0	1987	0	1877	750	6030	17160
WI 38 - 7							wt	0	6181	461	897	0	988	1033	12862	13392
HeLa - 1							HPV E6	0	2972	1049	125	0	783	381	8680	13286
HeLa - 3							HPV E6	0	6135	203	2588	0	206	308	18037	12311
HeLa - 4							HPV E6	0	1902	787	1330	0	283	619	11306	10796
HeLa - 5							HPV E6	0	6774	348	2858	0	2129	834	36267	18512
HeLa - 7							HPV E6	0	8057	0	1004	0	1873	860	16576	19187
H1299 - 1							mutant	0	6732	0	1878	0	488	789	13309	13626
H1299 - 3							mutant	0	7988	0	3638	0	581	947	4846	12467
H1299 - 4							mutant	0	11579	0	3803	0	1907	567	32308	13225
H1299 - 5							mutant	0	3290	0	3068	0	1547	552	6675	17847
H1299 - 7							mutant	0	6749	57	2847	0	866	234	13578	13794
A549 - 2							wt	0	1778	0	7923	0	369	470	7747	14837
EKVX - 2							mutant	0	4310	0	1255	0	866	386	16174	16568
HCT-116 - 1							wt	0	802	0	1151	0	1687	1682	13342	61832
HCT-116 - 2							wt	0	16450	0	3292	0	5168	886	86458	12691
HT29 - 2							mutant	0	1416	606	2202	0	1581	561	28757	15526
SF539 - 1							wt	0	7391	187	102	0	774	285	5026	16647
SF539 - 2							wt	0	10800	0	513	0	0	247	10468	14833
SF-268 - 1							mutant	0	11769	0	1105	0	3283	1120	18384	18521
SF-268 - 2							mutant	0	6717	0	10047	0	2007	1179	22525	14395
OVCAR-4 - 1							wt	0	2988	705	1397	0	1685	675	9858	24261
OVCAR-4 - 2							wt	0	4382	688	3277	0	1872	583	23042	58463
OVCAR-5 - 1							mutant	0	3130	350	338	0	851	269	12736	11007
OVCAR-5 - 2							mutant	0	2975	0	829	0	368	278	6086	11598
MCF-7 - 2							wt	0	2290	291	4687	0	630	122	7463	11766
ADR-RES - 2							mutant	0	6143	0	2038	0	814	854	8841	10902
HeLa - 2							HPV E6	0	5468	3367	5308	0	4474	842	40273	13088
SW480 - 1							mutant	0	6848	33	2511	0	1590	1182	44883	23143
SW480 - 2							mutant	0	2850	0	3398	0	915	638	28976	19496
H1299 - 2							mutant	0	7012	0	1635	0	1502	864	23857	24481
C33A - 1							mutant	0	5679	0	0	0	570	230	47320	12514
C33A - 2							mutant	0	3255	804	426	0	878	208	8221	8813
U2OS - 1							mutant	0	10292	0	5780	0	2118	1980	62566	31158
U2OS - 2							mutant	0	5298	748	8373	0	3282	1051	56322	27447
Hs68 - 1							wt	0	7177	447	1091	0	1155	416	11483	11084
Hs68 - 2							wt	0	8434	403	2864	0	3356	746	8708	17887
WI 38 - 2							wt	0	13825	488	1083	0	1883	732	11794	15250
[illegible] - 1								0	8886	0	2718	0	1113	399	12501	14913
[illegible] - 2								0	12729	0	128	0	1618	386	13386	14118
[illegible] - 3								0	12108	0	255	0	686	406	44133	14628
[illegible] - 4								0	32887	0	0	0	1087	540	4312	20874
[illegible] - 5								0	8005	0	0	0	0	404	0	11982
[illegible] - 6								0	13524	0	0	0	3368	1256	8031	21144
[illegible] - 8								0	15247	0	5682	0	3784	1358	20629	23061
[illegible] - 9								0	12139	0	309	0	2077	1090	4831	20644

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor-ts	Tumor cells	Normal	Endos	p53	SEQ 56 AA	SEQ 57 W	SEQ 60 AA	SEQ 63 NF	SEQ 64 CA	SEQ 68 NB	SEQ 110 R	SEQ 73 NR	SEQ 78 AA
DuPang-7								0	80728	3134	2300	0	2775	1021	16539	11948
DuPang-8								0	35361	84	3297	0	2619	349	23678	14951
DuPang-9								0	29319	0	4208	0	4247	714	57757	12234
DuPang-11								0	40536	0	6022	0	3724	1086	49305	13176
DuPang-12								0	16274	0	1652	0	2614	892	56963	11807
DuPang-10								0	18015	0	1366	0	4278	801	34062	11401
DuPang-1								0	11738	0	21443	0	2076	1022	20201	22149
DuPang-2								0	8371	0	13705	0	1528	783	13252	18196
DuPang-3								0	6905	1171	85151	0	503	823	31807	25563
DuPang-4								0	4899	0	610	0	1746	630	20143	25155
DuPang-5								0	3723	0	219	0	1618	848	8831	13544
DuPang-6								0	38584	0	0	0	465	462	1929	8565
A549-8							wt	0	4018	637	1675	0	2780	308	19012	13833
EKVX-8							mutant	0	6749	0	5081	0	4381	803	24768	14160
HCT-116-7							wt	0	2945	697	80	0	812	478	8413	12963
HCT-116-8							wt	0	5165	3415	808	0	302	301	11432	16808
HT29-1							mutant	0	2474	0	1363	0	1494	451	25516	21737
HT29-7							mutant	0	3253	0	94	0	307	305	9185	13182
HT29-8							mutant	0	4333	0	2802	0	709	594	16207	19784
SF539-7							wt	0	8602	8	866	0	1074	1086	13408	17989
SF539-8							wt	0	6864	0	150	0	856	811	14376	16088
SF-268-7							mutant	0	6810	1806	708	8	1316	420	14248	15443
SF-268-8							mutant	0	8205	0	1884	0	2052	568	12101	14424
OVCAR-4-7							wt	0	1789	0	507	0	601	100	3378	14758
OVCAR-4-8							wt	0	8000	786	12121	0	3077	730	17308	16846
OVCAR-5-7							mutant	0	8291	0	1758	0	19	1300	20088	37871
OVCAR-5-8							mutant	0	3818	11046	46	0	2528	288	8074	10561
MCF-7-8							wt	0	4047	348	1309	0	542	451	15891	15873
ADR-RES-8							mutant	0	4033	465	2605	0	479	99	7975	12562
HeLa-8							HPV E6	0	4132	914	1078	0	1823	706	11483	19305
SW480-7							mutant	0	3941	659	846	0	1028	212	13765	11456
SW480-8							mutant	0	3695	386	1133	0	215	439	19827	10513
H1299-8							mutant	0	8441	8274	1442	0	987	460	8507	12989
C33A-7							mutant	0	8465	0	131	0	304	331	1068	11745
C33A-8							mutant	0	4384	0	456	0	1800	1423	8025	35058
U2OS-7							mutant	0	6463	309	863	0	1824	251	21545	18584
U2OS-8							mutant	0	4223	197	1921	0	2486	614	33498	11293
Hs68-7							wt	0	4235	17844	462	0	888	614	10835	18314
Hs68-8							wt	0	4536	0	1101	0	673	843	3568	17704
WI38-8							wt	0	6860	0	0	0	2256	800	7101	12515
456 module RNA								219	10478	0	4687	322	11543	2388	4332	123911
CRL1572 3P17(0)								0	1475	79	288	0	0	1482	968	33047
Bov-4						84		1399	7178	0	471	66	4171	2041	13126	60734
HT308								415	10978	399	192	228	1211	1604	86	51232
HT378								394	1670	0	48	43	970	1344	481	84508
HT365								2694	23778	1052	187	825	1005	3483	3271	119825
HT308								484	4382	0	0	197	1806	2514	7486	73363
Bov-3						173		142	2983	0	68	40	1453	2563	2512	47784
Bov-5						175		1326	807	0	54	0	63	1943	676	27812
Bov-9						177		0	1932	619	109	0	315	1821	763	37803
h keratinocytes 2/25/02 #10								0	8382	0	0	878	1031	1484	280	44367
Bov-10						237		1100	3331	811	95	31	1233	2631	1895	63644
HTB10								0	6058	288	827	0	604	5317	197	84103
h fibroblasts 3/21/02 #12								165	4732	0	30	9	1843	2487	119	83251
prostate, h								97	709	86	151	47	840	1829	0	71260
MNNG-OS poly A+								0	8978	1806	300	186	2523	2510	9344	68836
SA-OS (Moody) poly A+								688	31235	0	101	1871	2913	2963	3973	62966
MK poly A+								272	28863	0	36	1131	4200	3844	5141	46333
HCT-116-3							wt	0	2284	630	2801	0	808	457	8561	14135
HCT-116-4							wt	0	3670	177	639	0	388	241	10248	13244
HCT-116-5							wt	0	6838	209	724	0	477	389	13563	18473
HCT-116-6							wt	0	5158	1378	2077	0	383	483	11660	12955
A549-6							wt	0	777	0	42	0	988	315	2191	14884
HT29-3							mutant	0	3211	1117	2356	0	1884	511	18891	15622
EKVX-6							mutant	0	819	80	0	0	367	636	9048	16148
HT29-4							mutant	0	771	1454	876	0	988	409	13595	21159
HT29-5							mutant	0	3498	1303	4091	0	1393	1063	28245	27154
HT29-6							mutant	0	3158	811	2404	0	143	1080	29241	38150
OVCAR-4-3							wt	0	808	1624	4736	0	764	229	6102	12980
OVCAR-4-4							wt	0	3487	0	1105	0	385	88	11844	11188
OVCAR-4-5							wt	0	12820	1901	4206	0	807	375	8613	14135
OVCAR-4-6							wt	0	3819	1285	0	0	1030	84	20408	15714
SF539-3							wt	0	6954	177	706	0	920	188	8632	15368
SF539-4							wt	0	11231	435	204	0	413	194	14686	10833
SF539-5							wt	0	12548	386	489	0	642	352	4084	13677
SF539-6							wt	0	5756	0	0	0	2221	362	14823	20785
OVCAR-5-3							mutant	0	4326	296	1341	0	1507	27	8822	14804
OVCAR-5-4							mutant	0	3508	0	1061	0	843	488	8731	13868
OVCAR-5-6							mutant	0	2838	0	88	0	706	105	319	11271
ADR-RES-6							mutant	0	3371	328	1852	0	553	195	8837	10873
MCF-7-6							wt	0	3709	0	222	0	0	141	20634	15834
HeLa-6							HPV E6	0	8105	0	2138	0	1130	874	28925	22168
H1299-6							mutant	0	1457	70	10	0	1106	448	6018	16346
SW480-3							mutant	0	1242	0	5328	0	380	304	15616	14058
SW480-4							mutant	0	4798	0	3600	0	461	543	47025	14272
SW480-5							mutant	0	7067	582	6067	0	1519	684	37625	18105
SW480-6							mutant	0	4158	0	1304	0	0	205	38247	17087
C33A-3							mutant	0	4670	885	485	0	823	173	7118	8840
C33A-4							mutant	0	2983	0	331	0	869	635	6046	7717
C33A-5							mutant	0	4227	186	2982	0	1128	484	11376	13418
C33A-6							mutant	0	1901	0	0	0	467	666	8687	17506
Hs68-6							wt	0	5858	0	384	0	581	535	4849	13363
U2OS-3							mutant	0	6180	8849	13081	0	1440	473	84885	18092
U2OS-4							mutant	0	4268	2979	8586	0	819	580	38448	17859
U2OS-5							mutant	0	9188	4213	4061	0	1083	478	60416	21270
U2OS-6							mutant	0	9431	0	0	0	1983	389	39463	18157
WI38-6							wt	0	9068	837	868	0	1864	940	2095	12948
Hs68-3							wt	0	10577	10235	1233	0	2412	880	20817	13348
Hs68-4							wt	0	17277	1853	3075	0	2413	1902	29235	20590
SF-268-3							mutant	0	4453	0	2302	0	1910	482	9499	17460
SF-268-4							mutant	0	8837	760	11168	0	1348	925	16909	18347
SF-268-5							mutant	0	13125	0	2498	0	614	1137	27875	19868
SF-268-6							mutant	0	4068	0	0	0	369	406	2400	18754
DuPang-13								0	15808	0	36386	0	3019	852	32106	24789
Mitchell-20								0	15885	0	4210	0	2461	740	11291	20203
Mitchell-21								0	14060	0	7219	0	2419	777	19057	20805
Mitchell-22								0	13878	0	3119	0	2675	897	44815	21250
OVCAR-5-5							mutant	0	7248	1	5016	0	1167	823	16627	19178
Mitchell-10								0	6712	0	3909	0	2058	367	1837	7830
Mitchell-11								0	6270	0	4708	0	937	129	688	4771
Mitchell-12								0	10644	0	2680	0	2250	826	43027	19005
Mitchell-13								0	13881	0	893	0	1883	810	57512	17026
Mitchell-14								0	18818	0	1380	0	432	1229	21693	17484
Mitchell-15								0	10792	0	3885	0	934	958	20174	15732
Mitchell-16								0	7517	0	54	0	1777	710	18220	12001
Mitchell-17								0	9770	0	295	0	1223	679	1698	16522
Mitchell-18								0	13084	8	224	0	2444	1438	12986	21852
Mitchell-19								0	8691	0	0	0	1173	849	22262	14100

Table 3 (cont'd)

Tissue	Tumor-syn	Normal-syn	Tumor - 1o	Tumor cells	Normal	Endo	p53	SEQ 79 AA	SEQ 882s	SEQ 82 MU	SEQ 84 RS	SEQ 88 AA	SEQ 89 AA	SEQ 89 MS	SEQ 93 TS	SEQ 94 AA
adrenal gland - h		1						0	338	18727	28487	169725	3877	1388	305	13731
lymph node - h		2						0	180	25285	38356	133216	11022	818	281	22717
bone marrow - h		3						0	407	8824	25850	80880	6274	447	0	12523
mammary gland - h		4						0	0	4132	3261	30833	30	34	100	2064
brain - h		5						0	0	11468	8876	138486	8157	3530	61	12106
pancreas - h		6						0	530	8084	17022	100224	2001	1052	241	11580
cerebellum - h		7						0	336	18448	41680	84237	10828	4741	486	21132
pituitary gland - h		8						127	162	6620	82715	134453	8087	4401	29	11637
fetal brain - h		9						171	354	10859	23941	183430	3445	812	55	23358
placenta - h		10						717	388	10004	74254	187867	6384	358	2011	16851
fetal kidney - h		11						256	538	28118	24194	87526	6311	803	224	14839
prostate, h		12						51	68	11315	8847	222874	217	1870	74	11687
fetal liver - h		13						436	207	10229	8406	116434	1804	430	256	8614
salivary gl. - h		14						0	532	13840	7790	102290	8583	2036	75	9485
fetal lung - h		15						0	658	27774	19719	158848	8148	1076	177	13841
skeletal muscle - h		16						191	1989	164918	11019	184752	1936	22013	56	3341
heart - h		17						364	1084	115085	8506	82087	2290	6761	0	4512
small intestine - h		18						330	288	25312	14109	103840	3385	1228	48	7578
kidney - h		19						318	5	6142	18392	81581	3888	388	0	6650
spinal cord - h		20						85	340	7758	11094	84387	7363	877	41	3903
liver - h		21						372	254	4036	13651	165877	1734	304	500	2807
Spleen - h		22						78	286	8082	14889	95360	2294	345	333	4083
lung - h		23						178	642	18806	13532	88815	2203	337	183	5781
stomach - h		24						0	28	12942	12134	71122	1805	1227	8	3742
testis - h		25						0	373	21247	22043	193540	8854	855	882	28800
thymus - h		27						177	436	21278	27103	112750	3463	700	290	30798
HPAEC		28				28		0	128	5788	13178	104784	240	529	289	13138
thyroid gland - h		29						0	229	13848	8080	110349	7250	1484	322	10434
RPTEC		30				30		122	0	0	4221	115750	11	378	7	6048
trachea - h		31						8	438	15832	13708	86718	2751	1477	162	15045
HMEC		32						0	797	18746	6112	158864	1037	368	421	20117
uterus - h		33						105	1371	61570	11725	84358	3629	1884	81	10387
HCAEC		34						30	0	11102	3715	222808	280	320	0	6100
Pancreas - h		35						0	130	20503	3244	127701	2384	1026	0	7344
lymph node - h		36						0	104	7145	4841	17524	816	0	84	2563
Skeletal muscle - h		37						0	0	33826	1929	187218	302	813	0	3018
fetal liver - h		38						436	37	6637	8083	85098	411	0	0	8065
Heart - h		39						124	232	20525	4908	128875	629	23	333	4438
thymus, h		40						382	0	3423	14735	15106	423	168	0	4408
Duodenum - h		41						0	0	0	4472	83230	76	87	88	6253
Fetal brain - h		42						534	204	1307	18012	1837	1024	330	280	7758
Salivary gl. - h		43						4	178	4203	8535	110729	1547	56	187	3288
testis - h		44						441	218	8677	17243	33097	4086	370	394	5357
HT218-normal					365			156	34	0	1327	1811	0	384	40	2573
HT213-normal					363			0	0	0	1256	0	0	300	82	883
HT157-normal					361			44	0	0	5096	0	238	19	67	4004
Bsv-13					356	356		2541	0	0	4970	39918	47	1438	180	9885
Bsv-12					354	354		4181	44	188	8006	38483	530	675	363	19146
cerebellum - h					344			76	41	0	3634	0	419	80	0	2922
brain - h					342			253	156	230	2481	0	229	87	0	2843
RPTEC					334	334		280	0	0	8463	4848	0	423	0	296
lymph node - h					332			15	0	0	15025	0	106	82	0	884
h adult SMC 10/21/92 #17					330			0	0	603	6905	0	126	0	0	1881
Fetal brain - h					328			840	0	6021	28088	83113	442	988	147	7317
HT308-normal					327			98	0	272	2277	0	0	118	146	3862
thymus, h					325			2858	85	417	11255	20108	196	871	0	5060
HT 140 - normal					321			8	20	0	2956	0	0	246	8	2382
HEPM 3d untreated					320			253	0	8480	8511	77932	1048	307	204	1980
uterus - h					318			447	2480	8764	17780	110877	6288	1031	124	13291
trachea - h					316			327	250	28285	8849	19058	2428	893	79	9214
thyroid gland - h					314			230	470	20840	12986	4852	10043	1002	273	14507
salivary gl. - h					311			80	62	42	7345	316	173	8	152	1713
prostate, h					309			0	21	300	2037	0	145	49	0	1845
pituitary gland - h					307			256	8	325	8486	19	189	670	158	1446
pancreas - h					305			0	11	186	4777	857	436	58	0	2540
mammary gland - h					303			146	756	3408	7475	735	1802	150	34	5067
bladder - h					302			0	558	27864	14461	181733	505	400	10	3863
testis - h					298			2409	1136	7085	11747	8708	3878	2577	1281	15783
liver - h					297			1360	344	14941	7284	12355	1178	1089	385	9920
Spleen - h					296			0	244	702	10569	466	2547	132	153	7560
spinal cord - h					294			456	45	516	6105	12809	6275	885	311	11646
small intestine - h					292			136	84	1930	4923	229	419	331	134	5612
skeletal muscle - h					290			633	1809	28493	18470	6789	3133	1326	224	15798
bone marrow - h					279			0	0	0	1113	0	18	0	188	1010
adrenal gland - h					277			0	0	652	1687	746	29	0	0	2444
HPAEC					275	275		190	124	87	2787	172	0	8	73	1817
HT302-normal					268			0	0	0	1285	8	113	62	108	5486
HT282-normal					266			0	0	0	2508	0	8	19	0	7622
Bsv-11					238	238		0	1002	0	8325	687	18	11	31	7456
Bsv-8					236	236		527	98	213	4728	1702	313	17	130	6438
HT372-normal					234			168	0	0	4079	2181	734	0	52	2258
Bsv-7					233	233		192	112	0	2948	0	136	64	0	5213
Bsv-6					231	231		0	8	194	4468	0	179	82	8	4709
Bsv-2					229	229		0	0	247	3875	0	59	50	171	6602
Bsv-1					227	227		208	62	0	1775	208	10	0	32	9127
bladder - h					222			61	0	1051	3512	0	185	133	40	2038
heart - h					216			200	0	0	7286	674	0	131	0	1679
stomach - h					214			0	204	0	8474	0	1257	315	108	2857
fetal liver - h					213			35	0	0	3881	0	125	0	0	843
placenta - h					212			0	93	243	28636	186	888	153	75	3806
HCAEC					211	211		0	0	0	2921	1	190	0	38	1167
fetal brain - h					210			186	145	0	4763	0	873	108	182	5873
HMEC					208			115	0	58	2285	0	198	0	70	2710
Duodenum - h					205			235	80	125	2970	0	1785	72	18	2887
Skeletal muscle - h					203			128	15	320	3074	183	63	30	0	831
Pancreas - h					201			0	0	194	2780	0	93	101	7	2500
testis - h					199			188	25	0	3811	0	154	83	0	1438
Salivary gl. - h					197			33	49	2102	2486	12568	193	119	0	3805
HEPM 3d TGFB1 detergent+DNase					195			0	30	558	1988	2238	787	117	0	841
thymus - h					193			444	155	213	5844	0	366	8	76	2951
WI-38 72h					179			0	67	0	1834	0	548	71	0	712
lymph node - h					61			0	57	0	1846	0	0	172	0	2302
lung - h					59			409	386	447	2183	0	1374	867	25	13413
kidney - h					57			0	213	191	3339	0	977	475	112	4583
heart - h					55			155	198	3427	2345	0	880	281	404	4283
fetal lung - h					53			149	113	416	35	0	0	0	21	844
fetal liver - h					51			0	83	204	1747	28	362	168	0	2927
fetal kidney - h					49			0	79	280	5458	1233	275	215	0	5812
HELA-2h-031899				79				213	887	121	3227	605	61	190	0	8488
HELA-4h-031899				81				72	174	0	3529	0	0	69	0	5410
HELA-5h-031899				83				0	253	215	2891	208	0	218	0	6647
HELA-0h-031899				86				83	0	257	2676	0	0	298	0	4962
HELA-6h-031899				88				140	380	0	8084	2708	0	247	0	4351
HELA-8h-031899				90				242	203	0	5776	0	64	0	183	7038
HELA-10h-031899				92				33	515	616	5068	0	180	0	0	7001
HELA-11h-031899				94				138	143	224	4108	0	0	0	0	3639
HELA-12h-031899				96				43	0	388	5810	0	105	67	0	3080
NCI-H322M				146				0	0	13071	1104	3218	514	285	38	6636
NCI-H460				148				0	18	8702	7871	1230	1730	36	0	5485
NCI-H522				150				0	76	9165	1557	245	71	0	34	2372
SNB-19				152				0	158	6995	730	4151	518	0	0	1600
SNB-75				154				81	108	24358	898	500	1175	89	194	5215
SF-268				156				242	0	3462	0	884	37	102	0	1189
SF-295				158				52	0	1780	705	0	97	3	27	957
CCRF-CEM				160				0	0	893	4451	3	287	0	121	1619
DU-145				162				98	0	7045	175	6522	186	202	57	690
HCT 116				164				0	30	1437	817	372	0	0	147	781

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - Tx	Tumor cells	Normal	Endos	p53	SEQ 79 AA	SEQ 80 2s	SEQ 82 NU	SEQ 86 RN	SEQ 88 AA	SEQ 89 AA	SEQ 90 NT	SEQ 93 TS	SEQ 94 AA
Caki-1				186				279	236	18781	1332	0	782	0	0	1300
786-0				168				132	88	28330	4542	3083	4183	138	0	3588
T-47D				169				0	235	19538	3870	85	2554	414	0	11858
Km-3				171				49	0	0	1822	8713	0	61	0	2573
CRL 1441 RNA 8/30				181				0	244	0	0	1791	0	1	128	543
791T untreated + DNase				183				28	0	0	321	111	0	0	0	284
KB poly A+				184				114	0	541	2325	0	58	136	0	3703
HOS poly A+				186				218	0	1363	3268	0	9	101	190	3424
ACHN				198				0	122	10672	1171	849	147	159	63	1671
UACC-62				200				166	0	3877	0	2173	244	0	183	4827
MCF-7/ADR-RES				202				100	0	1497	402	215	140	0	0	2877
UTOS (Mandy) poly a+				204				112	0	0	330	0	79	252	124	498
WISH (Collagen) poly A+				206				0	309	613	637	315	0	0	0	1576
458 ... mRNA				208				1146	0	2134	2543	826	880	0	107	8071
CCL 137 RinA 3/21/88				218				0	0	292	1884	0	25	143	6	2128
WI-38 72h 0.5%FBS, 24h 10% FBS				219				0	0	981	3363	416	835	194	0	3256
CRL 1441 + TPA (24hr) 8/30				220				0	154	0	177	0	9	5	71	1173
Km-1				221				18	66	0	2177	0	0	41	94	2956
Km-2				223				85	0	45	1182	144	0	133	0	2250
Km-4				226				0	238	0	822	0	11	24	0	1278
HOP-62				241				0	0	1788	1888	983	185	216	0	2505
MOLT-4				242				85	183	8063	1028	2895	153	980	48	5219
EKVX				243				0	0	22076	1594	866	311	200	0	8045
HL-60				244				0	226	14060	2051	0	44	215	0	4254
NCI-H23				245				0	1087	77132	1403	0	700	225	5	8646
RPMI 8226				246				0	0	0	811	928	57	0	7	24
A549/ATCC				247				0	0	4447	356	0	168	88	0	2544
SR				248				0	183	10413	855	1682	589	17	0	2103
OVCAR-3				249				0	148	8905	1324	168	0	60	218	4524
HCT-15				250				129	0	45256	1486	201	589	0	55	5053
OVCAR-4				251				171	0	2361	94	0	189	0	167	1032
UO-31				252				209	0	307	480	0	38	0	151	1421
OVCAR-5				253				0	80	577	3409	0	1477	8	0	4319
SN12C				254				486	0	6836	173	0	0	322	192	4185
OVCAR-8				255				181	56	17468	486	0	58	128	0	1761
LOX IMVI				256				0	2638	82575	1953	3515	1363	0	154	5249
IGROV1				257				140	73	32974	1309	565	128	0	326	4424
SK-MEL-2				258				0	167	4482	224	1854	0	48	567	1286
SK-OV-3				259				0	18	4761	313	1949	581	0	71	1009
SK-MEL-5				260				0	101	3676	172	0	28	0	41	1617
SF-539				261				159	0	73832	1603	2988	825	498	174	4144
SK-MEL-28				262				187	0	14342	546	0	0	86	8	1275
K-562				263				0	118	38831	825	1578	433	74	40	2880
UACC-257				264				0	83	6638	1900	775	91	109	0	1237
M14				265				0	21	1255	873	3737	0	121	0	2709
MCF7				267				128	298	23780	5268	7080	0	715	0	14982
MDA-MB-435				268				0	0	8781	383	0	147	280	126	4095
HT279				270				38	26	0	3084	0	67	170	29	3072
MDA-N				271				0	0	14738	415	0	441	336	0	4138
Y79 poly A+				273				11	361	6884	4474	0	1320	0	345	17179
XHOS poly A+				290				35	380	15860	6570	1854	2113	1081	0	21610
HT838_24h TPA RNA 8/23				300				71	0	0	6308	0	0	40	153	756
HELA-EXP-031800				313				37	62	0	4774	0	0	153	97	3084
HT838_0h RNA				322				344	0	618	6652	16719	0	800	0	4427
HT347				323				292	0	89	4109	270	377	462	83	5452
458 ... RNA				324				842	14	0	8157	6597	481	558	170	1953
NCI-H226				336				262	21	11463	1217	1515	0	171	0	0
HOP-62				337				0	0	10827	2336	0	236	139	0	3071
MDA-MB-231				338				833	1127	131888	15088	39722	8588	1067	45	13815
U251				339				488	1740	734467	8066	80562	28673	1974	0	18852
P1 cells poly A+				340				0	112	8025	779	0	445	178	27	2088
PC-3				341				613	215	25875	1044	16117	1417	1087	0	5852
HCC-2998				343				0	3	7505	1212	708	170	529	0	3085
SW-620				345				68	0	23834	1150	1491	32	243	0	3467
HT192				346				46	0	1966	8307	0	15	245	0	8568
COLO 205				347				17	60	3855	846	634	0	481	0	840
HT218				348				1	0	812	6365	0	72	0	0	2261
KM-12				349				0	81	8008	2006	913	0	158	0	1180
HT191				350				32	207	352	7122	0	192	305	22	8687
A498				351				837	11	8123	3778	2336	0	398	0	2292
HT383				352				235	131	0	14819	186	0	193	0	3522
RXF 393				353				350	0	8025	2120	3003	152	219	0	1987
TK-10				355				2370	1931	58088	4635	36193	4080	868	173	8202
Malme-3M				357				1422	1373	162135	14630	51277	8889	967	89	6366
Hs 578T				359				184	48	21188	1288	1167	1033	150	12	6287
HT213			50					0	0	797	2103	0	880	336	0	14318
HT288			52					146	0	647	3338	0	89	884	0	19288
HT139			54					174	0	0	2329	0	59	307	27	8584
HT155			56					0	0	13	2363	8	0	86	0	15006
HT163			58					375	0	118	1588	0	412	181	117	6438
HT170			60					713	0	2417	1484	1868	0	719	0	13133
HT172			62					111	8	85	2348	0	0	29	0	8824
HT138			63					384	34	82	3379	0	0	0	0	6638
HT178			64					0	78	147	3414	0	671	40	0	8823
HT154			65					208	0	374	2620	0	0	607	0	12319
HT180			66					43	122	437	3689	0	0	0	46	3531
HT169			67					0	118	0	1881	0	0	340	182	2859
HT189			68					43	836	2833	3850	0	894	83	78	8023
HT143			69					327	0	0	2961	0	0	182	0	632
HT198			70					382	71	1398	6366	0	208	288	0	1551
HT146			71					84	88	2084	4726	0	0	238	0	828
HT227			72					12	0	215	3473	0	1015	484	0	2304
HT302			73					143	0	2818	7386	1850	4134	721	174	25415
HT314			74					230	0	674	3847	0	938	348	0	11481
HT317			76					285	0	348	7380	706	979	885	238	13106
Medulloblastoma 8425 11/8			77					0	0	0	2082	21	0	88	0	67
HT323			79					0	0	608	4645	0	292	198	0	9445
HT327			80					0	83	230	1542	1133	0	16	45	2807
HT335			82					0	0	0	4194	0	288	0	0	8152
HT146			85					48	5	93	0	0	38	0	182	1384
HT348			87					69	156	150	5629	0	1017	0	0	3424
HT311			170					238	0	0	3176	0	130	5	111	5105
HT308			185					673	0	0	1126	1616	0	382	0	8621
HT140			187					230	117	0	0	0	0	186	159	746
HT291			189					303	0	0	1384	399	0	301	0	406
HT372			191					43	220	0	2713	0	298	133	144	438
TCGP			207					94	17	0	1450	0	0	10	0	3112
HT180			216					0	0	80	1395	308	0	40	0	1331
HT307			217					0	80	0	2222	0	46	149	0	4196
HT368			224					343	0	0	894	12719	127	327	115	4816
HT370			225					116	0	0	1365	0	0	0	0	3849
HT371			228					170	888	32	1671	0	0	129	0	8422
HT377			230					38	191	122	3185	87	135	53	0	3819
HT382			236					186	81	0	4305	162	520	208	132	2719
...blastoma RNA			281					0	0	103	555	0	30	41	0	280
HT334			290					0	127	0	8791	1382	66	123	0	8375
HT338			301					816	62	0	2712	0	195	241	279	6756
HT382			315					198	0	2288	322	354	107	31	208	3177
HT384			317					83	2474	0	5804	0	981	188	0	7782
HT312			319					208	68	164	3247	0	17	28	158	5742
HT182			325					415	0	228	2151	0	0	0	0	20
HT385			354					380	908	0	3119	0	0	0	0	2471
HT157			360					460	0	0	4419	1081	2685	69	0	585
T-47D	163							437	128	38188	3059	170678	3616	113	0	2621
MDA-N	161							485	135	80419	6019	157582	1445	523	114	4261
MDA-MB-435	158							79	0	55236	4048	124701	2831	197	0	5068
MDA-MB-231	157							816	202	82816	3658	284882	7911	528	445	4671

Table 3 (cont'd)

Tissue	Tumor-organ	Normal-organ	Tumor - ts	Tumor cells	Normal	Endoc	p53	SEQ 79 AA	SEQ 80 2s	SEQ 82 AS	SEQ 84 BR	SEQ 86 AA	SEQ 89 AA	SEQ 90 AS	SEQ 93 TS	SEQ 94 AA
Hs 578T	155							235	136	133245	4602	281680	3072	326	83	5383
MCF-7/ADR-RES	153							454	0	82589	3763	173547	840	234	71	4602
MCF7	151							0	88	23491	3845	219251	402	453	56	6546
M14	149							34	8	102635	5726	69626	734	463	78	8105
UACC-257	147							0	198	44804	4488	40556	1177	177	77	5052
UACC-62	145							0	33	105560	8515	47818	1123	348	0	8145
SK-MEL-28	144							0	103	35141	6515	65338	675	133	24	1529
UO-31	143							508	100	20849	9249	73274	520	189	275	4290
SK-MEL-5	142							104	0	29587	6758	73371	1055	79	11	2500
KM-12	141							416	0	3484	3354	80653	109	127	182	3180
SK-MEL-2	140							171	0	22819	3246	134829	27	167	132	2782
HCT-15	139							0	47	15005	3813	104930	598	0	103	7894
Malme-3M	138							149	150	22488	5785	137583	877	279	0	3758
COLO 205	137							0	213	21011	5643	114441	642	9	74	5403
LOX IMVI	136							158	1464	58887	3350	112245	1470	0	0	3197
SW-620	135							168	0	11595	3617	104047	788	0	210	6275
TK-10	134							0	137	23087	4148	75724	1988	130	0	4536
HCT 116	133							1060	58	7185	2016	119724	702	83	283	7449
786-0	132							225	0	28315	3030	102477	3314	0	47	6736
HCC-2998	131							0	190	17087	5568	127191	495	16	0	9800
ACHN	130							0	138	35733	4255	97808	473	165	144	2382
PC-3	129							180	104	8373	2715	90476	1017	242	0	7409
RXF 393	128							134	204	39080	3502	89683	377	298	65	7346
DU-145	127							0	79	8334	2431	17432	258	54	0	2877
Caki-1	126							0	141	60187	2848	64362	2136	0	0	5700
SR	125							0	79	8485	2584	28629	1849	80	47	10019
A498	124							0	153	28456	2600	91356	15	1182	0	8892
RPMI 8226	123							24	0	80	2614	12804	102	473	168	4276
SN12C	122							0	0	35753	7382	30641	542	572	84	11656
HL-60	121							613	108	825	8301	450	368	314	173	21438
MOLT-4	120							0	0	909	8372	83742	1346	27	0	3085
OVCAR-5	119							425	0	920	4872	41219	4613	1202	171	9433
K-562	118							298	0	10918	4997	106477	2277	97	70	6579
OVCAR-4	117							654	248	21540	2514	133148	8057	231	0	3791
CCRF-CEM	116							0	8	16290	3482	113784	8077	144	8	5240
OVCAR-3	115							464	37	13067	2665	86433	1585	33	0	3061
SF-539	114							217	0	14103	3082	85278	2383	119	0	6606
HOP-62	113							404	153	36836	1330	72109	2588	0	0	6448
SF-295	112							281	6	21130	3579	90198	3313	0	5	13804
A549/ATCC	111							1009	321	44888	4014	138108	3808	225	0	8485
SF-268	110							0	0	23677	2917	128764	808	446	416	2828
NCI-H522	109							364	213	33088	7465	81138	3557	225	113	4126
U251	108							282	0	34503	5609	148017	1964	183	253	7311
NCI-H460	107							170	216	27031	2888	46575	3614	27	5	4206
SNB-75	106							0	335	5681	1862	88012	1608	143	0	6291
NCI-H322M	105							212	0	23147	4126	72818	1194	0	0	6616
SNB-19	104							138	58	8408	2982	17270	1903	0	87	6176
NCI-H226	103							211	119	21514	5630	11321	4083	0	298	10800
SK-OV-3	102							0	0	5634	2381	18630	8044	212	171	5061
NCI-H23	101							319	432	81716	2984	2378	1016	187	64	9311
IGROV1	100							0	282	6158	2107	15131	1772	413	215	12724
EKVX	99							82	132	28193	4584	5729	613	373	0	8753
OVCAR-8	98							106	23	5123	8386	2088	2072	116	0	9109
HOP-92	97							0	254	16507	7191	3804	19079	305	0	12100
h fibroblasts 3/31/92 #12	48							315	200	22448	6764	190845	4808	414	0	4865
h adult SMC 10/21/92 #17	47							0	0	1880	7249	123385	634	456	204	4382
h keratinocytes 2/25/92 #10	46							0	9	13009	9192	188016	116	117	0	5760
TCCP	26							0	16	11006	6235	81405	341	228	0	14132
A549 - 1							wt	0	48	3563	63185	0	3072	0	48	110
A549 - 3							wt	0	22	0	46138	0	0	0	276	808
A549 - 4							wt	0	67	118	46247	0	1943	0	342	754
A549 - 5							wt	0	300	2509	72967	0	2142	0	0	1102
A549 - 7							wt	0	58	831	38890	0	880	0	0	1377
EKVX - 1							mutant	0	286	2806	86934	0	4756	0	132	330
EKVX - 4							mutant	0	223	714	150081	0	16061	0	128	1609
EKVX - 3							mutant	0	359	49	77798	0	6784	0	0	824
EKVX - 5							mutant	0	16	1208	37631	0	808	0	187	2202
EKVX - 7							mutant	0	1153	80	74369	0	703	0	0	4508
MCF-7 - 1							wt	0	650	0	41581	0	322	0	8	1185
MCF-7 - 3							wt	0	234	0	37845	0	0	0	124	574
MCF-7 - 4							wt	0	182	1025	32082	0	848	0	81	581
MCF-7 - 5							wt	0	0	0	25875	0	880	0	429	650
MCF-7 - 7							wt	0	264	20	27865	0	0	0	0	807
ADR-RES - 1							mutant	0	744	1810	88435	0	2747	0	912	1775
ADR-RES - 3							mutant	0	911	2497	43852	0	860	0	175	1127
ADR-RES - 4							mutant	0	449	218	40637	0	1142	0	0	1422
ADR-RES - 5							mutant	0	0	4	30547	0	1779	0	24	249
ADR-RES - 7							mutant	0	473	4304	27945	0	1085	0	0	924
WI38 - 1							wt	0	853	3984	67921	0	19059	0	110	2042
WI38 - 3							wt	0	362	1018	49671	0	10258	0	0	1308
WI38 - 4							wt	0	0	1422	44081	0	8330	0	0	1232
WI38 - 5							wt	0	16	1564	48543	0	7404	0	0	1057
WI38 - 7							wt	0	27	366	32973	0	10729	0	189	1050
HeLa - 1							HPV E6	0	287	0	36078	0	857	0	140	1118
HeLa - 3							HPV E6	0	143	1254	48790	0	758	0	0	842
HeLa - 4							HPV E6	0	80	3030	41448	0	903	0	0	823
HeLa - 6							HPV E6	0	148	884	73772	0	1303	0	0	679
HeLa - 7							HPV E6	0	0	140	49804	0	858	0	151	1152
H1299 - 1							mutant	0	857	330	22779	0	1805	0	0	959
H1299 - 3							mutant	0	1745	1070	26134	0	4089	0	0	441
H1299 - 4							mutant	0	3594	1828	35500	0	14641	0	94	1027
H1299 - 5							mutant	0	0	80	15450	0	6835	0	0	1528
H1299 - 7							mutant	0	813	4627	23886	0	1127	0	115	577
A549 - 2							wt	0	0	2762	38578	0	1166	0	0	511
EKVX - 2							mutant	0	1047	85	73357	0	8238	0	60	1408
HCT-116 - 1							wt	0	1062	308	62248	0	1884	0	0	1781
HCT-116 - 2							wt	0	17	84	122523	0	7698	0	0	1283
HT29 - 2							mutant	0	148	506	34858	0	121	0	170	877
SF539 - 1							wt	0	0	830	22587	0	2652	0	0	488
SF539 - 2							wt	0	182	21	25240	0	4926	0	0	731
SF-268-1							mutant	0	0	3808	43016	0	3529	0	436	1744
SF-268-2							mutant	0	258	1236	65884	0	6088	0	170	383
OVCAR-4 - 1							wt	0	1449	220	42305	0	7178	0	220	1914
OVCAR-4 - 2							wt	0	5263	790	46589	0	1149	0	388	3634
OVCAR-5 - 1							mutant	0	253	0	39085	0	913	0	0	475
OVCAR-5 - 2							mutant	0	1238	0	25748	0	623	0	53	1084
MCF-7 - 2							wt	0	0	0	28132	0	93	0	0	923
ADR-RES - 2							mutant	0	582	82	19243	0	0	0	297	1312
HeLa - 2							HPV E6	0	0	900	18042	0	586	0	197	815
SW480 - 1							mutant	0	2207	1291	61986	0	5196	0	0	1342
SW480 - 2							mutant	0	1156	433	34858	0	6893	0	16	190
H1299 - 2							mutant	0	2428	0	28010	0	7738	0	113	882
C33A - 1							mutant	0	817	0	39805	0	205	0	47	823
C33A - 2							mutant	0	677	0	28147	0	484	0	34	956
U2OS - 1							mutant	0	1584	5519	88346	0	4065	0	0	2314
U2OS - 2							mutant	0	278	1546	88620	0	1257	0	0	777
Hs68 - 1							wt	0	105	87	80212	0	3856	0	71	569
Hs68 - 2							wt	0	124	4250	68067	0	10711	0	57	2035
WI 38 - 2							wt	0	2168	694	65770	0	13181	0	334	2020
Mikhail - 1								0	0	245	23671	0	0	0	0	973
Mikhail - 2								0	0	0	49133	0	78	0	92	164
Mikhail - 3								0	0	0	145384	0	252	0	0	1088
Mikhail - 4								0	0	0	55686	0	232	0	145	480
Mikhail - 5								0	0	0	1560079	0	82	0	179	483
Mikhail - 6								0	0	131	50757	0	0	0	77	1086
Mikhail - 8								0	0	0	62530	0	14485	0	3535	1395
Mikhail - 9								0	260	0	77385	0	1094	0	0	1986

Table 3 (cont'd)

Tissue	Tumor-sync	Normal-sync	Tumor - to	Tumor cells	Normal	Endos	p53	SEQ 79 AA	SEQ [illegible]	SEQ 82 [illegible]	SEQ 84 [illegible]	SEQ 86 AA	SEQ 88 AA	SEQ 90 [illegible]	SEQ 93 TS	SEQ 94 AA
DuPerg-2								0	1167	2287	84067	0	7232	0	238	1528
DuPerg-8								0	2758	83	72826	0	8513	0	48	623
DuPerg-9								0	2323	15	38853	0	14281	0	103	750
DuPerg-11								0	11	2578	73585	0	8754	0	0	1268
DuPerg-12								0	0	1083	47835	0	7809	0	0	1778
DuPerg-10								0	34	0	33803	0	10777	0	0	915
DuPerg-1								0	257	704	80021	0	2318	0	56	308
DuPerg-2								0	408	285	146948	0	1211	0	46	393
DuPerg-3								0	213	6567	105946	0	3713	0	0	584
DuPerg-4								0	52	561	68183	0	558	0	354	801
DuPerg-5								0	2855	0	45709	0	0	0	249	623
DuPerg-6								0	1846	0	54508	0	58	0	19	492
A549-8							wt	0	28	4742	85151	0	2090	0	0	545
EKVX-8							mutant	0	184	4621	74530	0	7705	0	0	2327
HCT-116-7							wt	0	173	836	22256	0	1578	0	72	1568
HCT-116-8							wt	0	205	779	28245	0	2302	0	0	1781
HT29-1							mutant	0	167	1381	47837	0	276	0	315	852
HT29-7							mutant	0	0	80	14674	0	80	0	85	441
HT29-8							mutant	0	45	643	38186	0	342	0	0	458
SF539-7							wt	0	254	114	28008	0	1532	0	124	933
SF539-8							wt	0	1007	176	38168	0	4118	0	0	1851
SF-268-7							mutant	0	0	2013	52411	0	2540	0	167	1488
SF-268-8							mutant	0	1385	1825	38782	0	4138	0	126	1371
OVCAR-4-7							wt	0	809	0	24881	0	534	0	140	2424
OVCAR-4-8							wt	0	8	2400	66208	0	6738	0	0	768
OVCAR-5-7							mutant	0	1141	680	98680	0	2132	0	0	3745
OVCAR-5-8							mutant	0	79	478	13621	0	1	0	0	571
MCF-7-8							wt	0	204	0	40587	0	258	0	8	342
ADR-RES-8							mutant	0	108	0	23503	0	181	0	323	1207
HeLa-8							HPV E6	0	1303	1036	31952	0	384	0	208	651
SW480-7							mutant	0	236	483	29435	0	1176	0	89	1435
SW480-8							mutant	0	1123	0	27332	0	1872	0	330	879
H1299-8							mutant	0	215	7208	20150	0	2891	0	53	724
C33A-7							mutant	0	1006	204	19811	0	8	0	0	650
C33A-8							mutant	0	7777	373	70434	0	3386	0	215	1883
U2OS-7							mutant	0	720	1497	83571	0	3482	0	113	879
U2OS-8							mutant	0	1325	826	33247	0	112	0	38	858
Hs68-7							wt	0	88	522	76356	0	8382	0	0	855
Hs68-8							wt	0	0	530	40810	0	1024	0	0	1105
WI 38-8							wt	0	56	0	82606	0	142	0	0	860
458 medulla RNA								56	318	18715	14760	157513	855	80	0	2438
CRL1572 3/17/89								0	0	154	1378	926	83	21	0	2241
Bov-4						84		110	70	107	3788	616	605	254	0	12872
HT308								0	33	0	4338	137	22	988	548	7852
HT378								0	30	0	4042	18	0	44	0	3843
HT365								892	115	251	5218	14108	1123	1190	133	10627
HT308								308	185	874	6319	0	297	336	0	8480
Bov-3						173		105	0	0	1494	249	0	8	0	4067
Bov-5						175		45	115	220	154	44	0	0	0	2716
Bov-8						177		0	0	0	1789	0	54	0	103	3483
h keratinocytes 2/25/92 #10								19	0	0	2152	2734	0	81	80	5086
Bov-10						237		87	58	0	4051	650	416	154	77	2480
HTB10								49	73	821	8012	740	165	181	6	1021
h fibroblasts 3/31/92 #12								0	0	381	3370	0	518	0	111	1882
prostate, h								0	0	0	4530	0	0	0	0	474
MNNG-OS poly A+								235	87	4368	4893	296	485	375	11	12888
SA-OS (Mundy) poly A+								532	0	3011	1291	8062	49	789	249	8785
MK poly A+								830	0	7825	1853	8543	271	1030	147	4771
HCT-116-3							wt	0	0	817	28838	0	1747	0	0	0
HCT-116-4							wt	0	211	234	30197	0	5346	0	52	307
HCT-116-5							wt	0	7	37	34589	0	2413	0	0	1024
HCT-116-6							wt	0	188	383	35883	0	1888	0	68	1306
A549-6							wt	0	6	0	21787	0	0	0	0	807
HT29-3							mutant	0	302	1078	18879	0	193	0	150	880
EKVX-6							mutant	0	0	41	24371	0	187	0	82	1103
HT29-4							mutant	0	132	0	25089	0	484	0	0	2528
HT29-5							mutant	0	31	1363	76872	0	829	0	0	822
HT29-6							mutant	0	470	0	42341	0	152	0	8	1325
OVCAR-4-3							wt	0	236	328	29521	0	6217	0	0	679
OVCAR-4-4							wt	0	438	387	30765	0	2862	0	0	1088
OVCAR-4-5							wt	0	100	934	38312	0	8860	0	85	940
OVCAR-4-6							wt	0	308	458	18032	0	312	0	515	1063
SF539-3							wt	0	112	4506	32580	0	1361	0	0	1253
SF539-4							wt	0	0	2466	27211	0	2208	0	36	1067
SF539-5							wt	0	38	176	22984	0	1587	0	236	1238
SF539-6							wt	0	211	1013	59830	0	0	0	282	827
OVCAR-5-3							mutant	0	181	882	27675	0	1461	0	0	424
OVCAR-5-4							mutant	0	402	984	18852	0	1208	0	362	817
OVCAR-5-6							mutant	0	183	418	9373	0	483	0	0	477
ADR-RES-6							mutant	0	34	87	24285	0	908	0	0	579
MCF-7-6							wt	0	982	0	50348	0	32	0	54	961
HeLa-6							HPV E6	0	72	873	48407	0	1196	0	72	962
H1299-6							mutant	0	0	0	28441	0	4028	0	0	881
SW480-3							mutant	0	1767	444	24371	0	2777	0	99	984
SW480-4							mutant	0	797	50	38290	0	2235	0	0	1019
SW480-5							mutant	0	1245	884	62347	0	5806	0	289	1571
SW480-6							mutant	0	94	1207	31434	0	594	0	79	1080
C33A-3							mutant	0	1553	0	44175	0	1873	0	32	185
C33A-4							mutant	0	1129	155	28446	0	388	0	18	135
C33A-5							mutant	0	1808	711	29892	0	0	0	60	656
C33A-6							mutant	0	80	376	21348	0	56	0	30	350
Hs68-5							wt	0	434	0	23074	0	8	0	123	412
U2OS-3							mutant	0	58	2847	62228	0	6362	0	0	1217
U2OS-4							mutant	0	685	984	60322	0	4816	0	202	1229
U2OS-5							mutant	0	197	3251	76104	0	8848	0	120	1287
U2OS-6							mutant	0	44	359	25411	0	93	0	0	1349
WI 38-6							wt	0	68	0	16761	0	112	0	0	575
Hs68-3							wt	0	0	856	46605	0	4973	0	0	838
Hs68-4							wt	0	72	4286	68862	0	10191	0	481	2144
SF-268-3							mutant	0	111	148	47205	0	5538	0	33	719
SF-268-4							mutant	0	1	226	46902	0	4135	0	0	805
SF-268-5							mutant	0	80	981	54184	0	8455	0	0	1182
SF-268-6							mutant	0	0	804	27680	0	7780	0	0	814
DuPerg-13								0	0	1183	136780	0	4570	0	0	353
Mitchell-20								0	0	238	221297	0	1384	0	213	765
Mitchell-21								0	0	0	98785	0	6561	0	114	1116
Mitchell-22								0	0	0	118508	0	6553	0	0	1156
OVCAR-5-5							mutant	0	81	0	65962	0	2188	0	0	586
Mitchell-10								0	53	0	27408	0	888	0	0	416
Mitchell-11								0	12	1	16044	0	232	0	22	0
Mitchell-12								0	28	887	91131	0	8219	0	0	1103
Mitchell-13								0	32	0	75780	0	3867	0	64	964
Mitchell-14								0	93	18	88826	0	8687	0	231	1106
Mitchell-15								0	9	0	98153	0	6341	0	228	1552
Mitchell-16								0	0	0	48202	0	6588	0	73	1049
Mitchell-17								0	170	0	257777	0	17930	0	0	1258
Mitchell-18								0	0	2354	218279	0	6606	0	148	1116
Mitchell-19								0	141	68	45120	0	7770	0	0	822

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - 1o	Tumor cells	Normal	Endos	p53	SEQ 85 AA	SEQ 86 AA	SEQ 87 NC	SEQ 100 A	SEQ 101 A	SEQ 110 A	SEQ 111 A	SEQ 112 A	SEQ 114 N
adrenal gland - h		1						0	520	8317	16583	5311	3706	82946	580	18327
lymph node - h		2						145	1228	11829	24718	19927	8388	19401	867	19498
bone marrow - h		3						0	833	3234	4004	8045	4181	18648	1113	4801
mammary gland - h		4						121	306	849	403	453	1581	1216	553	3851
brain - h		5						400	947	2451	11046	2517	5005	85845	745	12780
pancreas - h		6						543	805	1776	11768	4289	4397	15743	1117	11146
cerebellum - h		7						342	1137	14444	44712	4832	3000	76814	1388	51344
pituitary gland - h		8						615	531	4852	21432	8817	4163	27271	1158	19044
fetal brain - h		9						0	1302	3571	20240	4881	7301	58138	1589	26240
placenta - h		10						863	818	7524	4384	8283	3481	51723	1725	28256
fetal kidney - h		11						1080	1190	8450	16797	9585	4326	34771	2576	49585
prostate, h		12						583	1511	798	7309	610	2972	14650	1414	30914
fetal liver - h		13						246	1238	3559	4142	1439	4358	14560	907	11285
salivary gl. - h		14						841	488	3524	7769	2508	8848	30032	1120	18185
fetal lung - h		15						1184	809	3315	12136	8087	6222	18182	1638	87815
skeletal muscle - h		16						349	605	804	3019	633	2580	11311	1787	13487
heart - h		17						32	708	3722	3365	1198	1491	41330	1154	37255
small intestine - h		18						0	524	2431	8421	3280	2070	10971	1713	19816
kidney - h		19						891	366	8028	14631	4876	4812	36866	1331	12278
spinal cord - h		20						9080	294	1535	4310	1760	946	18459	1055	8030
liver - h		21						0	429	1811	9137	1685	3116	19447	1435	4737
Spleen - h		22						336	348	4862	8027	3412	1381	6898	1008	4254
lung - h		23						8	182	5215	8947	4125	1031	13028	862	28815
stomach - h		24						8	443	2248	3228	1851	2148	6008	1235	8363
testis - h		25						16438	2514	35048	4231	29181	8520	67369	880	34003
thymus - h		27						750	414	6026	19572	11138	4767	11803	382	13311
HPAEC		28				28		703	187	0	238	1152	3658	4277	881	0
thyroid gland - h		29						681	680	1230	4784	3196	2998	21987	919	24405
RPTEC		30				30		181	516	0	380	1053	3123	1920	723	0
trachea - h		31						606	740	4384	8881	10717	2088	13172	1556	56880
HMEC		32						0	844	250	65	115	3044	1023	1192	2008
uterus - h		33						0	818	2915	8458	3860	1347	20090	1100	67028
HCAEC		34						0	299	0	454	0	3400	1110	805	0
Pancreas - h		35						0	451	0	312	222	1822	868	630	0
lymph node - h		36						746	473	443	301	11	1081	883	846	1325
Skeletal muscle - h		37						0	375	168	0	0	1441	1986	720	0
fetal liver - h		38						0	842	0	363	0	3211	1382	1054	901
Heart - h		39						0	338	1343	0	0	1194	3363	658	149
thymus,h		40						143	522	0	408	362	2819	541	1719	0
Duodenum - h		41						906	290	618	138	11	2838	0	1084	0
Fetal brain - h		42						829	409	0	573	464	1788	377	2223	0
Salivary gl. - h		43						0	421	154	0	145	1860	1341	1265	0
testis - h		44						1653	636	2190	425	3878	2371	878	1846	0
HT218-normal					365			0	323	0	0	0	734	53	348	0
HT213-normal					363			0	0	288	151	0	120	0	134	0
HT157-normal					361			0	0	0	18	0	83	2404	163	0
Bav-13					356	354		4165	9850	345	634	323	8777	296	3419	16347
Bav-12					354	354		7295	3210	1250	308	60	4806	182	1521	16386
cerebellum - h					344			0	254	82	225	35	297	84	989	0
brain - h					342			0	0	32	268	0	348	0	452	284
RPTEC					334	334		0	348	0	0	0	748	0	1888	0
lymph node - h					332			0	0	11	19	24	81	45	838	0
h adult SMC 10/21/92 #17					330			80	91	0	87	0	71	0	687	0
Fetal brain - h					328			1687	2605	0	1912	109	2629	458	1452	7258
HT308-normal					327			0	591	0	171	0	118	411	429	0
thymus,h					325			309	4778	98	727	0	1869	92	1924	9621
HT148 - normal					321			218	45	0	0	0	0	72	755	0
HEPM 3d untreated					320			0	780	0	283	238	2579	21	1311	0
uterus - h					318			2810	1322	774	2029	2109	4202	471	1067	2888
trachea - h					316			812	74	0	1132	1683	2543	0	701	1532
thyroid gland - h					314			195	271	0	749	2547	2242	333	730	2522
salivary gl. - h					311			0	0	0	153	47	58	251	1072	0
prostate, h					309			50	551	47	135	242	100	167	462	0
pituitary gland - h					307			306	810	156	464	88	1874	0	401	0
pancreas - h					305			0	79	0	387	200	520	535	749	0
mammary gland - h					303			0	1875	0	1884	675	1375	48	833	0
bladder - h					302			0	0	3064	123	72	308	2554	888	226
testis - h					298			7748	6576	2195	2083	3729	4087	1220	1487	4479
liver - h					297			2005	4962	0	2022	2522	2776	0	2119	1673
Spleen - h					296			0	288	0	807	515	388	661	831	0
spinal cord - h					294			1237	1442	0	1953	900	2031	75	1715	480
small intestine - h					292			0	0	0	1415	285	810	0	546	85
skeletal muscle - h					290			1434	482	0	3317	685	1687	277	881	2243
bone marrow - h					279			2288	171	0	0	0	665	280	465	0
adrenal gland - h					277			0	744	0	0	249	1352	374	884	0
HPAEC					276	276		0	14	687	0	0	407	181	801	0
HT382-normal					268			0	7	0	500	113	286	154	863	0
HT383-normal					266			0	0	1147	981	0	0	245	738	752
Bav-11					239	239		0	300	222	357	980	831	2987	1400	0
Bav-8					235	235		0	89	88	127	40	0	481	781	0
HT372-normal					234			78	1472	0	191	104	1278	8	1532	0
Bav-7					233	233		0	338	447	153	0	70	1084	862	0
Bav-6					231	231		0	635	285	217	81	228	2538	817	0
Bav-2					229	229		316	815	0	12	25	864	484	719	0
Bav-1					227	227		864	287	0	0	2	82	1867	347	0
bladder - h					222			0	57	0	0	96	849	48	483	0
Heart - h					216			0	408	0	0	0	314	0	1007	0
stomach - h					214			0	209	291	183	230	741	883	978	0
fetal liver - h					213			36	84	147	0	87	0	182	1042	0
placenta - h					212			0	330	0	387	614	532	533	863	0
HCAEC					211	211		0	67	0	0	69	0	258	783	0
fetal brain - h					210			0	179	0	286	0	188	541	580	0
HMEC					208			0	317	0	981	0	284	0	751	0
Duodenum - h					205			0	180	92	0	0	733	0	765	21
Skeletal muscle - h					203			0	141	279	68	0	115	0	881	0
Pancreas - h					201			81	473	0	125	0	658	0	725	0
testis - h					199			95	904	0	111	148	123	0	461	0
Salivary gl. - h					197			143	0	0	222	118	43	422	536	0
HEPM 3d TGFB1 detergent+DNase					195			0	88	0	156	76	230	0	387	0
thymus - h					193			453	452	0	348	118	2341	107	608	0
WI-38 72h					179			0	178	0	0	78	368	0	377	0
lymph node - h					81			0	873	0	0	180	1195	84	839	0
lung - h					59			0	2301	0	778	740	2537	383	858	0
kidney - h					57			0	462	240	142	182	808	62	787	0
heart - h					55			64	625	0	279	119	338	0	522	0
fetal lung - h					53			681	400	655	88	0	614	0	447	0
fetal liver - h					51			0	0	314	30	45	456	386	328	0
fetal kidney - h					49			0	82	311	213	138	482	0	799	0
HELA-2h-031800				79				0	409	115	269	0	326	454	774	276
HELA-4h-031800				81				0	337	0	201	0	806	102	779	0
HELA-6h-031800				83				0	243	0	212	0	361	321	1374	0
HELA-0h-031800				86				491	687	0	255	51	483	0	846	0
HELA-8h-031800				88				294	680	0	448	78	8211	1347	2176	0
HELA-9h-031800				90				346	228	0	200	211	3141	170	1008	302
HELA-10h-031800				92				0	0	0	285	219	288	313	1114	35
HELA-11h-031800				94				0	126	0	123	11	0	108	1073	0
HELA-12h-031800				96				184	210	326	18	121	172	247	1208	0
NCI-H322M				146				540	77	240	330	2183	677	42	170	0
NCI-H460				148				0	0	0	236	1214	165	88	431	0
NCI-H522				150				275	154	105	144	1241	0	0	362	0
SNB-19				152				0	121	0	134	553	1020	81	220	263
SNB-75				154				0	342	0	260	527	801	327	568	0
SF-268				156				0	449	288	173	819	838	0	182	0
SF-295				158				0	87	0	221	342	0	0	742	4819
CCRF-CEM				160				231	343	465	175	256	20	253	484	1672
DU-145				162				346	0	8	0	238	352	0	294	0
HCT 116				164				322	285	344	55	102	0	0	198	0

Table 3 (cont'd)

Tissue	Tumor-syn	Normal-syn	Tumor - ts	Tumor cells	Normal	Endos	p53	SEQ 95 AA	SEQ 96 AA	SEQ 97 NN	SEQ 100 A	SEQ 101 A	SEQ 110 A	SEQ 111 A	SEQ 112 A	SEQ 114 A
Calu-1				179				0	377	308	131	1114	713	82	303	0
786-0				158				238	356	21	45	4121	1018	0	1855	0
T-47D				169				0	152	14	104	5001	1079	0	708	0
Kan-3				171				0	0	150	85	0	338	0	630	0
CRL 1441 RNA 8/30				181				31	447	0	1	811	747	0	536	0
7B1T untreated + DNase				183				0	203	0	0	123	64	236	303	0
KB poly A+				194				0	0	283	279	1030	237	0	446	0
HOS poly A+				196				0	0	131	139	183	258	0	474	0
ACHN				198				118	283	0	67	1044	883	0	553	0
UACC-62				200				227	481	0	64	1808	1221	167	808	0
MCF-7/ADR-RES				202				0	78	137	0	167	139	172	257	0
UTOS (Blundy) poly a+				204				305	524	846	0	73	3428	156	431	0
WISH (Collagen) poly A+				208				0	0	888	0	293	474	0	197	10
458 medulla mRNA				209				712	1711	0	351	360	1345	0	858	0
CCL137 RNA 3/21/88				218				347	151	680	27	188	0	0	452	0
WI-38 72h 0.5%FBS, 24h 10% FBS				219				0	186	0	111	30	115	0	306	0
CRL 1441 + TPA (24h) 8/30				220				0	0	82	138	41	322	0	477	0
Kan-1				221				0	80	0	8	42	212	104	877	0
Kan-2				223				0	140	181	117	100	117	0	478	545
Kan-4				225				0	172	205	31	0	88	0	467	0
HOP-62				241				0	0	197	155	365	80	0	68	1888
MOLT-4				242				10	0	173	804	2918	787	524	294	0
EKVX				243				882	302	19	379	2734	720	370	870	0
HL-60				244				2488	529	0	272	6737	330	66	18	817
NCI-H23				245				27	233	624	434	2576	193	0	337	0
RPMI 8226				246				0	450	847	146	1817	0	0	460	0
A549/ATCC				247				225	106	0	312	837	249	0	808	981
SR				248				0	122	0	229	298	823	0	425	0
OVCAR-3				249				0	0	1127	321	3870	467	215	308	270
HCT-15				250				18	423	54	448	1543	531	382	484	6882
OVCAR-4				251				0	84	421	79	463	453	0	196	0
UO-31				252				197	270	0	207	62	34	0	41	0
OVCAR-5				253				0	816	0	73	6728	1339	0	351	305
SN12C				254				880	308	982	0	1416	398	452	687	0
OVCAR-8				255				753	0	0	19	153	245	0	275	0
LOX IMVI				256				227	541	454	732	3180	814	357	703	0
IGROV1				257				0	880	564	458	1607	389	189	826	0
SK-MEL-2				258				0	212	0	63	47	346	0	204	0
SK-OV-3				259				0	572	0	0	624	448	415	653	0
SK-MEL-5				260				211	0	0	0	1528	325	0	453	0
SF-539				261				0	352	0	158	2049	1651	0	1121	0
SK-MEL-28				262				0	884	1839	0	1332	1027	0	837	0
K-562				263				82	0	700	207	473	91	32	544	302
UACC-257				264				0	0	0	70	2108	505	0	403	0
M14				265				406	0	0	70	414	119	114	186	0
MCF7				267				472	0	0	2572	17839	1425	0	1304	0
MDA-MB-435				269				0	73	0	138	1853	109	0	98	0
HT279				270				0	628	0	41	0	1085	0	800	400
MDA-N				271				76	278	0	0	1376	489	647	221	0
Y79 poly A+				273				0	810	527	318	1534	1167	0	1461	1821
KHOS poly A+				289				0	158	187	1711	2315	1851	0	513	0
HTB38 24h TPA RNA 6/23				300				0	383	85	218	37	0	0	404	0
HELA-EXP-031800				313				0	0	207	141	0	0	0	209	0
HTB38 0h RNA				322				805	1211	0	129	225	1206	0	1573	3086
HT347				323				0	346	0	222	211	117	0	749	0
458 medulla RNA				324				359	1854	0	0	58	1202	0	801	4136
NCI-H226				336				0	77	0	0	3402	484	0	514	0
HOP-62				337				0	0	219	657	413	390	0	16	0
MDA-MB-231				338				863	0	0	836	12057	4891	0	1033	3276
U251				339				2821	1673	53	3315	26387	11807	1155	1018	3184
PT cells poly A+				340				138	0	0	292	858	229	26	144	0
PC-3				341				383	1320	0	842	3005	1872	0	1051	858
HCC-2998				343				300	845	280	44	1152	482	0	485	0
SW-620				345				307	1338	0	20	1534	782	0	423	0
HT192				346				0	232	108	0	217	0	7	88	0
COLO 205				347				0	845	0	188	822	87	115	396	0
HT218				348				0	300	41	0	0	272	0	446	0
KM-12				349				0	1263	0	56	980	327	150	181	0
HT151				350				0	476	0	0	42	0	832	725	0
A498				351				453	2054	628	277	273	587	298	672	1028
HT383				352				0	491	160	435	54	700	4	1086	0
FOF 303				353				173	1630	0	96	446	195	279	638	1403
TK-10				355				4314	2783	0	658	3339	4922	402	1376	8137
Malme-3M				357				1135	4390	0	1484	22112	4861	1635	1624	2340
Hs 578T				358				0	458	0	0	327	205	842	543	354
HT213			50					0	951	848	257	17	1388	0	248	0
HT288			52					0	502	0	0	2784	1622	190	438	0
HT138			54					0	648	130	37	0	365	0	354	0
HT156			56					0	280	0	0	387	752	0	925	0
HT163			58					0	298	0	47	0	870	0	462	0
HT170			60					402	2258	0	412	26	1722	72	1136	0
HT172			62					0	1113	0	0	41	822	0	698	0
HT136			63					0	812	78	254	0	0	0	552	0
HT178			64					0	148	0	163	98	0	78	680	37
HT154			65					0	194	85	64	270	852	0	383	0
HT180			66					0	0	0	384	81	681	0	679	0
HT168			67					0	819	0	178	7	868	0	451	391
HT188			68					329	428	0	77	134	190	188	1028	0
HT143			69					0	20	68	20	0	61	0	729	0
HT190			70					0	268	658	478	27	410	0	1802	0
HT145			71					448	880	0	330	84	1127	0	2057	277
HT227			72					312	1060	358	167	701	1787	55	1137	708
HT302			73					0	194	0	294	115	2880	1837	828	0
HT214			74					0	33	0	222	6	834	727	812	0
HT317			76					100	568	0	750	100	2488	782	887	0
Medulloblastoma #425 114			77					0	2	0	308	6	446	0	380	0
HT323			78					0	836	0	488	7	839	435	1116	0
HT327			80					201	873	260	112	0	560	173	687	0
HT336			82					45	349	0	128	0	576	161	809	0
HT146			85					0	0	289	20	0	218	0	173	0
HT348			87					0	450	0	126	51	112	373	1349	182
HT311			170					221	27	0	0	26	0	101	916	138
HT398			185					0	1087	0	52	0	887	0	946	0
HT140			187					0	277	0	105	0	858	0	517	0
HT291			189					0	0	0	63	0	661	0	453	0
HT372			191					0	581	7	197	0	390	0	576	0
TCGP			207					421	898	0	109	96	375	142	653	0
HT169			216					0	0	0	45	64	135	67	345	0
HT307			217					0	0	0	275	2031	403	0	291	1888
HT389			224					224	1068	173	384	0	1186	0	773	2580
HT370			226					0	219	0	0	851	408	0	856	0
HT371			228					0	347	0	385	1	902	256	720	0
HT377			230					0	172	0	250	98	207	87	774	0
HT382			236					0	71	286	69	11	0	83	738	0
Neuroblastoma RNA			281					0	38	0	0	0	387	298	842	0
HT334			299					0	1349	828	383	758	797	241	1030	0
HT338			301					0	2033	0	796	0	860	137	802	0
HT392			315					570	44	0	280	162	347	0	400	0
HT394			317					0	0	0	185	0	127	19	471	0
HT312			319					0	60	0	0	36	147	201	548	469
HT182			325					308	0	0	0	34	0	174	406	0
HT395			358					0	0	0	105	0	0	100	680	0
HT157			360					0	0	0	10	14	470	0	896	0
T-47D	163							4583	169	545	825	1180	8222	1026	668	1143
MDA-N	161							1043	208	871	1441	814	8740	5757	730	8208
MDA-MB-435	158							4564	370	1164	1987	936	6884	4457	976	2908
MDA-MB-231	157							11137	2218	0	1820	1456	38345	3387	1639	388

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - ts	Tumor cells	Normal	Endoo	p53	SEQ 95 AA	SEQ 96 AA	SEQ 97 NN	SEQ 100 A	SEQ 101 A	SEQ 110 A	SEQ 111 A	SEQ 112 A	SEQ 114 N
Hs 578T	155							3029	943	0	1780	2069	12004	10483	665	14282
MCF-7/ADR-RES	153							491	517	1977	881	686	10679	8354	882	0
MCF7	151							8433	1235	180	6836	3980	23634	2094	1308	2238
M14	149							3831	0	450	2401	1983	3478	1359	1035	0
UACC-257	147							4023	388	1258	2276	2137	11053	8220	679	947
UACC-62	145							2545	157	726	756	1215	4403	3438	585	429
SK-MEL-28	144							6634	62	3806	1173	721	3098	1531	805	2945
UO-31	143							5324	487	2107	504	442	3000	1020	1536	11987
SK-MEL-5	142							1336	0	1008	2261	2526	18384	2884	881	3356
KM-12	141							261	319	0	488	0	3403	379	443	0
SK-MEL-2	140							2814	185	1844	1741	479	19872	1717	918	3811
HCT-15	139							4882	486	855	1930	389	8858	682	979	1620
Malme-3M	138							1296	46	565	2361	1148	7870	2354	943	2809
COLO 205	137							3539	181	1983	1864	1417	11150	231	1214	1103
LOX IMVI	136							3534	52	1973	1526	677	23802	2457	867	1985
SW-620	135							4581	483	1395	1150	826	12216	571	850	1756
TK-10	134							4648	318	1845	685	484	9644	2033	821	1147
HCT 116	133							1234	384	579	1534	323	6648	355	768	0
786-0	132							2284	182	1883	628	782	11840	2318	722	0
HCC-2998	131							2684	29	0	1232	719	5838	858	904	0
ACHN	130							2267	488	2068	1078	836	30009	2858	852	0
PC-3	129							5813	370	0	719	646	13846	2580	543	0
RXF 393	128							614	317	8314	911	640	2571	7582	524	105
DU-145	127							1412	83	621	806	481	3331	1531	866	312
Caki-1	126							2183	41	0	1328	635	8406	3126	502	1586
SR	125							3471	320	0	841	330	19003	1183	345	841
A498	124							5481	0	1125	1967	268	25034	10429	628	1032
RPMI 8226	123							1951	46	44	228	354	1876	0	563	654
SN12C	122							2080	194	802	178	1833	11740	11038	834	837
HL-60	121							830	0	0	294	845	2164	385	634	0
MOLT-4	120							6083	0	1010	522	1507	4271	753	1205	0
OVCAR-5	119							1580	119	1758	1606	2515	8853	1900	825	5625
K-562	118							3767	0	0	850	252	8345	1008	1001	268
OVCAR-4	117							1258	284	0	1029	2228	11490	3863	1253	857
CCRF-CEM	116							8623	86	1508	2572	1628	25692	2316	981	1348
OVCAR-3	115							2080	150	1853	834	1582	12158	1242	552	0
SF-539	114							3527	457	10	717	387	14856	893	882	1468
HOP-62	113							456	0	1559	673	265	19248	3406	282	1027
SF-295	112							2817	639	75	1118	801	17864	1580	941	0
A549/ATCC	111							1680	940	1723	2304	1701	30228	3221	1074	751
SF-268	110							2259	208	1443	583	1814	11938	4509	643	1866
NCI-H522	109							1284	0	1176	1767	1721	7210	1406	876	1034
U251	108							2200	209	729	877	738	8651	3516	526	2250
NCI-H460	107							2274	449	1277	926	936	17629	1892	676	0
SNB-75	106							1146	228	0	405	288	4322	1334	722	0
NCI-H322M	105							3388	436	0	3525	1047	20442	338	559	327
SNB-19	104							2006	316	0	1863	456	4358	2106	812	1909
NCI-H226	103							6463	125	0	1140	758	4785	1552	1081	0
SK-OV-3	102							6105	418	0	1085	615	13274	5271	587	3219
NCI-H23	101							8803	311	0	1182	841	7912	446	380	0
IGROV1	100							212	0	0	1683	858	10757	0	483	0
EKVX	99							1881	170	77	1733	916	17090	1357	340	842
OVCAR-8	98							3654	0	477	422	150	7006	376	762	0
HOP-92	97							2307	158	0	886	928	13230	5619	687	481
h fibroblasts 3/31/92 #12	48							334	84	16	280	21	1718	823	1424	0
h adult SMC 10/21/92 #17	47							269	10	109	231	0	1286	802	1342	0
h keratinocytes 2/25/92 #10	46							534	336	0	193	62	6234	8718	1436	7982
TCGP	28							1086	737	4718	402	836	2721	1845	34	1742
A549 - 1							wt	0	0	0	8421	18	0	353	825	0
A549 - 3							wt	0	0	0	4212	30	0	0	402	0
A549 - 4							wt	0	0	0	5323	49	0	587	404	0
A549 - 5							wt	0	0	0	2872	210	0	60	635	0
A549 - 7							wt	0	0	0	162	118	0	630	583	0
EKVX - 1							mutant	0	0	0	1343	0	0	438	617	0
EKVX - 4							mutant	0	0	0	43800	11	0	557	705	0
EKVX - 3							mutant	0	0	0	934	0	0	0	706	0
EKVX - 5							mutant	0	0	0	0	207	0	283	758	0
EKVX - 7							mutant	0	0	0	1576	72	0	126	802	0
MCF-7 - 1							wt	0	0	0	718	64	0	0	621	0
MCF-7 - 3							wt	0	0	0	9245	85	0	536	641	0
MCF-7 - 4							wt	0	0	0	1155	73	0	353	896	0
MCF-7 - 5							wt	0	0	0	1060	189	0	0	685	0
MCF-7 - 7							wt	0	0	0	1337	145	0	217	639	0
ADR-RES - 1							mutant	0	0	0	3885	0	0	58	2343	0
ADR-RES - 3							mutant	0	0	0	575	88	0	160	988	0
ADR-RES - 4							mutant	0	0	0	851	0	0	0	835	0
ADR-RES - 5							mutant	0	0	0	472	112	0	0	569	0
ADR-RES - 7							mutant	0	0	0	7502	0	0	329	670	0
WI 38 - 1							wt	0	0	0	0	222	0	2187	854	0
WI 38 - 3							wt	0	0	0	217	672	0	581	558	0
WI 38 - 4							wt	0	0	0	751	79	0	548	546	0
WI 38 - 5							wt	0	0	0	3721	134	0	1014	829	0
WI 38 - 7							wt	0	0	0	4617	0	0	0	856	0
HeLa - 1							HPV E6	0	0	0	12621	108	0	0	1073	0
HeLa - 3							HPV E6	0	0	0	643	253	0	74	884	0
HeLa - 4							HPV E6	0	0	0	3311	270	0	305	871	0
HeLa - 6							HPV E6	0	0	0	1186	816	0	1402	1155	0
HeLa - 7							HPV E6	0	0	0	1048	460	0	0	801	0
H1299 - 1							mutant	0	0	0	0	0	0	0	703	0
H1299 - 3							mutant	0	0	0	0	0	0	212	988	0
H1299 - 4							mutant	0	0	0	2070	530	0	147	1342	0
H1299 - 6							mutant	0	0	0	1806	183	0	864	578	0
H1299 - 7							mutant	0	0	0	0	0	0	0	719	0
A549 - 2							wt	0	0	0	4270	141	0	408	565	0
EKVX - 2							mutant	0	0	0	2003	86	0	0	373	0
HCT-116 - 1							wt	0	0	0	5587	143	0	1327	1078	0
HCT-116 - 2							wt	0	0	0	3758	44	0	2853	816	0
HT29 - 2							mutant	0	0	0	1380	188	0	1005	1046	0
SF539 - 1							wt	0	0	0	1840	198	0	220	650	0
SF539 - 2							wt	0	0	0	2474	10	0	397	719	0
SF-268-1							mutant	0	0	0	317	2004	0	1212	585	0
SF-268-2							mutant	0	0	0	660	282	0	451	953	0
OVCAR-4 - 1							wt	0	0	0	89	619	0	375	1271	0
OVCAR-4 - 2							wt	0	0	0	1543	196	0	214	1200	0
OVCAR-5 - 1							mutant	0	0	0	581	154	0	430	914	0
OVCAR-5 - 2							mutant	0	0	0	10	90	0	535	632	0
MCF-7 - 2							wt	0	0	0	1433	48	0	0	420	0
ADR-RES - 2							mutant	0	0	0	731	138	0	23	786	0
HeLa - 2							HPV E6	0	0	0	0	107	0	1170	780	0
SW480 - 1							mutant	0	0	0	0	632	0	0	685	0
SW480 - 2							mutant	0	0	0	7826	1023	0	543	879	0
H1299 - 2							mutant	0	0	0	2573	19	0	1147	1143	0
C33A - 1							mutant	0	0	0	18707	0	0	0	865	0
C33A - 2							mutant	0	0	0	1155	1	0	114	748	0
U2OS - 1							mutant	0	0	0	85	198	0	559	887	0
U2OS - 2							mutant	0	0	0	0	183	0	1008	871	0
Hs68 - 1							wt	0	0	0	582	457	0	40	657	0
Hs68 - 2							wt	0	0	0	885	0	0	846	931	0
WI 38 - 2							wt	0	0	0	2478	0	0	861	1129	0
[illegible] - 1								0	0	0	285	57	0	178	636	0
[illegible] - 2								0	0	0	2267	402	0	8	672	0
[illegible] - 3								0	0	0	886	386	0	1724	610	0
[illegible] - 4								0	0	0	0	143	0	178	583	0
[illegible] - 5								0	0	0	0	71	0	319	461	0
[illegible] - 6								0	0	0	8430	1	0	0	414	0
[illegible] - 8								0	0	0	1897	6531	0	2589	867	0
[illegible] - 9								0	0	0	0	0	0	0	1224	0

Table 3 (cont'd)

Tissue	Tumor-syn	Normal-syn	Tumor - 1o	Tumor cells	Normal	Embos	p53	SEQ 95 AA	SEQ 96 AA	SEQ 97 NS	SEQ 100 A	SEQ 101 A	SEQ 110 A	SEQ 111 A	SEQ 112 A	SEQ 114 N
DuPang-7								0	0	0	4153	258	0	1186	768	0
DuPang-8								0	0	0	0	72	0	1136	384	0
DuPang-9								0	0	0	352	17	0	2407	803	0
DuPang-11								0	0	0	2910	477	0	1191	732	0
DuPang-12								0	0	0	0	50	0	5703	388	0
DuPang-10								0	0	0	11437	702	0	910	582	0
DuPang-1								0	0	0	0	80	0	120	636	0
DuPang-2								0	0	0	282	0	0	206	737	0
DuPang-3								0	0	0	5080	88	0	332	870	0
DuPang-4								0	0	0	3575	67	0	3508	784	0
DuPang-5								0	0	0	217	72	0	1090	645	0
DuPang-6								0	0	0	0	40	0	62	1567	0
A549 - 8							wt	0	0	0	1853	79	0	58	822	0
EKVX - 8							mutant	0	0	0	6488	207	0	324	847	0
HCT-116 - 7							wt	0	0	0	0	208	0	84	573	0
HCT-116 - 8							wt	0	0	0	846	122	0	176	675	0
HT29 - 1							mutant	0	0	0	3501	0	0	655	844	0
HT29 - 7							mutant	0	0	0	3147	20	0	214	530	0
HT29 - 8							mutant	0	0	0	467	0	0	200	768	0
SF539 - 7							wt	0	0	0	375	55	0	21	654	0
SF539 - 8							wt	0	0	0	0	252	0	21	883	0
SF-268-7							mutant	0	0	0	446	164	0	706	829	0
SF-268-8							mutant	0	0	0	0	183	0	203	848	0
OVCAR-4 - 7							wt	0	0	0	1305	423	0	0	835	0
OVCAR-4 - 8							wt	0	0	0	527	329	0	2772	802	0
OVCAR-5 - 7							mutant	0	0	0	328	0	0	603	2184	0
OVCAR-5 - 8							mutant	0	0	0	0	316	0	311	558	0
MCF-7 - 8							wt	0	0	0	740	194	0	610	860	0
ADR-RES - 8							mutant	0	0	0	3013	0	0	255	1032	0
HeLa - 8							HPV E6	0	0	0	2243	117	0	138	875	0
SW480 - 7							mutant	0	0	0	1081	452	0	0	1825	0
SW480 - 8							mutant	0	0	0	7328	417	0	302	712	0
H1299 - 8							mutant	0	0	0	2363	0	0	0	737	0
C33A - 7							mutant	0	0	0	3128	0	0	163	760	0
C33A - 8							mutant	0	0	0	1813	0	0	528	1083	0
U2OS - 7							mutant	0	0	0	2184	0	0	13	851	0
U2OS - 8							mutant	0	0	0	0	167	0	658	868	0
H460 - 7							wt	0	0	0	4024	909	0	171	615	0
H460 - 8							wt	0	0	0	4497	0	0	301	578	0
WI 38 - 8							wt	0	0	0	67	8	0	904	973	0
450 medulla RNA								0	206	0	304	1464	1336	1421	1814	0
CRL 1572 3/17/99								0	104	154	32	0	42	445	338	1013
Bw-4						84		274	404	0	25	153	872	2372	1229	2098
HT368								1326	1327	0	217	70	5103	0	822	0
HT378								20	184	0	183	65	723	0	839	0
HT385								278	2601	0	870	60	4081	375	1937	3835
HT308								0	234	0	449	0	484	85	2033	62054
Bw-3						173		0	0	188	34	115	0	0	637	0
Bw-6						175		0	336	790	0	0	19	101	345	0
Bw-8						177		576	386	241	104	0	483	119	821	0
h keratinocytes 3/25/02 #10								0	1129	365	0	0	706	166	819	0
Bw-10						237		0	0	14	0	16	0	1516	898	0
HT910								0	188	0	242	0	483	406	1306	0
h fibroblasts 3/31/02 #12								0	362	208	91	46	0	94	1057	0
prostate, h								0	182	69	187	69	186	0	1021	0
MNNG-OS poly A+								52	0	0	492	846	1535	0	632	0
SA-OS (Mundy) poly A+								1046	78	0	572	838	2116	211	606	850
MK poly A+								1104	1914	0	778	1306	2290	268	1231	186
HCT-116 - 3							wt	0	0	0	2064	180	0	382	615	0
HCT-116 - 4							wt	0	0	0	0	56	0	1404	189	0
HCT-116 - 5							wt	0	0	0	377	14	0	754	414	0
HCT-116 - 6							wt	0	0	0	248	0	0	1034	589	0
A549 - 6							wt	0	0	0	4346	0	0	245	815	0
HT29 - 3							mutant	0	0	0	3771	100	0	378	803	0
EKVX - 6							mutant	0	0	0	0	0	0	175	366	0
HT29 - 4							mutant	0	0	0	0	0	0	813	644	0
HT29 - 5							mutant	0	0	0	1280	296	0	238	711	0
HT29 - 6							mutant	0	0	0	0	154	0	0	810	0
OVCAR-4 - 3							wt	0	0	0	1208	42	0	650	660	0
OVCAR-4 - 4							wt	0	0	0	487	93	0	0	644	0
OVCAR-4 - 5							wt	0	0	0	3826	734	0	877	585	0
OVCAR-4 - 6							wt	0	0	0	822	93	0	190	753	0
SF539 - 3							wt	0	0	0	0	131	0	315	862	0
SF539 - 4							wt	0	0	0	0	99	0	484	824	0
SF539 - 5							wt	0	0	0	1450	79	0	864	896	0
SF539 - 6							wt	0	0	0	617	0	0	0	1057	0
OVCAR-5 - 3							mutant	0	0	0	2513	92	0	278	898	0
OVCAR-5 - 4							mutant	0	0	0	3086	438	0	72	758	0
OVCAR-5 - 6							mutant	0	0	0	444	0	0	0	397	0
ADR-RES - 6							mutant	0	0	0	882	175	0	0	723	0
MCF-7 - 6							wt	0	8	0	2112	35	0	843	1137	0
HeLa - 6							HPV E6	0	0	0	0	853	0	0	1363	0
H1299 - 6							mutant	0	0	0	358	1111	0	674	771	0
SW480 - 3							mutant	0	0	0	228	300	0	388	841	0
SW480 - 4							mutant	0	0	0	3044	90	0	0	708	0
SW480 - 5							mutant	0	0	0	0	577	0	379	1149	0
SW480 - 6							mutant	0	0	0	240	450	0	1271	1267	0
C33A - 3							mutant	0	0	0	0	88	0	163	1108	0
C33A - 4							mutant	0	0	0	0	0	0	0	521	0
C33A - 5							mutant	0	0	0	211	0	0	861	1143	0
C33A - 6							mutant	0	0	0	676	313	0	1994	1256	0
H460 - 6							wt	0	0	0	0	807	0	0	818	0
U2OS - 3							mutant	0	0	0	86	838	0	201	728	0
U2OS - 4							mutant	0	0	0	2742	15	0	146	881	0
U2OS - 5							mutant	0	0	0	1378	219	0	622	718	0
U2OS - 6							mutant	0	0	0	528	0	0	1097	826	0
WI 38 - 6							wt	0	0	0	4047	0	0	0	739	0
H460 - 3							wt	0	0	0	4744	204	0	755	806	0
H460 - 4							wt	0	0	0	1334	2368	0	2582	1018	0
SF-268-3							mutant	0	0	0	740	1284	0	0	864	0
SF-268-4							mutant	0	0	0	6402	1366	0	751	721	0
SF-268-5							mutant	0	0	0	1850	989	0	0	954	0
SF-268-6							mutant	0	0	0	1800	0	0	10	780	0
DuPang-13								0	0	0	1829	47	0	1567	1099	0
Mikhail - 20								0	0	0	6046	0	0	0	845	0
Mikhail - 21								0	0	0	67	78	0	1398	831	0
Mikhail - 22								0	0	0	2514	236	0	227	828	0
OVCAR-5 - 5							mutant	0	0	0	0	95	0	312	741	0
Mikhail - 10								0	0	0	15	3	0	96	343	0
Mikhail - 11								0	0	0	0	69	0	1	361	0
Mikhail - 12								0	0	0	0	290	0	2124	801	0
Mikhail - 13								0	0	0	0	1044	0	4091	842	0
Mikhail - 14								0	0	0	0	207	0	521	806	0
Mikhail - 15								0	0	0	0	597	0	1083	880	0
Mikhail - 16								0	0	0	0	2	0	0	376	0
Mikhail - 17								0	0	0	0	0	0	0	380	0
Mikhail - 18								0	0	0	667	33	0	1234	584	0
Mikhail - 19								0	0	0	4	55	0	448	489	0

Table 3 (cont'd)

Tissue	Tumor-cryo	Normal-cryo	Tumor - ts	Tumor cells	Normal	Endos	p53	SEQ 116 S
adrenal gland - h		1						84
lymph node - h		2						634
bone marrow - h		3						822
mammary gland - h		4						0
brain -h		5						2001
pancreas - h		2						235
cerebellum - h		7						686
pituitary gland - h		8						2327
fetal brain - h		9						2719
placenta - h		10						1303
fetal kidney - h		11						717
prostate, h		12						782
fetal liver- h		13						537
salivary gl. - h		14						546
fetal lung - h		15						410
skeletal muscle - h		16						0
heart - h		17						154
small intestine - h		18						514
kidney - h		16						292
spinal cord - h		20						230
liver - h		21						51
Spleen - h		22						167
lung - h		23						436
stomach -h		24						884
testis - h		25						68
thymus -h		27						141
HPAEC		28				28		332
thyroid gland - h		29						0
RPTEC		30				30		168
trachea - h		31						3128
HMEC		32						91
uterus - h		33						198
HCAEC		34						100
Pancreas - h		35						0
lymph node - h		36						178
Skeletal muscle - h		37						71
fetal liver- h		38						1036
Heart - h		39						102
thymus,h		40						145
Duodenum - h		41						123
Fetal brain - h		42						537
Salivary gl. - h		43						140
testis - h		44						0
HT219-normal					365			0
HT213-normal					363			0
HT157-normal					361			0
Bev-13					358	358		1292
Bev-12					354	354		1237
cerebellum - h					344			85
brain -h					342			0
RPTEC					334	334		0
lymph node - h					332			138
h adult SMC 10/21/92 #17					330			141
Fetal brain - h					329			70
HT380-normal					327			68
thymus,h					326			386
HT149 - normal					321			0
HEPM 3d untreated					320			0
uterus - h					318			149
trachea - h					316			203
thyroid gland - h					314			173
salivary gl. - h					311			0
prostate, h					309			86
pituitary gland - h					307			190
pancreas - h					305			0
mammary gland - h					303			0
bladder - h					302			307
testis - h					298			16
liver - h					297			80
Spleen - h					296			21
spinal cord - h					294			111
small intestine - h					292			0
skeletal muscle - h					290			0
bone marrow - h					279			267
adrenal gland - h					277			136
HPAEC					271	275		0
HT382-normal					268			0
HT382-normal					266			69
Bev-11					238	239		331
Bev-8					235	235		222
HT372-normal					234			0
Bev-7					233	233		356
Bev-6					231	231		467
Bev-2					229	229		82
Bev-1					227	227		442
bladder - h					222			80
Heart - h					215			0
stomach -h					214			1000
fetal liver- h					213			0
placenta - h					212			123
HCAEC					211	211		0
fetal brain - h					210			0
HMEC					208			0
Duodenum - h					205			267
Skeletal muscle - h					203			0
Pancreas - h					201			0
testis - h					199			0
Salivary gl. - h					197			0
HEPM 3d TGFB1 detergent+QIAmp					195			48
thymus -h					193			0
WI-38 72h					179			0
lymph node - h					61			0
lung - h					59			0
kidney - h					57			0
heart - h					55			0
fetal lung - h					53			0
fetal liver- h					51			39
fetal kidney - h					49			0
HELA-2h-031899				79				0
HELA-4h-031899				81				534
HELA-6h-031899				33				71
HELA-6h-031899				86				674
HELA-8h-031899				88				97
HELA-9h-031899				98				151
HELA-10h-031899				92				0
HELA-11h-031899				94				91
HELA-12h-031899				98				0
NCI-H322M				146				120
NCI-H460				148				9
NCI-H522				150				66
SNB-19				152				294
SNB-75				154				0
SF-268				156				137
SF-295				158				0
CCRF-CEM				160				185
DU-145				162				0
HCT 116				164				0

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - lu	Tumor cells	Normal	Embryo	p53	SEQ 116 S
Calu-1				166				4
786-0				168				0
T-47D				169				0
Kan-3				171				72
CRL 1441 RNA 8/30				181				0
781T untreated + DMSO				183				160
KB poly A+				194				47
HOS poly A+				195				0
ACHN				196				52
UACC-62				200				0
MCF-7/ADR-RES				202				55
UTOS ([illegible]) poly a+				204				0
WISH (Collagen) poly A+				205				34
458 medulla mRNA				206				208
CCL 137 RNA 3/21/99				218				0
WI-38 72h 0.5%FBS, 24h 10% FBS				219				0
CRL 1441 + TPA (24h) 8/30				220				242
Kan-1				221				58
Kan-2				223				79
Kan-4				225				0
HOP-62				241				0
MOLT-4				242				0
EKVX				243				0
HL-60				244				0
NCI-H23				245				0
RPMI 8226				246				60
A549/ATCC				247				241
SR				248				0
OVCAR-3				249				85
HCT-15				250				0
OVCAR-4				251				0
UO-31				252				0
OVCAR-5				253				248
SN12C				254				0
OVCAR-8				255				0
LOX IMVI				256				0
IGROV1				257				0
SK-MEL-2				258				153
SK-OV-3				259				0
SK-MEL-5				260				0
SF-539				261				0
SK-MEL-28				262				0
K-562				263				22
UACC-257				264				30
M14				265				0
MCF7				267				48
MDA-MB-435				269				108
HT279				270				0
MDA-N				271				0
Y79 poly A+				273				0
KHOS poly A+				280				26
HT838 24h TPA RNA 8/23				308				147
HELA-EXP-031800				313				83
HT838 0h RNA				322				0
HT347				323				0
458 medulla RNA				324				125
NCI-H226				336				0
HOP-92				337				0
MDA-MB-231				338				61
U251				339				0
PT cells poly A+				340				0
PC-3				341				0
HCC-2998				343				0
SW-620				345				0
HT192				346				148
COLO 205				347				0
HT218				348				0
KM 12				349				0
HT151				350				20
A498				351				0
HT383				352				400
RXF 393				353				0
TK-10				356				363
Malme-3M				357				241
Hs 578T				358				0
HT213			50					312
HT288			52					0
HT139			54					0
HT155			56					0
HT163			58					165
HT170			60					61
HT172			62					137
HT138			63					0
HT178			64					32
HT154			65					19
HT180			66					40
HT169			67					140
HT189			68					0
HT143			69					0
HT190			70					99
HT145			71					130
HT227			72					191
HT302			73					0
HT314			74					0
HT317			76					0
Medulloblastoma 8425 11/8			77					0
HT323			78					21
HT327			80					137
HT335			82					0
HT146			85					98
HT348			87					29
HT311			170					18
HT308			185					0
HT140			187					0
HT281			189					205
HT372			191					75
TCGP			207					40
HT160			216					48
HT307			217					62
HT389			224					258
HT370			226					0
HT371			228					114
HT377			230					125
HT382			236					112
neuroblastoma RNA			281					488
HT334			298					231
HT339			301					0
HT392			315					93
HT394			317					0
HT312			319					0
HT142			325					0
HT391			358					46
HT157			360					13
T-47D	163							63
MDA-N	161							0
MDA-MB-435	159							0
MDA-MB-231	157							36

Table 3 (cont'd)

Tissue	Tumor-cyto	Normal-cyto	Tumor - 1x	Tumor cells	Normal	Endos	p53	SEQ 116
Hs 578T	155							0
MCF-7ADR-RES	153							0
MCF7	151							0
M14	149							7
UACC-257	147							22
UACC-62	145							0
SK-MEL-28	144							33
UO-31	143							0
SK-MEL-5	142							91
KM-12	141							4
SK-MEL-2	140							263
HCT-15	139							328
Malme-3M	138							181
COLO 205	137							230
LOX IMVI	136							0
SW-620	135							0
TK-10	134							0
HCT 116	133							0
786-0	132							82
HCC-2998	131							76
ACHN	130							276
PC-3	129							0
RXF 393	128							336
DU-145	127							88
Caki-1	126							276
SR	125							0
A498	124							137
RPMI 8226	123							8
SN12C	122							136
HL-60	121							0
MOLT-4	120							116
OVCAR-5	119							0
K-562	118							36
OVCAR-4	117							842
CCRF-CEM	116							806
OVCAR-3	115							181
SF-539	114							87
HOP-62	113							0
SF-295	112							181
A549/ATCC	111							110
SF-268	110							133
NCI-H522	109							0
U251	108							204
NCI-H460	107							0
SNB-75	106							30
NCI-H322M	105							430
SNB-19	104							78
NCI-H226	103							82
SK-OV-3	102							6
NCI-H23	101							777
IGROV1	100							0
EKVX	99							54
OVCAR-8	98							0
HOP-92	97							43
h fibroblasts 3/31/92 #12	48							148
h adult SMC 10/21/92 #17	47							210
h keratinocytes 2/25/92 #19	46							135
TCGP	28							0
A549 - 1							wt	8
A549 - 3							wt	379
A549 - 4							wt	454
A549 - 5							wt	347
A549 - 7							wt	73
EKVX - 1							mutant	96
EKVX - 4							mutant	280
EKVX - 3							mutant	0
EKVX - 5							mutant	483
EKVX - 7							mutant	877
MCF-7 - 1							wt	0
MCF-7 - 3							wt	885
MCF-7 - 4							wt	315
MCF-7 - 5							wt	0
MCF-7 - 7							wt	0
ADR-RES - 1							mutant	3049
ADR-RES - 3							mutant	158
ADR-RES - 4							mutant	79
ADR-RES - 5							mutant	18
ADR-RES - 7							mutant	96
WI 38 - 1							wt	0
WI 38 - 3							wt	383
WI 38 - 4							wt	880
WI 38 - 6							wt	[illegible]
WI 38 - 7							wt	0
HeLa - 1							HPV E6	0
HeLa - 3							HPV E6	58
HeLa - 4							HPV E6	185
HeLa - 5							HPV E6	308
HeLa - 7							HPV E6	105
H1299 - 1							mutant	0
H1299 - 3							mutant	0
H1299 - 4							mutant	0
H1299 - 5							mutant	0
H1299 - 7							mutant	1
A549 - 2							wt	193
EKVX - 2							mutant	0
HCT-116 - 1							wt	0
HCT-116 - 2							wt	820
HT29 - 2							mutant	68
SF539 - 1							wt	0
SF539 - 2							wt	3
SF-268-1							mutant	208
SF-268-2							mutant	631
OVCAR-4 - 1							wt	0
OVCAR-4 - 2							wt	0
OVCAR-5 - 1							mutant	523
OVCAR-5 - 2							mutant	208
MCF-7 - 2							wt	86
ADR-RES - 2							mutant	221
HeLa - 2							HPV E6	173
SW480 - 1							mutant	0
SW480 - 2							mutant	191
H1299 - 2							mutant	1083
C33A - 1							mutant	0
C33A - 2							mutant	0
U2OS - 1							mutant	271
U2OS - 2							mutant	557
Hs68 - 1							wt	0
Hs68 - 2							wt	24
WI 38 - 2							wt	239
Mixed - 1								0
Mixed - 2								0
Mixed - 3								0
Mixed - 4								14520
Mixed - 5								532
Mixed - 6								0
Mixed - 8								0
Mixed - 9								0

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - 1o	Tumor cells	Normal	Embryo	p53	SEQ 116 3
DuPong-7								1582
DuPong-8								2331
DuPong-9								603
DuPong-11								2503
DuPong-12								518
DuPong-10								358
DuPong-1								474
DuPong-2								0
DuPong-3								222
DuPong-4								0
DuPong-5								0
DuPong-6								0
A549 - 8							wt	0
EKVX - 8							mutant	58
HCT-116 - 7							wt	0
HCT-116 - 8							wt	0
HT29 - 1							mutant	310
HT29 - 7							mutant	89
HT29 - 8							mutant	0
SF539 - 7							wt	155
SF539 - 8							wt	258
SF-268-7							mutant	218
SF-268-8							mutant	503
OVCAR-4 - 7							wt	405
OVCAR-4 - 8							wt	0
OVCAR-5 - 7							mutant	831
OVCAR-5 - 8							mutant	107
MCF-7 - 8							wt	35
ADR-RES - 8							mutant	857
HeLa - 8							HPV E6	0
SW480 - 7							mutant	0
SW480 - 8							mutant	0
H1299 - 8							mutant	0
C33A - 7							mutant	0
C33A - 8							mutant	0
U2OS - 7							mutant	729
U2OS - 8							mutant	37
HeG8 - 7							wt	0
HeG8 - 8							wt	0
WI 38 - 8							wt	0
K56 medulla RNA								0
CRL 1672 3/17/00								71
Bov-4						94		221
HT365								80
HT378								151
HT385								88
HT308								0
Bov-5						173		487
Bov-5						175		117
Bov-6						177		481
h keratinocytes 2/25/02 #10								0
Bov-10						237		0
HTB18								0
h fibroblasts 3/31/02 #12								0
prostate, h								0
MNNG-OS poly A+								32
SA-OS (bloody) poly A+								0
MK poly A+								0
HCT-116 - 3							wt	384
HCT-116 - 4							wt	0
HCT-116 - 5							wt	0
HCT-116 - 6							wt	0
A549 - 6							wt	0
HT29 - 3							mutant	974
EKVX - 6							mutant	121
HT29 - 4							mutant	540
HT29 - 5							mutant	0
HT29 - 6							mutant	177
OVCAR-4 - 3							wt	338
OVCAR-4 - 4							wt	0
OVCAR-4 - 5							wt	16
OVCAR-4 - 6							wt	0
SF539 - 3							wt	728
SF539 - 4							wt	83
SF539 - 5							wt	0
SF539 - 6							wt	0
OVCAR-5 - 3							mutant	2219
OVCAR-5 - 4							mutant	266
OVCAR-5 - 6							mutant	0
ADR-RES - 6							mutant	0
MCF-7 - 6							wt	279
HeLa - 6							HPV E6	371
H1299 - 6							mutant	0
SW480 - 3							mutant	61
SW480 - 4							mutant	0
SW480 - 5							mutant	293
SW480 - 6							mutant	225
C33A - 3							mutant	173
C33A - 4							mutant	162
C33A - 5							mutant	0
C33A - 6							mutant	55
HeG8 - 6							wt	0
U2OS - 3							mutant	620
U2OS - 4							mutant	561
U2OS - 5							mutant	644
U2OS - 6							mutant	0
WI 38 - 6							wt	0
HeG8 - 3							wt	286
HeG8 - 4							wt	821
SF-268-3							mutant	277
SF-268-4							mutant	0
SF-268-5							mutant	125
SF-268-6							mutant	33
DuPong-13								21
Mixed - 20								308
Mixed - 21								0
Mixed - 22								0
OVCAR-5 - 5							mutant	811
Mixed - 10								98
Mixed - 11								260
Mixed - 12								684
Mixed - 13								309
Mixed - 14								180
Mixed - 15								332
Mixed - 16								0
Mixed - 17								129
Mixed - 18								0
Mixed - 19								172

Table 4

Gene Name	SP	ID# na	ID# aa	Family	Group	Length_AA	Extra-Catalytic Domains (Amino acid positions)
X69117_h beta_adrene	H	1	122	AGC	GRK	688	Regulator of G protein signaling domain 54-175; PH domain 559-652
AA144574_m	M	2	123	AGC	GRK	378	PH domain 249-337
AA210825_h	H	9	130	AGC	PKC	978	Phorbol esters/diacylglycerol binding domain (C1 domain) 238-287; PH domain 497-577
AA316804_h	H	11	132	AGC	PKC	890	Phorbol esters/diacylglycerol binding domain (C1 domain) 155-204 and 272-321; PH domain 417-532
AA887783_h	H	21	142	AGC	SGK	446	PX domain 13-120
AA021445_h 3	H	32	152	CAMK	EMK	1311	Vitamin K-dependent carboxylation/gamma-carboxyglutamic (GLA) domain 1072-1113
R31237_1_h, AAC3348	H	34	154	CAMK	EMK	729	UBA domain 327-365
406786.5_h	H	36	156	CAMK	EMK	1330	PAS domain 133-186, 247-280, 354-386
Z36720_h	H	41	161	CAMK	MLCK	874	WD domain, G-beta repeat 674-711
SGK088_h	H	42	162	CAMK	Trio	2287	Immunoglobulin domain 1-62, 97-153, 221-277, 518-578, 1617-1678; Fibronectin type III domain 301-390, 1697-1779
R19772_h	H	44	164	CAMK	Trio	1287	RhoGEF domain 235-405; Fibronectin type III domain 870-955; Immunoglobulin domain 786-851; PH domain419-528
17000139801197_h, IRA	H	76	195	Other	IRAK	596	Death domain 26-108
AA088547_h	H	78	197	Other	IRE	922	PQQ enzyme repeat 39-76
AA232253_h	H	82	201	Other	MLK	800	SAM domain (Sterile alpha motif) 337-408
AA599286_h	H	89	208	Other	SLOB	649	PX domain 16-122
AA836348_h	H	113	232	STE	NEK	836	Regulator of chromosome condensation (RCC1) 387-427, 427-480, 483-532, 598-650
PAK6_h	H	115	234	STE	STE20-02	719	P21-Rho-binding domain 11-69

FIGURE 1A

SEQ ID NO: 122_X69117_H BARK2_H
MADLEAVLADVSYLMAMEKSKATPAARASKRIVLPEPSIRSVMQKYLAERNEITFDKIFN
QKIGFLLFKDFCLNEINEAVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSC
SHPFSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGDIFQKFMESDKFTRFCQWKNV
ELNIHLTMNEFSVHRIIGRGGFGEVYGCRKADTGKMYAMKCLDKKRIKMKQGETLALNER
IMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYATE
IILGLEHVHNRFVVYRDLKPANILLDEHGHARISDLGLACDFSKKKPHASVGTHGYMAPE
VLQKGTAYDSSADWFSLGCMLFKLLRGHSPFRQHKTKDKHEIDRMTLTVNVELPDTFSPE
LKSLLEGLLQRDVSKRLGCHGGGSQEVKEHSFFKGVDWQHVYLQKYPPPLIPPRGEVNAA
DAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERWQQEVTETVYEAVNADTDKIEARK
RAKNKQLGHEEDYALGKDCIMHGYMLKLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQNL
LTMEQILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKKELNETFKEAQRLLRR
APKFLNKPRSGTVELPKPSLCHRNSNGL

SEQ ID NO: 123_AA144574_M BARK2_M
CFVVYRDLKPANILLDEYGHVRISDLGLACDFSKKKPHASVGTHGYMAPEVLQKGTCYDS
SADWFSLGCMLFKLLRGHSPFRQHKTKDKHEIDRMTLTVNVQLPDAFSPELRSLLEGLLQ
RDVSQRLGCGGGGARELKEHIFFKGIDWQHVYLRKYPPPLIPPRGEVNAADAFDIGSFDE
EDTKGIKLLDCDQDLYKNFPLVISERWQQEVVETIYDAVNADTDKIEARKKAKNKQLGQE
EDYAMGKDCIMHGYMLKLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQSLLTMEQIMSVE
ETQIKDRKCILLRIKGGKQFVLQCESDPEFAQWLKELTCTFNEAQRLLRRAPKFLNKPRA
AILEFSKPPLCHRNSSGL

SEQ ID NO: 124_AA826850_H
MGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFGKVCIVQKRDTEKMYAMKYMNKQ
QCIERDEVRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQ
FSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNIATIIKDGERA
TALAGTKPYMAPEIFXSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLV
QLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVE
PGFVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRDSSQSENDYLQDCLD
AIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCGPICPSAGSG

SEQ ID NO: 125_AA960957_H
MGGNHSHKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKMYAMKYMNKQKCI
ERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFTE
GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATVVKGAERASSM
AGTKPYMAPEVFQVYMDRGPGYSYPVDWWSLGITAYELLRGWRPYEIHSVTPIDEILNMF
KVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDAVFKKALMPGF
VPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTKDSCPLNGHLQHCLETVRE
EFIIFNREKLRRQQGQGSQLLDTDSRGGGQAQSKLQDGCNNNLLTHTCTRGCSS

SEQ ID NO: 126_TBK1_H
MQSTSNHLWLLSDILGQGATANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMREFEVLK
KLNHKNIVKLFAIEEETTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDVV
GGMNHLRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQFVSLYGTEEYL
HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVMYKIITG
KPSGAISGVQKAENGPIDWSGDMPVSCSLSRGLQVLLTPVLANILEADQEKCWGFDQFFA
ETSDILHRMVIHVFSLQQMTAHKIYIHSYNTATIFHELVYKQTKIISSNQELIYEGRRLV
LEPGRLAQHFPKTTEENPIFVVSREPLNTIGLIYEKISLPKVHPRYDLDGDASMAKAITG
VVCYACRIASTLLLYQELMRKGIRWLIELIKDDYNETVHKKTEVVITLDFCIRNIEKTVK

FIGURE 1B

VYEKLMKINLEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSLADAWAHQE
GTHPKDRNVEKLQVLLNCMTEIYYQFKKDKAERRLAYNEEQIHKFDKQKLYYHATKAMTH
FTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDIEEEVSKYQEYTNELQETLPQ
KMFTASSGIKHTMTPIYPSSNTLVEMTLGMKKLKEEMEGVVKELAENNHILERFGSLTMD
GGLRNVDCL

SEQ ID NO: 127_AA305176_H
MDPTAGSKKEPGGGAATEEGVNRIAVPKPPSIEEFSIVKPISRGAFGKVYLGQKGGKLYA
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIGGDVKS
LLHIYGYFDEEMAVKYISEVALALDYLHRHGIIHRDLKPDNMLISNEGHIKLTDFGLSKV
TLNRDINMMDILTTPSMAKPRQDYSRTPGQVLSLISSLGFNTPIAEKNQDPANILSACLS
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS
SASSQSHTFISSVESECHSSPKWEKDCQV

SEQ ID NO: 128_AA116841_M
TRPIPWPEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFV
PQPDDETDTSYFEARNNAQHLTVSGFSL

SEQ ID NO: 129_AA256100_H
MAMTAGTTTTFPMSNHTRERVTVAKLTLENFYSNLILQHEERETRQKKLEVAMEEEGLAD
EEKKLRRSQHARKETEFLRLKRTRLGLDDFESLKVIGRGAFGEVRLVQKKDTGHIYAMKI
LRKSDMLEKEQVAHIRAERDILVEADGAWVVKMFYSFQDKRNLYLIMEFLPGGDMMTLLM
KKDTLTEEETQFYISETVLAIDAIHQLGFIHRDIKPDNLLLDAKGHVKLSDFGLCTGLKK
AHRTEFYRNLTHNPPSDFSFQNMNSKRKAETWKKNRRQLAYSTVGTPDYIAPEVFMQTGY
NKLCDWWSLGVIMYEMLIGYPPFCSETPQETYRKVMNWKETLVFPPEVPISEKAKDLILR
FCIDSENRIGNSGVEEIKGHPFFEGVDWEHIRERPAAIPIEIKSIDDTSNFDDFPESDIL
QPVPNTTEPDYKSKDWVFLNYTYKRFEGLTQRGSIPTYMKAGKL

SEQ ID NO: 130_AA210825_H
DSLLPTPALGTPLPIPWPVGSLRTPLSLESTRSPTQRLLPSTPKDPAILRSPPPARSFLG
SPLSHHLLTRSRGSRTQGPPGPPGGSRVGSRRAVPGLPPWPPPPHYPAGLPGSPGPGSPP
PPGGLELQSPPPLLPQIPAPGSGVSFHIQIGLTREFVLLPAASELAHVKQLACSIVDQKF
PECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQEGDLVEVVLSASATFEDFQIRPHAL
TVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCGLNYHKRCAFSIPNNCSGARKRRLSSTSL
ASGHSVRLGTSESLPCTAEELSRSTTELLPRRPPSSSSSSSASSYTGRPIELDKMLLSKV
KVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDCKFNCHKRCATRVPNDCLGEALIN
GDVPMEEATDFSEADKSALMDESEDSGVIPGSHSENALHASEEEEGEGGKAQSSLGYIPL
MRVVQSVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQNNTTNRYYKEI
PLSEILTVESAQNFSLVPPGTNPHCFEIVTANATYFVGEMPGGTPGGPSGQGAEAARGLX
ETAIRQALMPVILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSG
QFGVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLRHPGIVNLECMFETP
EKVFVVMEKLHGDMLEMILSSEKGRLPERLTKFLITQILVALRHLHFKNIVHCDLKPENV
LLASADPFPQVKLCDFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVGVI
MYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAIDLINNLLQVKMRKRYSVDK
SLSHPWLQEYQTWLDLRELEGKMGERYITHESDDARWEQFAAEHPLPGSGLPTDRDLGGA
CPPQDHDMQGLAERISVL

SEQ ID NO: 131_AA127299_H
IQFIIVGAKDLLAMDSNGLSDPYIKITNLSQKTKVIKKTLTPTWNETFFVHFPEKTTLEL
ECWDHDTFSDDFIGKASISLAEIPALAEVDMWIDMKTKKGEFAGK

FIGURE 1C

SEQ ID NO: 132_AA316804_H
MSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSARLSNGSFSAPSLTNSRGSVHTV
SFLLQIGLTRESVTIEAQELSLSAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSEN
ILQLITSADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDYCGEMLWGLVR
QGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSNVSLPGPGLSVPRPLQPEYVALPSEES
HVHQEPSKRIPSWSGRPIWMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGM
QCKDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDNNDINSDSSRGLDDT
EEPSPPEDKMFFLDPSDLDVERDEEAVKTISPSTSNNIPLMRVVQSIKHTKRKSSTMVKE
GWMVHYTSRDNLRKRHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNISQG
SNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQSWEKAIRQALMPVTPQASV
CTSPGQGKDHKDLSTSISVSNCQIQENVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGR
DVAIKVIDKMRFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEKLHGDML
EMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHCDLKPENVLLASAEPFPQVKLCD
FGFARIIGEKSFRRSVVGTPAYLAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDE
DINDQIQNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHPWLQDYQTWLD
LREFETRIGERYITHESDDARWEIHAYTHNLVYPKHFIMAPNPDDMEEDP

SEQ ID NO: 133_PKNBETA_H
MEEGAPRQPGPSQWPPEDEKEVIRRAIQKELKIKEGVENLRRVATDRRHLGHVQQLLRSS
NRRLEQLHGELRELHARILLPGPGPGPAEPVASGPRPWAEQLRARHLEALRRQLHVELKV
KQGAENMTHTCASGTPKERKLLAAAQQMLRDSQLKVALLRMKISSLEASGSPEPGPELLA
EELQHRLHVEAAVAEGAKNVVKLLSSRRTQDRKALAEAQAQLQESSQKLDLLRLALEQLL
EQLPPAHPLRSRVTRELRAAVPGYPQPSGTPVKPTALTGTLQVRLLGCEQLLTAVPGRSP
AAALASSPSEGWLRTKAKHQRGRGELASEVLAVLKVDNRVVGQTGWGQVAEQSWDQTFVI
PLERARELEIGVHWRDWRQLCGVAFLRLEDFLDNACHQLSLSLVPQGLLFAQVTFCDPVI
ERRPRLQRQERIFSKRRGQDFLRRSQMNLGMAAWGRLVMNLLPPCSSPSTISPPKGCPRT
PTTLREASDPATPSNFLPKKTPLGEEMTPPPKPPRLYLPQEPTSEETPRTKRPHMEPRTR
RGPSPPASPTRKPPRLQDFRCLAVLGRGHFGKVLLVQFKGTGKYYAIKALKKQEVLSRDE
IESLYCEKRILEAVGCTGHPFLLSLLVCFQTSSHARFVTEFVPGGDLMMQIHEDVFPEPQ
ARFYVACVVLGLQFLHEKKIIYRDLKLDNLLLDAQGFLKIADFGLCKEGIGFGDRTSTFC
GTPEFLAPEVLTQEAYTQAVDWWALGVLLYEMLVGECPFPGDTEEEVFDCIVNMDAPYPG
FLSVQGLEFIQKLLQKCPEKRLGAGEQDAEEIKVQPFFRTTNWQALLARTIQPPFVPTLC
GPADLRYFEGEFTGLPPALTPPAPHSLLTARQQAAFRDFDFVSERFLEP

SEQ ID NO: 134_AI021023_M PKNBETA_M
LKWDNLLLDAQGFLKIADFGLCKEGIGFGDRTSTFCGTPEFLAPEVLTQEAYTRAVDWWG
LGVLLYEMLVGECPFPGDTEEEVFDCIVNMDAPYPGFLSVQGLEFIQKLLQKCPEKRLGA
GEQDAEEIKVQPFFRTTNWQALLARTIQPPFVPTLCGPADLRYFEGEFTGLPPALTPPAP
HSLLTARQQAAFRDFDFVSERFLEP

SEQ ID NO: 135_H19102_H
GGNIRGPWARGWKSLWTGLGTIRSDLEELWELRGHHYLHQESLKPAPVLVEKPLPEWPVP
QFINLFLPEFPIRPIRGQQQLKILGLVAKGSFGTVLKVLDCTQKAVFAVKVVPKVKVLQR
DTVRQCKEEVSIQRQINHPFVHSLGDSWQGKRHLFIMCSYCSTDLYSLWSAVGCFPEASI
RLFAAELVLVLCYLHDLGIMHRDVKMENILLDERGHLKLTDFGLSRHVPQGAQAYTICGT
LQYMAPEVLSGGPYNHAADWWSLGVLLFSLATGKFPVAAERDHVAMLASVTHSDSEIPAS
LNQGLSLLLHELLCQNPLHRLRYLHHFQVHPFFRGVAFDPELLQKQPVNFVTETQATQPS
SAETMPFDDFDCDLESFLLYPIPA

FIGURE 1D

SEQ ID NO: 136_AA476563_H
MEFFRIDSKDSASELLGLDFGEKLYSLKSEPLKPFFTLPDGDSASRSFNTSESKVEFKAQ
DTISRGSDDSVPVISFKDAAFDDVSGTDEGRPDLLVNLPGELESTREAAAMGPTKFTQTN
IGIIENKLLEAPDVLCLRLSTEQCQAHEEKGIEELSDPSGPKSYSITEKHYAQEDPRMLF
VAAVDHSSSGDMSLLPSSDPKFQGLGVVESAVTANNTEESLFRICSPLSGANEYIASTDT
LKTEEVLLFTDQTDDLAKEEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALAS
RFYIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHIQLTYFSRWSEVEDS
CDSDAIERMYCAPEVGAITEETEACDWWSLGAVLFELLTGKTLVECHPAGINTHTTLNMP
ECVSEEARSLIQQLLQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR

SEQ ID NO: 137_AA626690_H
MLPFAPQDEPWDREMEVFSGGGASSGEVNGLKMVDEPMEEGEADSCHDEGVVKEIPITHH
VKEGYEKADPAQFELLKVLGQGSFGKVFLVRKKTGPDAGQLYAMKVLKKASLKVRDRVRT
KMERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGDVFTRLSKEVLFTEEDVKFYLA
ELALALDHLHQLGIVYRDLKPENILLDEIGHIKLTDFGLSKESVDQEKKAYSFCGTVEYM
APEVVNRRGHSQSADWWSYGVLMFEMLTGTLPFQGKDRNETMNMILKAKLGMPQFLSAEA
QSLLRMLFKRNPANRLGSEGVEEIKRHLFFANIDWDKLYKREVQPPFKPASGKPDDTFCF
DPEFTAKTPKDSPGLPASANAHQLFKGFSFVATSIAEEYKITPITSANVLPIVQINGNAA
QFGEVYELKEDIGVGSYSVCKRCIHATTNMEFAVKIIDKSKRDPSEEIEILMRYGQHPNI
ITLKDVFDDGRYVYLVTDLMKGGELLDRILKQKCFSEREASDILYVISKTVDYLHCQGVV
HRDLKPSNILYMDESASADSIRICDFGFAKQLRGENGLLLTPCYTANFVAPEVLMQQGYD
AACDIWSLGVLFYTMLAGYTPFANGPNDTPEEILLRIGNGKFSLSGGNWDNISDGAKDLL
SHMLHMDPHQRYTAEQILKHSWITHRDQLPNDQPKRNDVSHVVKGAMVATYSALTHKTFQ
PVLEPVAASSLAQRRSMKKRTSTGL

SEQ ID NO: 138_AA215680_H
MSLVACECLPSPGLEPEPCSRARSQAHVYLEQIRNRVALGVPDMTKRDYLVDAATQIRLA
LERDVSEDYEAAFNHYQNGVDVLLRGIHVDPNKERREAVKLKITKYLRRAEEIFNCHLQR
PLSSGASPSAGFSSLRLRPIRTLSSAVEQLRGCRVVGVIEKVQLVQDPATGGTFVVKSLP
RCHMVSRERLTIIPHGVPYMTKLLRYFVSEDSIFLHLEHVQGGTLWSHLLSQAHSRHSGL
SSGSTQERMKAQLNPHLNLLTPARLPSGHAPGQDRIALEPPRTSPNLLLAGEAPSTRPQR
EAEGEPTARTSTSGSSDLPKAPGGHLHLQARRAGQNSDAGPPRGLTWVPEGAGPVLGGCG
RGMDQSCLSADGAGRGCGRATWSVREEQVKQWAAEMLVALEALHEQGVLCRDLHPGNLLL
DQAGHIRLTYFGQWSEVEPQCCGEAVDNLYSAPEVGGISELTEACDWWSFGSLLYELLTG
MALSQSHPSGIQAHTQLQLPEWLSRPAASLLTELLQFEPTRRLGMGEGGVSKLKSHPFFS
TIQWSKLVG

SEQ ID NO: 139_SGK_H
MTVKTEAAKGTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIANNSYACKHPEVQSILKI
SQPQEPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKAE
EVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
FGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSR
NTAEMYDNILNKPLQLKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINW
DDLINKKITPPFNPNVSGPNELRHFDPEFTEEPVPNSIGKSPDSVLVTASVKEAAEAFLG
FSYAPPTDSFL

SEQ ID NO: 140_AA107515_M
MTVKAEAARSTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSILKM
SHPQEPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKAE

FIGURE 1E

EVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
XFQLRRIEHNGTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSRN
TAEMYDNILNKPLQLKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHIFFSLINWD
DLINKKITPPFNPNVSGPSDLRHFDPEFTEEPVPSSIGRSPDSILVTASVKEAAEAFLGF
SYAPPVDSFL

SEQ ID NO: 141_AA109508_M
HLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDFGLCKE
GVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSQDVSQMY
ENILHQPLQIPGGRTVAACDLLQSLLHKDQRQRLGSKADFLEIKNHVFFSPINWDDLYHK
RLTPPFNPNVTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDD
ILDC

SEQ ID NO: 142_AA887783_H
MQRDHTMDYKESCPSVXIPSSDEHREKKKRFTVYKVLVSVGRSEWFVFRRYAEFDKLYNT
LKKQFPAXALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMD
SPKHQSDPSEDEDERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKVLLAK
RKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVL
DFVNGGEGHVVLTDFGLCKEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAV
LYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELLEKDRQNRLGAKEDF
LEIQNHPFFESLSWADLVQKKIPPPFNPNVAGPDDIRNFDTAFTEETVPYSVCVSSDYSI
VNASVLEADDAFVGFSYAPPSEDLFL

SEQ ID NO: 143_R47805_H
MAHQTGIHATEELKEFFAKARAGSVRLIKVVIEDEQLVLGASQEPVGRWDQDYDRAVLPL
LDAQQPCYLLYRLDSQNAQGFEWLFLAWSPDNSPVRLKMLYAATRATVKKEFGGGHIKDE
LFGTVKDDLSFAGYQKHLSSCAAPAPLTSAERELQQIRINEVKTEISVESKHQTLQGLAF
PLQPEAQRALQQLKQKMVNYIQMKLDLERETIELVHTEPTDVAQLPSRVPRDAARYHFFL
YKHTHEGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIAKKIEIGDG
AELTAEFLYDEVHPKQHAFKQAFAKPKGPGGKRGHKRLIRGPGENGDDS

SEQ ID NO: 144_H60215_H
MSKLRMKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLAR
KDGTDDFYQLKILTLEERGDQGIESQEERQGKMLLHTEYSLLSLLHTQDGVVHHHGLFQD
RTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFSDKTADLINLQHYVIKEKRLSERETV
VIFYDVVRVVEALHQKNIVHRDLKLGNMVLNKRTHRITITNFCLGKHLVSEGDLLKDQRG
SPAYISPDVLSGRPYRGKPSDMWALGVVLFTMLYGQFPFYDSIPQELFRKIKAAEYTIPE
DGRVSENTVCLIRKLLVLDPQQRLAAADVLEALSAIIASWQSLSSLSGPLQVVPDIDDQM
SNADSSQEAKVTEECSQYEFENYMRQQLLLAEEKSSIHDTRSWVPKRQFGSAPPVRRLGH
DAQPMTSLDTAILAQRYLRK

SEQ ID NO: 145_SGK324_H
MASTRSIELEHFEERDKRPRPGSRRGAPSSSGGSSSSGPKGNGLIPSPAHSAHCSFYRTR
TLQALSSEKKAKKARFYRNGDRYFKGLVFAISSDRFRSFDALLIELTRSLSDNVNLPQGV
RTIYTIDGSRKVTSLDELLEGESYVCASNEPFRKVDYTKNINPNWSVNIKGGTSRALAAA
SSVKSEVKESKDFIKPKLVTVIRSGVKPRKAVRILLNKKTAHSFEQVLTDITEAIKXASG
VVKRLCTLDGKQVRVTCVHLPDFFGDDDVFIACGPEKFRYAQDDFVLDHSECRVLKSSYS
RSSAVKYSGSKSPGPSRRSQISAHGRSSSNVNGGPELDRCISPEGVNGNRCSESSTLLEK
YKIGKVIGDGNFAVVKECIDRSTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNII

FIGURE 1F

MLVEEMETATELFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHGLSIVH
RDIKPENLLVCEYPDGTKSLKLGDFGLATVVEGPLYTVCGTPTYVAPXIIAETGYGLKVD
IWAAGVITYILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQ
VNVEARCTAGQILSHPWVSDDASQENNMQAEVTGKLKQHFNNALPKQNSTTTGVSVIMVS
GRRQVWPDCGAGLEVFELGSRELPSHGSWCLP

SEQ ID NO: 146_W30246_M SGK324_M
TKSSSSSPTSPGSFRGLKISAQGRSSSNVNGGPELDRCLSPEGVNGNRCSESFPLLEKYR
IGKVIGDGNFAVVKECVDRYTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNIIML
VEEMETATDLFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHSLSIVHRD
IKPENLLVCEYPDGTKSLKLGDFGLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDVW
AAGVITYILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSPCVCFRKCL

SEQ ID NO: 147_AA383293_H
PAAKRVVVYRNGDPFFPGSQLVVTQRRFPTMEAFLCEVTSAVQAPLAVRALYTPCHGHPV
TNLADLKNRGQYVAAGFERFHKLPPYQAFCLSVFRNGDLVSPPFSLKLSQAASQDWETVL
KLLTEKVKLQSGAVRLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDLPYPALSTRGLLAA
GNEAHLRSGVGTVAGSPKPLGRKAKKETCLIVTLTLKYQQSETSRDGQSFPSGVIGVYGA
PHRRKETAGALEVADDEDTQTEEPLDQRAAQIVEQVTCLQDFFGDDDVFIACGPEKFRYA
QDDFVLDHSRRRLLREHQAGFEKLRRTRGEEKEAEKEKKPCMSGGRRMTLRDDQPAKLEK
EPKTRPEENKPERPSGRKPRPMGIIAANVEKHYETGRVIGDGNFAVVKECRHRETRQAYA
MKIIDKSRLKGKEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYLILEYVQGGDLFDAI
IESVKFPEPDAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNEDKSTTLKLADFGLA
KHVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPPFRSPXXGDQDE
LFNIIQLGHFEFLPPYWDNISDAAKDLVSRLLVVDPKKRYTAHQVLQHPWIETAGKTNTV
KRQKQVSPSSDGHFRSQHKRVVEQVS

SEQ ID NO: 148_AA197883_M
MPTAPVLRPPPPPATPAPPAPSRPAPPIPGHRGPCDHSLKCLSSKISERKLPGPWLPAGR
GPLEKPVLGPRGAVMPLFSPQSSLHSVRAEHSPLKPRVVTVVKLGGQPLRKATLLLNRRS
VQTFEQLLSDISEALGFPRWKNDRVRKLFTLKGREVKSVSDFFREGDAFIAMGKEPLTLK
SIQLAMEELYPKNRALALAPHSRVPSPRLRSRLPSKLLKGSHRCGEAGSYSAEMESKAVS
RHQGKTSTVLAPEDKARAQKWVRGKQESEPGGPPSPGAATQEETHASGEKHLGVEIEKTS
GEIVRCEKCKRERELQLGLQREPCPLGTSELDLGRAQKRDSEKLVRTKSCRRPSKAKFTD
GEEGWKGDSHRGSPRDPPQEMRRPNSNSDKKEIRGSESQDSYPQGAPKAQKDFVEGPPAV
EEGPIDMRREDRHTCRSKHAAWLRREQQAEPPQLPRTRGEEKQAEHEKKPGGLGERRAPE
KESKRKLEEKRPERPSGRKPRPKGIISADVEKHYDIGGVIGDGNFATVKECRHRETKQAY
AMKMIDKSQLKGKEDIVDSEILIIQSLSHPNIVKLHEVYETEAEIYLIMEYVQGGDLFDA
IVENVKFPEPEAAVMITDLCKAFVHMHDKNIVHRDVKPENLLVQRNEDKSITLKLADFGL
AKYVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPPFRSPERDQDE
LFNIIQVGQFEFLSPYWDNISDAAKDLVRNLLEVDPKKRYTAEQVLQHPWIEMVGHTNTG
NSQKEESPNSLGHFQSQHKKVAEQMP

SEQ ID NO: 149_DRAK2_H
MSRRRFDCRSISGLLTTTPQIPIKMENFNNFYILTSKELGRGKFAVVRQCISKSTGQEYA
AKFLKKRRRGQDCRAEILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFS
LCLPELAEMVSENDVIRLIKQILEGVYYLHQNNIVHLDLKPQNILLSSIYPLGDIKIVDF
GMSRKIGHACELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYLNISQVNVDYSEETFSSVSQLATDFIQSLLVKNPEKRPTAEICLSHSWLQQWDFEN

FIGURE 1G

LFHPEETSSSSQTQDHSVRSSEDKTSKSSCNGTCGDREDKENIPEDSSMVSKRFRFDDSL
PNPHELVSDLLC

SEQ ID NO: 150_W44160_M DRAK2_M
MSRRRFDCRSVSGLLTTTPQTPIKTENFNNFYTLTPKELGRGKFAVVRQCISKSTGQEYA
AKSLKKRRRGQDCRAEILHEIAVLELARSCPHVINLHEVYENATEIILVLEYAAGGEIFN
LCLPELAEMVSENDVIRLIKQILEGVHYLHQNNIVHLDLKPQNILLSSIYPLGDIKIVDF
GMSRKIGNASELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYLNISQVNVDYSEEMFSSVSQLATDFIQSLLVKNPEKRPTAESCLSHSWLQQWDFGS
LFHPEETSGSSQIQDLTLRSSEEKTSKSSCNGSCGAREDKENIPEDGSLVSKRFRFDDSL
PSPHELVPDLFC

SEQ ID NO: 151_H01248_H, DRAK1_H
MIPLEKPGSGGSSPGATSGSGRAGRGLSGPCRPPPPPQARGLLTEIRAVVRTEPFQDGYS
LCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKRRKGQDCRMEIIHEIAVLELAQDNPW
VINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEKDVQRLMRQILEGVHFLHTR
DVVHLDLKPQNILLTSESPLGDIKIVDFGLSRILKNSEELREIMGTPEYVAPEILSYDPI
SMATDMWSIGVLTYVMLTGISPFLGNDKQETFLNISQMNLSYSEEEFDVLSESAVDFIRT
LLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEANALQEGHSVPEINSDTDKSE
TEESIVTEELIVVTSYTLGQCRQSEKEKMEQKAISKRFKFEEPLLQEIPGEFIY

SEQ ID NO: 152_AA021445_H
MPARIGYYEIDRTIGKGNFAVVKRATHLVTKAKVAIKIIDKTQLDEENLKKIFREVQIMK
MLCHPHIIRLYQVMETERMIYLVTEYASGGEIFDHLVAHGRMAEKEARRKFKQIVTAVYF
CHCRNIVHRDLKAENLLLDANLNIKIADFGFSNLFTPGQLLKTWCGSPPYAAPELFEGKE
YDGPKVDIWSLGVVLYVLVCGALPFDGSTLQNLRARVLSGKFRIPFFMSTECEHLIRHML
VLDPNKRLSMEQICKHKWMKLGDADPNFDRLIAECQQLKEERQVDPLNEDVLLAMEDMGL
DKEQTLQSLRSDAYDHYSAIYSLLCDRHKRHKTLRLGALPSMPRALAFQAPVNIQAEQAG
TAMNISVPQVQLINPENQIVEPDGTLNLDSDEGEEPSPEALVRYLSMRRHTVGVADPRTE
VMEDLQKLLPGFPGVNPQAPFLQVAPNVNFMHNLLPMQNLQPTGQLEYKEQSLLQPPTLQ
LLNGMGPLGRRASDGGANIQLHAQQLLKRPRGPSPLVTMTPAVPAVTPVDEESSDGEPDQ
EAVQRYLANRSKRHTLAMTNPTAEIPPDLQRQLGQQPFRSRVWPPHLVPDQHRSTYKDSN
TLHLPTERFSPVRRFSDGAASIQAFKAHLEKMGNNSSIKQLQQECEQLQKMYGGQIDERT
LEKTQQQHMLYQQEQHHQILQQQIQDSICPPQPSPPLQAACENQPALLTHQLQRLRIQPS
SPPPNHPNNHLFRQPSNSPPPMSSAMIQPHGAASSSQFQGLPSRSAIFQQQPENCSSPPN
VALTCLGMQQPAQSQQVTIQVQEPVDMLSNMPGTAAGSSGRGISISPSAGQMQMQHRTNL
MATLSYGHRPLSKQLSADSAEAHSLNVNRFSPANYDQAHLHPHLFSDQSRGSPSSYSPST
GVGFSPTQALKVPPLDQFPTFPPSAHQQPPHYTTSALQQALLSPTPPDYTRHQQVPHILQ
GLLSPRHSLTGHSDIRLPPTEFAQLIKRQQQQRQQQQQQQQQQEYQELFRHMNQGDAGSL
APSLGGQSMTERQALSYQNADSYHHHTSPQHLLQIRAQECVSQASSPTPPHGYAHQPALM
HSESMEEDCSCEGAKDGFQDSKSSSTLTKGCHDSPLLLSTGGPGDPESLLGTVSHAQELG
IHPYGHQPTAAFSKNKVPSREPVIGNCMDRSSPGQAVELPDHNGLGYPARPSVHEHHRPR
ALQRHHTIQNSDDAYVQLDNLPGMSLVAGKALSSARMSDAVLSQSSLMGSQQFQDGENEE
CGASLGGHEHPDLSDGSQHLNSSCYPSTCITDILLSYKHPEVSFSMEQAGV

SEQ ID NO: 153_2R22-5-11_H
MTAVYMNGGGLVNPHYARWDRRDSVESGCQTESSKEGEEGQPRQLTPFEKLTQDMSQDEK
VVREITLGKRIGFYRIRGEIGSGNFSQVKLGIHSLTKEKVAIKILDKTKLDQKTQRLLSR
EISSMEKLHHPNIIRLYEVVETLSKLHLVMEYAGGGELFGKISTEGKLSEPESKLIFSQI
VSAVKHMHENQIIHRDLKAENVFYTSNTCVKVGDFGFSTVSKKGEMLNTFCGSPPYAAPE

FIGURE 1H

LFRDEHYIGIYVDIWALGVLLYFMVTGTMPFRAETVAKLKKSILEGTYSVPPHVSEPCHR
LIRGVLQQIPTERYGIDCIMNDEWMQGVPYPTPLEPFQLDPKHLSETSTLKEEENEVKST
LEHLGITEEHIRNNQGRDARSSITGVYRIILHRVQRKKALESVPVMMLPDPKERDLKKGS
RVYRGIRHTSKFCSIL

SEQ ID NO: 154_R31237_1_H, AAC33487
MSTRTPLPTVNERDTENHTSHGDGRQEVTSRTSRSGARCRNSIASCADEQPHIGNYRLLK
TIGKGNFAKVKLARHILTGREVAIKIIDKTQLNPTSLQKLFREVRIMKILNHPNIVKLFE
VIETEKTLYLIMEYASGGEVFDYLVAHGRMKEKEARSKFRQIVSAVQYCHQKRIVHRDLK
AENLLLDADMNIKIADFGFSNEFTVGGKLDTFCGSPPYAAPELFQGKKYDGPEVDVWSLG
VILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFLVLNPIKRGTLEQ
IMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMVGMGYSQEEIQESLSKMKYDEITAT
YLLLGRKSSELDASDSSSSSNLSLAKVRPSSDLNNSTGQSPHHKVQRSVSSSQKQRRYSD
HAGPAIPSVVAYPKRSQTSTADGDLKEDGISSRKSSGSAVGGKGIAPASPMLGNASNPNK
ADIPERKKSSTVPSSNTASGGMTRRNTYVCSERTTADRHSVIQNGKENSTIPDQRTPVAS
THSISSAATPDRIRFPRGTASRSTFHGQPRERRTATYNGPPASPSLSHEATPLSQTRSRG
STNLFSKLTSKLTRSRNVSAEQKDENKEAKPRSLRFTWSMKTTSSMDPGDMMREIRKVLD
ANNCDYEQRERFLLFCVHGDGHAENLVQWEMEVCKLPRLSLNGVRFKRISGTSIAFKNIA
SKIANELKL

SEQ ID NO: 155_W90839_M
KGPSWSSRSLGARCRNSIASCPEEQPHVGNYRLLRTIGKGNFAKVKLARHILTGREVAIK
IIDKTQLNPSSLQKLFREVRIMKGLNHPNIVKLFEVIETEKTLYLVMEYASAGEVFDYLV
SHGRMKEKEARAKFRQIVSAVHYCHQKNIVHRDLKAENLLLDAEANIKIADFGFSNEFTL
GSKLDTFCGSPPYAAPELFQGKKYDGPEVDIWSLGVILYTLVSGSLPFDGHNLKELRERV
LRGKYRVPFYMSTDCESILRRFLVLNPAKRCTLEQIMKDKWINIGYEGEELKPDTELKEE
RMPGRKASCSAVGSGSRGLPPSSPMVSSAHNPNKAEIPERRKDSTSTPNNLPPSMMTRRN
TYVCTERPGSERPSLLPNGKENSSGTSRVPPASPSSHSLAPPSGERSRLARGSTIRSTFH
GGQVRDRRAGSGSGGGVQNGPPASPTLAHEAAPLPSGRPRPTTNLFTKLTSKLTRRVTDE
PERIGGPEVTSCHLPWDKTETAPRLLRFPWSVKLTSSRPS

SEQ ID NO: 156_406786.5_H
MEVGGLTVFEEDQRCLSQSLPLPVSAEGPAAQTTAEPSRSFSSAHRHLSRRNGLSRLCQS
RTALSEDRWSSYCLSSLAAQNICTSKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSSGWSS
PLLPAPVCNPNKAIFTVDAKTTEILVANDKACGLLGYSSQDLIGQKLTQFFLRSDSDVVE
ALSEEHMEADGHAAVVFGTVVDIITRSGEKIPVSVWMKRMRQERRLCCVVVLEPVERVST
WVAFQSDGTITSCDSLFAHLHGYVSGEDVAGQHITDLIPSVQLPPSGQHIPKNLKIQRSV
GRARDGTTFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLPDGTIHGI
NHSFALTLFGYGKTELLGKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDVGNESGCGER
TLDPWQGQDPAEGGQDPRINVVLAGGHVVPRDEIRKLMESQDIFTGTQTELIAGGQLLSC
LSPQPAPGVDNVPEGSLPVHGEQALPKDQQITALGREEPVAIESPGQDLLGESRSEPVDV
KPFASCEDSEAPVPAEDGGSDAGMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQ
LAGGSLLMHCPCYGSEWGLWWRSQDLAPSPSGMAGLSFGTPTLDEPWLGVENDREELQTC
LIKEQLSQLSLAGALDVPHAELVPTECQAVTAPVSSCDLGGRDLCGGCTGSSSACYALAT
DLPGGLEAVEAQEVDVNSFSWNLKELFFSDQTDQTSSNCSCATSELRETPSSLAVGSDPD
VGSLQEQGSCVLDDRELLLLTGTCVDLGQGRRFRESCVGHDPTEPLEVCLVSSEHYAASD
RESPGHVPSTLDAGPEDTCPSAEEPRLNVQVTSTPVIVMRGAAGLQREIQEGAYSGSCYH
RDGLRLSIQFEVRRVELQGPTPLFCCWLVKDLLHSQRDSAARTRLFLASLPGSTHSTAAE
LTGPSLVEVLRARPWFEEPPKAVELEGLAACEGEYSQKYSTMSPLGSGAFGFVWTAVDKG
KNKEVVVKFIKKEKVLEDCWIEDPKLGKVTLEIAILSRVEHANIIKVLDIFENQGFFQLV

FIGURE 1I

MEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAGQSRLVSAVGYLRLKDIIHRDIKDEN
IVIAEDFTIKLIDFGSAAYLERGKLFYTFCGTIEYCAPEVLMGNPYRGPELEMWSLGVTL
YTLVFEENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQPVPERRTTLEKLVTDPWVTQ
PVNLADYTWEEVFRVNKPESGVLSAASLEMGNRSLSDVAQAQELCGGPVPGEAPNGQGCL
HPGDPRLLTS

SEQ ID NO: 157_AA544838_M 406786_M
TRPHPCLDEPLASFIFRQLVSAVGYLHSQGIIHRDIKDENIVIAEDFTIKLIDFGSAAYL
ERGKLFYTFCGTIEYCAPEVLIGNPYRGPELEMWSLGVTLYTLIFEENPFCEVEETMEAV
IHPPFLVSQELMSLLSGLLQPCPEQRTTLEKLIRDPWVTQPVNLASYTWEEVCRTNQPES
GLLSAASLEIGSRSPSEMAQREGLCGPPAPRETRGDQHCLHLKDPSLPVS

SEQ ID NO: 158_AA785735_H
MVMADGPRHLQRGPVRVGFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQLDAVN
LEKIYREVQIMKMLDHPHIIKLYQVMETKSMLYLVTEYAKNGEIFDYLANHGRLNESEAR
RKFWQILSAVDYCHGRKIVHRDLKAENLLLDNNMNIKIADFGFGNFFKSGELLATWCGSP
PYAAPEVFEGQQYEGPQLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRIPYFM
SEDCEHLIRRMLVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQV
LRLMHSLGIDQQKXIESLQNKSYNHFAAIYFLLVERLKSHRSSFPVEQRLDGRQRRPSTI
AEQTVAKAQTVGLPVTMHSPNMRLLRSALLPQASNVEAFSFPASGCQAEAAFMEEECVDT
PKVNGCLLDPVPPVLVRKGCQSLPSNMMETSIDEGLETEGEAEEDPAHAFEAFQSTRSGQ
RRHTLSEVTNQLVVMPGAGKIFSMNDSPSLDSVDSEYDMGSVQRDLNFLEDNPSLKDIML
ANQPSPRMTSPFISLRPTNPAMQALSSQKREVHNRSPVSFREGRRASDTSLTQGIVAFRQ
HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVST
LPASVHPQLSPRQSLETQYLQHRLQKPSLLSKAQNTCQLYCKEPPRSLEQQLQEHRLQQK
RLFLQKQSQLQAYFNQMQIAESSYPQPSQQLPLPRQETPPPSQQAPPFSLTQPLSPVLEP
SSEQMQYSPFLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQQPPPPPPPPPPRQPGAAPA
PLQFSYQTCELPSAASPAPDYPTPCQYPVDGAQQSDLTGPDCPRSPGLQEAPSSYDPLAL
SELPGLFDCEMLDAVDPQHNGYVLVN

SEQ ID NO: 159_AA207220_H
MESLVFARRSGPTPSAAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLG
KGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHIIAIHEVFE
NSSKIVIVMEYASRGDLYDYISERQQLSEREARHFFRQIVSAVHYCHQNRVVHRDLKLEN
ILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVDSWSLGVLL
YILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRRATLEDVAS
HWWVNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLLENGAKVCSFFKQHAP
GGGSTTPGLERQHSLKKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPKGILKKKVSASA
EGVQEDPPELSPIPASPGQAAPLLPKKGILKKPRQRESGYYSSPEPSESGELLDAGDVFV
SGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRPLARASRP
SGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDP
LGDSCFSLTDCQEVTATYRQALRVCSKLT

SEQ ID NO: 160_AA426580_H, MAK_V_H
MPAAAGDGLLGEPAAPGGGGGAEDAARPAAACEGSFLPAWVSGVPRERLRDFQHHKRVGN
YLIGSRKLGEGSFAKVREGLHVLTGEKVAIKVIDKKRAKKDTYVTKNLRREGQIQQMIRH
PNITQLLDILETENSYYLVMELCPGGNLMHKIYEKKRLEESEARRYIRQLISAVEHLHRA
GVVHRDLKIENLLLDEDNNIKLIDFGLSNCAGILGYSDPFSTQCGSPAYAAPELLARKKY
GPKIDVWSIGVNMYAMLTGTLPFTVEPFSLRALYQKMVDKEMNPLPTQLSTGAISFLRSL
LEPDPVKRPNIQQALANRWLNENYTGKVPCNVTYPNRISLEDLSPSVVLHMTEKLGYKNS

FIGURE 1J

DVINTVLSNRACHILAIYFLLNKKLERYLSGKSDIQDSLCYKTRLYQIEKYRAPKESYEA
SLDTWTRDLEFHAVQDKKPKEQEKRGDFLHRPFSKKLDKNLPSHKQPSGSLMTQIQNTKA
LLKDRKASKSSFPDKDSFGCRNIFRKTSDSNCVASSSMEFIPVPPPRTPRIVKKPEPHQP
GPGSTGIPHKEDPLMLDMVRSFESVDRDDHVEVLSPSHHYRILNSPVSLARRNSSERTLS
PGLPSGSMSPLHTPLHPTLVSFAHEDKNSPPKEEGLCCPPPVPSNGPMQPLGSPNCVKSR
GRFPMMGIGQMLRKRHQSLQPSADRPLEASLPPLQPLAPVNLAFDMADGVKTQC

SEQ ID NO: 161_Z36720_H
MDTKLNMLNEKVDQLLHFQEDVTEKLQSMCRDMGHLERGLHRLEASRAPGPGGADGVPHI
DTQAGWPEVLELVRAMQQDAAQHGARLEALFRMVAAVDRAIALVGATFQKSKVADFLMQG
RVPWRRGSPGDSPEEWVKEEEVCFMPPVPPAPGAAGQSLQKDKGELSAEQGIWATLMTLV
IMVTAANKERVEEEGGKPKHVLSTSGVQSDAREPGEESQKADVLEGTAERLPPIRASGLG
ADPAQAVVSPGQGDGVPGPAQAFPGHLPLPTKVEAKAPETPSENLRTGLELAPAPGRVNV
VSPSLEVAPGAGQGASSSRPDPEPLEEGTRLTPGPGPQCPGPPGLPAQARATHSGGETPP
RAALLKGAVAPGFSRRDLVFPSIFCACLGISIHIQEMDTPGEMLMTGRGSLGPTLTTEAP
AAAQPGKQGPPGTGRCLQAPGTEPGEQTPEGARELSPLQESSSPGGVKAEEEQRAGAEPG
TRPSLARSDDNDHEVGALGLQQGKSPGAGNPEPEQDCAARAPVRAEAVRRMPPGAEAGSV
VLDDSPAPPAPFEHRVVSVKETSISAGYEVCQHEVLGGGRFGQVHRCTEKSTGLPLAAKI
IKVKSAKDREDVKNEINIMNQLSHVNLIQLYDAFESKHSCTLVMEYVDGGELFDRITDEK
YHLTELDVVLFTRQICEGVHYLHQHYILHLDLKPENILCVNQTGHQIKIIDFGLARRYKP
REKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLLSGLSPFLGETDAETMNFIV
NCSWDFDADTFEGLSEEAKDFVSRLLVKEKSCRMSATQCLKHEWLNNLPAKASRSKTRLK
SQLLLQKYIAQRKWKKHFYVVTAANRLRKFPTSP

SEQ ID NO: 162_SGK088_H
GEMALFECLVAGPTDVEVDWLCRGRLLQPALLKCKMHFDGRKCKLLLTSVHEDDSGVYTC
KLSTAKDELTCSARLTVRPSLAPLFTRLLEDVEVLEGRAARFDCKISGTPPPVVTWTHFG
CPMEESENLRLRQDGGLHSLHIAHVGSEDEGLYAVSAVNTHGQAHCSAQLYVEEPRTAAS
GPSSKLEKMPSIPEEPEQGELERLSIPDFLRPLQDLEVGLAKEAMLECQVTGLPYPTISW
FHNGHRIQSSDDRRMTQYRDVHRLVFPAVGPQHAGVYKSVIANKLGKAACYAHLYVTDVV
PGPPDGAPQVVAVTGRMVTLTWNPPRSLDMAIDPDSLTYTVQHQVLGSDQWTALVTGLRE
PGWAATGLRKGVQHIFRVLSTTVKSSSKPSPPSEPVQLLEHGPTLEEAPAMLDKPDIVYV
VEGQPASVTVTFNHVEAQVVWRSCRGALLEARAGVYELSQPDDDQYCLRICRVSRRDMGA
LTCTARNRHGTQTCSVTLELAEAPRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKD
EVLLTESSHVSFVYEENECSLVVLSTGAQDGGVYTCTAQNLAGEVSCKAELAVHSAQTAM
EVEGVGEDEDHRGRRLSDFYDIHQEIGRGAFSYLRRIVERSSGLEFAAKFIPSQAKPKAS
ARREARLLARLQHDCVLYFHEAFERRRGLVIVTELCTEELLERIARKPTVCESEIRAYMR
QVLEGIHYLHQSHVLHLDVKPENLLVWDGAAGEQQVRICDFGNAQELTPGEPQYCQYGTP
EFVAPEIVNQSPVSGVTDIWPVGVVAFLCLTGISPFVGENDRTTLMNIRNYNVAFEETTF
LSLSREARGFLIKVLVQDRLRPTAEETLEHPWFKTQAKGAEVSTDHLKLFLSRRRWQRSQ
ISYKCHLVLRPIPELLRAPPERVWVTMPRRPPPSGGLSSSSDSEEEELEELPSVPRPLQP
EFSGSRVSLTDIPTEDEALGTPETGAATPMDWQEQGRAPSQDQEAPSPEALPSPGQEPAA
GASPRRGELRRGSSAESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEG
EYAQRLQALRQRLLRGGPEDGKVSGLRGPLLESLGGRARDPRMARAASSEAAPHHQPPLE
NRGLQKSSSFSQGEAEPRGRHRRAGAPLEIPVARLGARRLQESPSLSALSEAQPSSPARP
SAPKPSTPKSAEPSATTPSDAPQPPAPQPAQDKAPEPRPEPVRASKPAPPPQALQTLALP
LTPYAQIIQSLQLSGHAQGPSQGPAAPPSEPKPHAAVFARVASPPPGAPEKRVPSAGGPP
VLAEKARVPTVPPRPGSSLSSSIENLESEAVFEAKFKRSRESPLSLGLRLLSRSRSEERG
PFRGAEEEDGIYRPSPAGTPLELVRRPERSRSVQDLRAVGEPGLVRRLSLSLSQRLRRTP
PAQRHPAWEARGGDGESSEGGSSARGSPVLAMRRRLSFTLERLSSRLQRSGSSEDSGGAS

FIGURE 1K

GRSTPLFGRLRRATSEGESLRRLGLPHNQLAAQAGATTPSAESLGSEASATSGSSAPGES
RSRLRWGFSRPRKDKGLSPPNLSASVQEELGHQYVRSESDFPPVFHIKLKDQVLLEGEAA
TLLCLPAACPAPHISWMKDKKSLRSEPSVIIVSCKDGRQLLSIPRAGKRHAGLYECSATN
VLGSITSSCTVAVARVPGKLAPPEVTQTYQDTALVLWKPGDSRAPCTYTLERRVDGESVW
HPVSSGIPDCYYNVTHLPVGVTVRFRVACANRAGQGPFSNSSEKVFVRGTQDSSAVPSAA
HQEAPVTSRPARARPPDSPTSLAPPLAPAAPTPPSVTVSPSSPPTPPSQALSSLKAVGPP
PQTPPRRHRGLQAARPAEPTLPSTHVTPSEPKPFVLDTGTPIPASTPQGVKPVSSSTPVY
VVTSFVSAPPAPEPPAPEPPPEPTKVTVQSLSPAKEVVSSPGSSPRSSPRPEGTTLRQGP
PQKPYTFLEEKARGRFGVVRACRENATGRTFVAKIVPYAAEGKPRVLQEYEVLRTLHHER
IMSLHEAYITPRYLVLIAESCGNRELLCGLSDRFRYSEDDVATYMVQLLQGLDYLHGHHV
LHLDIKPDNLLLAPDNALKIVDFGSAQPYNPQALRPLGHRTGTLEFMAPEMVKGEPIGSA
TDIWGAGVLTYIMLSGRSPFYEPDPQETEARIVGGRFDAFQLYPNTSQSATLFLRKVLSV
HPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAATRHKVLLR
SYPGGP

SEQ ID NO: 163_AA542015_M SGK088_M
ATDIWGAGVLTYIMLSGYSPFYEPDPQETEARIVGGRFDAFQLYPNTSQSATLFLRKVLS
VHPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAATRHKVLL
RSYPGSP

SEQ ID NO: 164_R19772_H
MKGGDRAYTRGPSLGWLFAKCCCCFPCRDAYSHSSSENGGKSESVANLQAQPSLNFIHSS
PGPKRSTNTLKKWLTSPVRRLNSGKADGNIKKQKKVRDGRKSFDLGSPKPGDETTPQGDS
ADESKKGWGEDEPDEESHTPLPPPMKIFDNDPTQDEMSSSLLAARQASTEVPTAADLVNA
IEKLVKNKLSLEGSSYRGSLKDPAGCLNEGMAPPTPPKNPEEEQKAKALRGRMFVLNELV
QTEKDYVKDLGIVVEGFMKRIEEKGVPEDMRGKDKIVFGNIHQIYDWHKDFFLAELEKCI
QEQDRLAQLFIKHERKLHIYVWYCQNKPRSEYIVAEYDAYFEEVKQEINQRLTLSDFLIK
PIQRITKYQLLLKDFLRYSEKAGLECSDIEKAVELMCLVPKRCNDMMNLGRLQGFEGTLT
AQGKLLQQDTFYVIELDAGMQSRTKERRVFLFEQIVIFSELLRKGSLTPGYMFKRSIKMN
YLVLEENVDNDPCKFALMNRETSERVVLQAANADIQQAWVQDINQVLETQRDFLNALQSP
IEYQRKERSTAVMRSQPARLPQASPRPYSSVPAGSEKPPKGSSYNPPLPPLKISTSNGSP
GFEYHQPGDKFEASKNDLGGCNGTSSMAVIKDYYALKENEICVSQGEVVQVLAVNQQNMC
LVYQPASDHSPAAEGWVPGSILAPLTKATAAESSDGSIKKSCSWHTLRMRKRAEVENTGK
NEATGPRKPKDILGNKVSVKETNSSEESECDDLDPNTSMEILNPNFIQEVAPEFLVPLVD
VTCLLGDTVILQCKVCGRPKPTITWKGPDQNILDTDNSSATYTVSSCDSGEITLKICNLM
PQDSGIYTCIATNDHGTTSTSATVKVQGVPAAPNRPIAQERSCTSVILRWLPPSSTGNCT
ISGYTVEYREEGSQIWQQSVASTLDTYLVIEDLSPGCPYQFRVSASNPWGISLPSEPSEF
VRLPEYDAAADGATISWKENFDSAYTELNEIGRGRFSIVKKCIHKATRKDVAVKFVNKKM
KKKEQAAHEAALLQHLQHPQYITLHDTYESPTSYILILELMDDGRLLDYLMNHDELMEEK
VAFYIRDIMEALQYLHNCRVAHLDIKPENLLIDLRIPVPRVKLIDLEDAVQISGHFHIHH
LLGNPEFAAPEVIQGIPVSLGTDIWSIGVLTYVMLSGVSPFLDESKEETCINVCRVDFSF
PHEYFCGVSNAARDFINVILQEDFRRRPTAATCLQHPWLQPHNGSYSKIPLDTSRLACFI
ERRKHQNDVRPIPNVKSYIVNRVNQGT

SEQ ID NO: 165_5R72_8_2_H
MADSGLDKKSTKCPDCSSASQKDVLCVCSSKTRVPPVLVVEMSQTSSIGSAESLISLERK
KEKNINRDITSRKDLPSRTSNVERKASQQQWGRGNFTEGKVPHIRIENGAAIEEIYTFGR
ILGKGSFGIVIEATDKETETKWAIKKVNKEKAGSSAVKLLEREVNILKSVKHEHIIHLEQ
VFETPKKMYLVMELCEDGELKEILDRKGHFSENETRWIIQSLASAIAYLHNNDIVHRDLK
LENIMVKSSLIDDNNEINLNIKVTDFGLAVKKQSRSEAMLQATCGTPIYMAPEVISAHDY

FIGURE 1L

SQQCDIWSIGVVMYMLLRGEPPFLASSEAKLFELIRKGELHFENAVWNSISDCAKSVLKQ
LMKVDPAHRITAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVEENTTEEKNKPS
TEEKLKSYQPWGNVPETNYTSDEEEEKQSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAE
IKGEMEKTPVTPSQGTATKYPAKSGALSRTKKKL

SEQ ID NO: 166_SGK309_H
MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTRENV
ALKVESAQQPKQVLKMEVAVLKKLQGSGLGQGDGKEEMMKPGAKRGKDHVCRFIGCGRNE
KFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHD
DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMIKEKYEHRMLLKHMPSEFHLFLDHIASLDY
FTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLSTSTSTPPPAEHPADGSHVWG
GQCDASAWGPAPGEHRGCATGRAPEXPGECTPNSAREALXGAGPQSPPCPPPRGSXGXSL
GGDRCQPEQTPDQHRQSNCRQGEGRGWPFLSPPIPSLVPLPCSSXAPCPPPISLLARPLF
PVPSPALASLCLPSSSSSVSFTLRRPSA

SEQ ID NO: 167_AA234451_H
MSGGGEQLDILSVGILVKERWKVLRKIGGGGFGEIYDALDMLTRENVALKVESAQQPKQV
LKMEVAVLKKLQGKDHVCRFIGCGRNDRFNYVVMQLQGRNLADLRRSQSRGTFTISTTLR
LGRQILESIESIHSVGSXHRDIKPSNFAMGRFPSTCRKCYMLDFGLARQFTNSCGDVRPP
RAVAGFRGTVRYASINAHRNREMGRHDDLWSLFYMLVEFVVGQLPWRKIKDKEQVGSIKE
RYDHRLMLKHLPPEFSIFLDHISSLDYFTKPDYQLLTSVFDNSIKTFGVIESDPFDWEKT
GNDGSLTTTTTSTTPQLHTRLTPAAIGIANATPIPGDLLRENTDEVFPDEQLSDGENGIP
VGVSPDKLPGSLGHPRPQEKDVWEEMDANKNKIKLGICKAATEEENSHGQANGLLNAPSL
GSPIRVRSEITQPDRDIPLVRKLRSIHSFELEKRLTLEPKPDTDKFLETWYKIVYFSF

SEQ ID NO: 168_AA435956_H
TFTIFFEMTVFDLEAKSARGGSNLLMDSVSSFQLFMFQLLRGLAYIHHQHVLHRDLKPQN
LLISHLGELKLADFGLARAKSIPSQTYSSEVVTLWYRPPDALLGATEYSSELDIWGAGCI
FIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYNPEWFPLPTPRSLHV
VWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQLPDEESLFTVSGV
RLKPEMCDLLASYQKGHHPAQFSKCW

SEQ ID NO: 169_AA626859_H
NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIPGD
AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR
TLGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRL
TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQNQLLPLIPGSHISPTPDGRKQVLQLK
FDHLPNI

SEQ ID NO: 170_AA061797_M
KIALREIRMLKLKHPNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVSDGVIKSV
LWQTLQALNFCHKHNCIHRDVKPENILITKQGMIKICDFGFARILIPGDAYTDYVATRWY
RAPELLVGDTKYGSSVDVWAVGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQS
IFRSNQFFRGISIPEPEDMETLEEKFSNVQPVALSFMKGCLKMNPDERLTCAQLLDSAYF
ESFQEDQMKRKARSEGRSRRRQQNQLLPLIPGSHISPTPDGRKQVVQLKFDHLPNI

SEQ ID NO: 171_AA397553_H
MPNSERHGGKKDGSGGASGTLQPSSGGGSSNSRERHRLVSKHKRHKSKHSKDMGLVTPEA
ASLGTVIKPLVEYDDISSDSDTFSDDMAFKLDRRENDERRGSDRSDRLHKHRHHQHRRSR

FIGURE 1M

DLLKAKQTEKEKSQEVSSKSGSMKDRISGSSKRSNEETDDYGKAQVAKSSSKESRSSKLH
KEKTRKERELKSGHKDRSKSHRKRETPKSYKTVDSPKRRSRSPHRKWSDSSKQDDSPSGA
SYGQDYDLSPSRSHTSSNYDSYKKSPGSTSRRQSVSPPYKEPSAYQSSTRSPSPYSRRQR
SVSPYSRRRSSSYERSGSYSGRSPSPYGRRRSSSPFLSKRSLSRSPLPSRKSMKSRSRSP
AYSRHSSSHSKKKRSSSRSRHSSISPVRLPLNSSLGAELSRKKKERAAAAAAAKMDGKES
KGSPVFLPRKENSSVEAKDSGLESKKLPRSVKLEKSAPDTELVNVTHLNTEVKNSSDTGK
VKLDENSEKHLVKDLKAQGTRDSKPIALKEEIVTPKETETSEKETPPPLPTIASPPPPLP
TTTPPPQTPPLPPLPPIPALPQQPPLPPSQPAFSQVPASSTSTLPPSTHSKTSAVSSQAN
SQPPVQVSVKTQVSVTAAIPHLKTSTLPPLPLPPLLPGGDDMDSPKETLPSKPVKKEKEQ
RTRHLLTDLPLPPELPGGDLSPPDSPEPKAITPPQQPYKKRPKICCPRYGERRQTESDWG
KRCVDKFDIIGIIGEGTYGQVYKARDKDTGELVALKKVRLDNEKEGFPITAIREIKILRQ
LIHRSVVNMKEIVTDKQDALDFKKDKGAFYLVFEYMDHDLMGLLESGLVHFSEDHIKSFM
KQLMEGLEYCHKKNFLHRDIKCSNILLNNSGQIKLADFGLARLYNSEESRPYTNKVITLW
YRPPELLLGEERYTPAIDVWSCGCILGELFTKKPIFQANLELAQLELISRLCGSPCPAVW
PDVIKLPYFNTMKPKKQYRRRLREEFSFIPSAALDLLDHMLTLDPSKRCTAEQTLQSDFL
KDVELSKMAPPDLPHWQDCHELWSKKRRRQRQSGVVVEEPPPSKTSRKETTSGTSTEPVK
NSSPAPPQPAPGKVESGAGDAIGLADITQQLNQSELAVLLNLLQSQTDLSIPQMAQLLNI
HSNPEMQQQLEALNQSISALTEATSQQQDSETMAPEESLKEAPSAPVILPSAEQMTLEAS
STPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGPQGPRRTPTMPQEEAAACPPHIL
PPEKRPPEPPGPPPPPPPPPLVEGDLSSAPQELNPAVTAALLQLLSQPEAEPPGHLPHEH
QALRPMEYSTRPRPNRTYGNTDGPETGFSAIDTDERNSGPALTESLVQTLVKNRTFSGSL
SHLGESSSYQGTGSVQFPGDQDLRFARVPLALHPVVGQPFLKAEGSSNSVVHAETKLQNY
GELGPGTTGASSSGAGLHWGGPTQSSAYGKLYRGPTRVPPRGGRGRGVPY

SEQ ID NO: 172_AA789239_H
MEMYETLGKVGEGSYGTVMKCKHKNTGQIVAIKIFYERPEQSVNKIAMREIKFLKQFHHE
NLVNLIEVFRQKKKIHLVFEFIDHTVLDELQHYCHGLESKRLRKYLFQILRAIDYLHSNN
VIIHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYTDYVATRWYRAPELVLKDTSYG
KYVPVDIWALGCMIIEMATGNPYLPSSSDLDLLHKIVLKVXFMPELKAKLLQEAKVNSLI
KPKESSKENELRKDERKTVYTNTLLSSSVLGKEIEKEKKPKEIKVRVIKVKGGRGDISEP
KKKEYEGGLGQQDANENVHPMSPDTKLVTIEPPNPINPSTNCNGLKENPHCGGSVTMPPI
NLTNSNLMAANLSSNLFHPSVRLTERAKKRRTSSQSIGQVMPNSRQEDPGPIQSQMEKGI
FNERTGHSDQMANENKRKLNFSRSDRKEFHFPELPVTIQSKDTKGMEVKQIKMLKRESKK
TESSKIPTLLNVDQNQEKQEFIPLSLLSACCPIFTNICSQLTIRVEMAIARGRI

SEQ ID NO: 173_AA124976_M
LADIVHACLQIDPAERTSSTDLLRHDYFTRDGFIEKFIPELRAKLLQEAKVNSFIKPKEN
FKENEPVRDEKKSVFTNTLLYGNPSLYGKEVDRDKRAKELKVRVIKAKGGKGDVPDQKKP
EYEGDHRQQGTADDTQPSSLDKKPSVLELTNPLNPSENSDGVKEDPHAGGCMIMPPINLT
SSNLLAANLSSNLSHPNSRLTERTKKRRTSSQTIGQTLSNSRQEDTGPTQVQTEKGAFNE
RTGQNDQISSGNKRKLNFPKCDRKEFHFPELPFTVQAKEMKGMEVKQIKVLKRESKKTDS
SKIPTLLSMDPNQEKQEGGDGDCEGKNLKRNRFFFSR

SEQ ID NO: 174_AA575635_M CCRK_M
SASGQLKIADFGLARVFSPDGGRLYTHQVATRWYRAPELLYGARQYDQGVDLWAVGCIMG
ELLNGSPLFPGENDIEQLCCVLRILGTPSPRVWPEITELPDYNKISFEEQAPVPLEEVLP
DASPQALDLLGQFLLYPPRQRIAASQALLHQYFFTAPLPAHPSELPIPQRPGGPAPKAHP
GPPHVHDFHVDRPIEESLLNPELIRPFIPEG

FIGURE 1N

SEQ ID NO: 175_AA631990_H
MITSISTEKSGHTHYPFMITTLQYYRGRGGKTAVWRHFSAEGPFAFAEMRHSKRTHCPDW
DSRESWGHESYRGSHKRKRRSHSSTQENRHCKPHHQFKESDCHYLEARSLNERDYRDRRY
VDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSRSXEIV
DTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAARSEIQVLEHLNSTDPNSVFRC
VQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKL
THTDLKPENILFVKSDYVVKYNSKMKRDERTLKNTDIKVVDFGSATYDDEHHSTLVSTRH
YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPQHMIQ
KTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQ
RITLDEALQHPFFDLLKKK

SEQ ID NO: 176_AA557536_H
MCTVVDPRIVRRYLLRRQLGQGRTFREITLLQVSGLGPPVQSPCPGTDLSRQERNWPSWA
PEHSPSWPSSRLRLSPQEFGDHPNIISLLDVIRAENDRDIYLVFEFMDTDLNAVIRKGGL
LQDVHVRSIFYQLLRATRFLHSGHVVHRDQKPSNVLLDANCTVKLCDFGLARSLGDLPEG
PEDQAVTEYVATRWYRAPEVLLSSHRYTASCPRYTLGVDMWSLGCILGEMLRGRPLFPGT
STLHQLELILETIPPPSEEXRPRQTLDALLPPDTSPEALDLLRRLLVFAPDKRLSATQAL
QHPYVQRFHCPSDEWAREADVRPRAHEGVQLSVPEYRSRVYQMILECGGSSGTSREKGPE
GVSPSQAHLHKPRADPQLPSRTPVQGPRPRPQSSPGHDPAEHESPRAAKNVPRQNSAPLL
QTALLGNGERPPGAKEAPPLTLSLVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV
RVASVQQVPPRLPPEARPGRRMFSTSALQGAQGGARALLGGYSQAYGTVCHSALGHLPLL
EGHHV

SEQ ID NO: 177_N28606_H, MOK_H
MKNYKAIGKIGEGTFSEVMKMQSLRDGNYYACKQMKQRFESIEQVNNLREIQALRRLNPH
PNILMLHEVVFDRKSGSLALICELMDMNIYELIRGRRYPLSEKKIMHYMYQLCKSLDHIH
RNGIFHRDVKPENILIKQDVLKLGDFGSCRSVYSKQPYTEYISTRWYRAPECLLTDGFYT
YKMDLWSAGCVFYEIASLQPLFPGVNELDQISKIHDVIGTPAQKILTKFKQSRAMNFDFP
FKKGSGIPLLTTNLSPQCLSLLHAMVAYDPDERIAAHQALQHPYFQEQRKTEKRALGSHR
KAGFPEHPVAPEPLSNSCQISKEGRKQKQSLKQEEDRPKRRGPAYVMELPKLKLSGVVRL
SSYSSPTLQSVLGSGTNGRVPVLRPLKCIPASKKTDPQKDLKPAPQQCRLPTIVRKGGR

SEQ ID NO: 178_AB023153_H, ICK_H
MNRYTTIRQLGDGTYGSVLLGRSIESGELIAIKKMKRKFYSWEECMNQREVKSLKKLNHA
NVVKLKEVIRENDHLYFIFEYMKENLYQLIKERNKLFPESAIRNIMYQILQGLAFIHKLG
FFHRDLKPENLLCMGPELVKIADFGLAREIRSKPPYTDYVSTRWYRAPEVLLRSTNYSSP
IDVWAVGCIMAEVYTLRPLFPGASEIDTIFKICQVLGTPKKTDWPEGYQLSSAMNFRWPQ
CVPNNLKTLIPNASSEAVQLLRDMLQWDPKKRPTASQALRYPYFQVGHPLGSTTQNLQDS
EKPQKGILERAGPPPYIKPVPPAQPPAKPHTRISSRQHQASQPPLHLTYPYKAEVSRTDH
PSHLQEDKPSPLLFPSLHNKHPQSKITAGLEHKNGEIKPKSRRRWGLISRSTKDSDDWAD
LDDLDFSPSLSRIDLKNKKRQSDDTLCRFESVLDLKPSEPVGTGNSAPTQTSYQRRDTPT
LRSAAKQHYLKHSRYLPGISIRNGILSNPGKEFIPPNPWSSSGLSGKSSGTMSVISKVNS
VGSSSTSSSGLTGNYVPSFLKKEIGSAMQRVHLAPIPDPSPGYSSLKAMRPHPGRPFLDT
QPRSTPGLIPRPPAAQPVHGRTDWASKYPSRR

SEQ ID NO: 179_AA839940_M
SSNNGGMSAEEEIGPGAEPMRGPSLATRDWRDETVGTTDLQQGIDPGAVSPEPGKDHAAQ
GPGRTEAGRVSSAAEAAIVVLDDSAAPPAPFEHRVVSIKDTLISAGYTVSQHEVLGGGRF
GQVHRCTERSTGLALAAKIIKVKNVKDREDVKNEVNIMNQLSHVNLIQLYDAFESKNSFT
LIMEYVDGGELFDRITDEKYHLTELDVVLFTRQICEGVHYLHQHYILHLDLKPENILCVS

FIGURE 10

QTGHQIKIIDFGLARRYKPREKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLL
SGLSPFLGETDAETMNFIVNCSWDFDADTFKGLSEEAKDFVSRLLVKEKSCRMSATQCLK
HEWLNHLPAKASGSNVRLRSQQLLQKYMAQSKWKKHFHVVAAVNRLRKFPTCP

SEQ ID NO: 180_AA460132_H
MAAARATTPADGEEPAPEAEALAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEEIEGSV
TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 181_SGK034_H
QREKVNQGNMPGLQSTFLAMDTEEGVEVVWNELHFGDRKAFAAHEEKIQTVFEQLVLVDH
PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKKNHKAMNARAWKRWCTQILS
ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALPDDLRSPIRAEREELR
NLHFFPPEYGEVADGTAVDIFSFGMCALEMAVLEIQTNGDTRVTEEAIARARHSLSDPNM
REFILCCLARDPARRPSAHSLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAM
DLHAVLAELPRPRRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAP
PPEEVQKAKTPTPEPFDSETRKVIQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLL
PTDSAQDLASELVHYGFLHEDDRMKLAAFLESTFLKYRGTQA

SEQ ID NO: 182_AA103218_M SGK034_M
HASAPEYGEVNDGTGFVDIFSFGMCALEMAVLEIQANGDTRVTEEAIARARHSLSDPNMR
EFILSCLARDPARRPSAHNLLFHRVLFEVHSLKLLAAHCFIQHQYLMPENVVEEKTKAMD
LHAVLAEMPQPHGPPMQWRYSEVSFLELDKFLEDVRNGIYPLMNFAAARPLGLPRVLAPP
PEEAQKAKTPTPEPFDSETRKVVQMQCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLP
TDSAQDLAAELVHYGFLHEDDRTKLAAFLETTFLKYRGTQA

SEQ ID NO: 183_NEK7_H, N34132_H
MSGGAAEKQSSTPGSLFLSPPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHT
MDKDSRGAAATTTTTEHRFFRRSVICDSNATALELPGLPLSLPQPSIPAAVPQSAPPEPH
REETVTATATSQVAQQPPAAAAPGEQAVAGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPP
ARSGSGGGSAKEPQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVYKGLD
TETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNIVRFYDSWESTVKGKKCIVLV
TELMTSGTLKTYLKRFKVMKIKVLRSWCRQILKGLQFLHTRTPLIIHRDLKCDNIFITGP
TGSVKIGDLGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEY
PYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEIIEGCIRQNKDERYSIKDLLNHAFFQ
EETGVRVELAEEDDGEKIAIKLWLRIEDIKKLKGKYKDNEAIEFCFDLERDVPEDVAQEM
VESGYVCEGDHKTMAKAIKDRVSLIKRKREQRQLVREEQENKKQEESSLKQQVEQSSASQ
TGIKQLPSASTGIPTASTTSASVSTQVEPEEPEADQHQQLQYQQPSISVLSDGTVDSGQG
SSVFTESRVSSQQTVSYGFPXHEQAHSTGTVPGHIPSTVQAQSQPHGVYPPSSVQQGIQQ
TAPPQQTVQYSLSQTSTSSEATTAQPVSQPQAPQVLPQVSAGKQSTQGVSQVAPAEPVAV
AQPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSVRSRSRHE
KTSRPKLRILNVSNKGDRVVECQLETHNRKMVTFKFDLDGDNPEEIATIMVNNDFILAIE
RESFVDQVREIIEKADEMLSEDVSVEPEGDQGLESLQGKDDYGFSGSQKLEGEFKQPIPA
SSMPQQIGIPTSSLTQVVHSAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPGMN
LSHSASSLSLQQAFSELRRAQMTEGPNTAPPNFSHTGPTFPVVPPFLSSIAGVPTTAAAT
APVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATSTGVVTSGGLPIPPVSESPVLSSVV
SSITIPAVVSISTTSPSLQVPTSTSEIVVSSTALYPSVTVSATSASAGGSTATPGPKPPA
VVSQQAAGSTTVGATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTS

FIGURE 1P

HSSTTGLAFSLSAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPL
LPQVPSIPPLVQPVANVPAVQQTLIHSQPQPALLPNQPHTHCPEVDSDTQPKAPGIDDIK
TLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVAPSKLLTSTTSTCLPP
TNLPLGTVALPVTPVVTPGQVSTPVSTTTSGVKPGTAPSKPPLTKAPVLPVGTELPAGTL
PSEQLPPFPGPSLTQSQQPLEDLDAQLRRTLSPEMITVTSAVGPVSMAAPTAITEAGTQP
QKGVSQVKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTSESS
VLSSSSPESTLVKPEPNGITIPGISSDVPESAHKTTASEAKSDTGQPTKVGRFQVTTTAN
KVGRFSVSKTEDKITDTKKEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSD
PEAAFLSRDVDDGSGSPHSPHQLSSKSLPSQNLSQSLSNSFNSSYMSSDNESDIEDEDLK
LELRRLRDKHLKEIQDLQSRQKHEIESLYTKLGKVPPAVIIPPAAPLSGRRRRPTKSKGS
KSSRSSSLGNKSPQLSGNLSGQSAASVLHPQQTLHPPGNIPESGQNQLLQPLKPSPSSDN
LYSAFTSDGAISVPSLSAPGQGNKATIIVQKQ

SEQ ID NO: 184_BCON3_H
MSEGESQTVLSSGSDPKVESSSSAPGLTSVSPPVTSTTSAASPEEEEESEDESEILEESP
CGRWQKRREEVNQRNVPGIDSAYLAMDTEEGVEVVWNEVQFSERKNYKLQEEKVRAVFDN
LIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLKKTKKNHKTMNEKAWKRW
CTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINNHVKTCREEQKNL
HFFAPEYGEVTNVTTAVDIYSFGMCALEMAVLEIQGNGESSYVPQEAISSAIQLLEDPLQ
REFIQKCLQSEPARRPTARELLFHPALFEVPSLKLLAAHCIVGHQHMIPENALEEITKNM
DTSAVLAEIPAGPGREPVQTLYSQSPALELDKFLEDVRNGIYPLTAFGLPRPQQPQQEEV
TSPVVPPSVKTPTPEPAEVETRKVVLMQCNIESVEEGVKHHLTLLLKLEDKLNRHLSCDL
MPNENIPELAAELVQLGFISEADQSRLTSLLEETLNKFNFARNSTLNSAAVTVSS

SEQ ID NO: 185_AA711829_M
LKQFLKKTKKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIK
IGSVAPDTINNHVKTCREEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEMAVLEIQGN
GESSYVPQEAISSAIQLLEDSLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLKLLA
AHCIVGHQHMIPENALEEITKNMDTSAVLAEIPAGPGREPVQTLYSQSPALELDKFLEDV
RNGIYPLTAFGLPRPQQPQQEEVTSPVVPPSVKTPTPEPAEVETRKVVLMQCNIESVEEG
VKHHLTLLLKLEDKLNRHLSCDLMPNESIPDLAAELVQLGFISEADQSRLTSLLEETLNK
FNFTRNSTLNTATVTVSS

SEQ ID NO: 186_AA099102_H
MSSCVSSQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGMESFIVVTECEP
GCAVDLGLARDRPLEADGQEVPLDTSGSQARPHLSGRKLSLQERSQGGLAAGGSLDMNGR
CICPSLPYSPVSSPQSSPRLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVK
LAYNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQPRGPIEQVYQEIAIL
KKLDHPNVVKLVEVLDDPNEDHLYMVFELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGI
EYLHYQKIIHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNYVGTPAFMAPESLS
ETRKIFSGKAKDVWAMGVTLYCFVFGQCPFMDERIMCLHSKIKSQALEFPDQPDIAEDLK
DLITRMLDKNPESRIVVPEIKLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPS
LATVILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESLSELKEARQRRQP
PGHRPAPRGGGGSALVRGSPCVESCWAPAPGSPARMHPLRPEEAMEPE

SEQ ID NO: 187_5R69_17_2_H
MQEIPQEQIKEIKKEQLSGSPWILLRENEVSTLYKGEYHRAPVAIKVFKKLQAGSIAIVR
QTFNKEIKTMKKFESPNILRIFGICIDETVTPPQFSIVMEYCELGTLRELLDREKDLTLG

FIGURE 1Q

KRMVLVLGAARGLYRLHHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQTSMSLGTT
REKTDRVKSTAYLSPQELEDVFYQYDVKSEIYSFGIVLWEIATGDIPFQGEECEDWLSQW
L

SEQ ID NO: 188_H85811_H
MAPVYEGMASHVQVFSPHTLQSSAFCSVKKLKIEPSSNWDMTGYGSHSKVYSQSKNIPLS
QPATTTVSTSLPVPNPSLPYEQTIVFPGSTGHIVVTSASSTSVTGQVLGGPHNLMRRSTV
SLLDTYQKCGLKRKSEEIENTSSVQIIEEHPPMIQNNASGATVATATTSTATSKNSGSNS
EGDYQLVQHEVLCSMTNTYEVLEFLGRGTFGQVVKCWKRGTNEIVAIKILKNHPSYARQG
QIEVSILARLSTESADDYNFVRAYECFQHKNHTCLVFEMLEQNLYDFLKQNKFSPLPLKY
IRPVLQQVATALMKLKSLGLIHADLKPENIMLVDPSRQPYRVKVIDFGSASHVSKAVCST
YLQSRYYRAPEIILGLPFCEAIDMWSLGCVIAELFLGWPLYPGDSEYDQIRYISQTQGLP
AEYLLSAGTKTTRFFNRDTDSPYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVN
MTTDLEGSDMLVEKADRREFIDLLKKMLTIDADKRITPIETLNHPFVTMTHLLDFPHSTH
VKSCFQNMEICKRRVNMYDTVNQSKTPFITHVAPSTSTNLTMTFNNQLTTVHNQPSAASM
AAVAQRSMPLQTGTAQICARPDPFQQALIVCPPGFQGLQASPSKHAGYSVRMENAVPIVT
QAPGAQPLQIQPGLLAQQAWPSGTQQILLPPAWQQLTGVATHTSVQHATVIPETMAGTQQ
LADWRNTHAHGSHYNPIMQQPALLTGHVTLPAAQPLNVGVAHVMRQQPTSTTSSRKSKQH
QSSVRNVSTCEVSSSQAISSPQRSKRVKENTPPRCAMVHSSPACSTSVTCGWGDVASSTT
RERQRQTIVIPDTPSPTVSVITISSDTDEEEEQKHAPTSTVSKQRKNVISCVTVHDSPYS
DSSSNTSPYSVQQRAGHNNANAFDTKGSLENHCTGNPRTIIVPPLKTQASEVLVECDSLV
PVNTSHHSSSYKSKSSSNVTSTSGHSSGSSSGAITYRQQRPGPHFQQQQPLNLSQAQQHI
TTDRTGSHRRQQAYITPTMAQAPYSFPHNSPSHGTVHPHLAAAAAAAHLPTQPHLYTYTA
PAALGSTGTVAHLVASQGSARHTVQHTAYPASIVHQVPVSMGPRVLPSPTIHPSQYPAQF
AHQTYISASPASTVYTGYPLSPAKVNQYPYI

SEQ ID NO: 189_DYRK3_H
MMIDETKCPPCSNVLCNPSEPPPPRRLNMTAEQFTGDHTQHFLDGGEMKVEQLFQEFGNR
KSNTIQSDGISDSEKCSPTVSQGKSSDCLNTVKSNSSSKAPKVVPLTPEQALKQYKHHLT
AYEKLEIINYPEIYFVGPNAKKRHGVIGGPNNGGYDDADGAYIHVPRDHLAYRYEVLKII
GKGSFGQVARVYDHKLRQYVALKMVRNEKRFHRQAAEEIRILEHLKKQDKTGSMNVIHML
ESFTFRNHVCMAFELLSIDLYELIKKNKFQGFSVQLVRKFAQSILQSLDALHKNKIIHCD
LKPENILLKHHGRSSTKVIDFGSSCFEYQKLYTYIQSRFYRAPEIILGSRYSTPIDIWSF
RCILAELLTGQPLFPGEDEGDQLACMMELLGMPPPKLLEQSKRAKYFINSKGIPRYCSVT
TQADGRVVLVGGRSRRGKKRGPPGSKDWGTALKGCDDYLFIEFLKRCLHWDPSARLTPAQ
ALRHPWISKSVPRPLTTIDKVSGKRVVNPASAFQGLGSKLPPVVGIANKLKANLMSETNG
SIPLCSVLPKLIS

SEQ ID NO: 190_AA589241_M DYRK3_M
TRPELLGMPPQKLLEQSKRAKYFINSKGLPRYCSVSTQTDGRVVLLGGRSRRGKKRGPPG
SKDWATALKGCGDYLFIEFLKRCLQWDPSARLTPAQALRHPWISKSTPKPLTMDKVPGKR
VVNPTNAFQGLGSKLPPVVGIASKLKANLMSETSGSIPLCSVLPKLIS

SEQ ID NO: 191_5R72_16_2_H
MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACGPVKEPPEINLVLY
PQGLTGEEVYVKVDLRVKCPPTYPDVVPEIELKNAKGLSNESVNLLKSRLEELAKKHCGE
VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQQRLLEAKRKEEQEQREILHEIQ
RRKEEIKEEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAILHGGSPDFVGNGKHR
ANSSGRSRRERQYSVCNSEDSPGSCEILYFNMGSPDQLMVHKGKCIGSDEQLGKLVYNAL
ETATGGFVLLYEWVLQWQKKMGPFLTSQEKEKIDKCKKQIQGTETEFNSLVKLSHPNVVR

FIGURE 1R

YLAMNLKEQDDSIVVDILVEHISGVSLAAHLSHSGPIPVHQLRRYTAQLLSGLDYLHSNS
VVHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKGD
VWRLGLLLLSLSQGQECGEYPVTIPSDLPADFQDFLKKCVCLDDKERWSPQQLLKHSFIN
PQPKMPLVEQSPEDSGGQDYVETVIPSNRLPSAAFFSETQRQFSRYFIEFEELQLLGKGA
FGAVIKVQNKLDGCCYAVKRIPINPASRQFRRIKGEVTLLSRLHHENIVRYYNAWIERHE
RPAGPGTPPPDSGPLAKDDRAARGQPASDTDGLDSVEAAAPPPILSSSVEWSTSGERSAS
ARFPATGPGSSDDEDDDEDEHGGVFSQSFLPASDSESDIIFDNEDENSKSQNQDEDCNEK
NGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH
EKGMIHRDLKPVNIFLDSDDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGHLTG
MVGTALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPTSP
KFPEDFDDGEHAKQKSVISWLLNHDPAKRPTATELLKSELLPPPQMEESELHEVLHHTLT
NVDGKAYRTMMAQIFSQRISPAIDYTYDSDILKGNFSIRTAKMQQHVCETIIRIFKRHGA
VQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIE
RVFRPRKLDRFHPKELLECAFDIVTSTTNSFLPTAEIIYTIYEIIQEFPALQERNYSIYL
NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSLSSNSLCRLYKF
IEQKGDLQDLMPTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYK
VQQHNGIIFQFVAFIKRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSIAIDK
ISAAVLNMEESVTISSCDLLVVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQ
EYCRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETELVDHVLQKLRTKVTDERNG
REASDNLAVQNLKGSFSNASGLFEIHGATVVPIVSVLAPEKLSASTRRRYETQVQTRLQT
SLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC
DEIYNIKVEKKVSVLFLYSYRDDYYRILF

SEQ ID NO: 192_R43524_H, HRI_H
MLGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQQPTFP
FAVANQLLLVSLLEHLSHVHEPNPLRSRQVFKLLCQTFIKMGLLSSFTCSDEFSSLRLHH
NRAITHLMRSAKERVRQDPCEDISRIQKIRSREVALEAQTSRYLNEFEELVILGKGGYGR
VYKVRNKLDGQYYAIKKILIKGATKTVCMKVLREVKVLAGLQHPNIVGYHTAWIEHVHVI
QPRADRAAIELPSLEVLSDQEEDREQCGVKNDESSSSSIIFAEPTPEKEKRFGESDTENQ
NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQLPLRRNSHLEESFTSTEE
SSEENVNFLGQTEAQYHLMLHIQMQLCELSLWDWIVERNKRGREYVDESACPYVMANVAT
KIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWTNRN
GKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSLGVVLLELFQPFGTEMERAEVLTGL
RTGQLPESLRKRCPVQAKYIQHLTRRNSSQRPSAIQLLQSELFQNSGNVNLTLQMKIIEQ
EKEIAELKKQLNLLSQDKGVRDDGKDGGVG

SEQ ID NO: 193_17000057519457_H
MAAARATTPADGEEPAPEAEALAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEEIEGSV
TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 194_AA013524_M
LVQQGAEARVFRGRFQGRAAVVKHRFPKSYRHPELEARLGRRRTVQEARALLRCRRAGIA
APVVFFVDYASNCLYMEEIEDSVTVRDYIQSTMETEKDPQCLLDLARRMGQVLAGMHDQD
LIHGDLTTSNMLLRRPLAQLHIVLIDFGLSFVSGLPEDKGVDLYVLEKAFLSTHPHTETA
FEAFLKSYGASSKKSSPVLKKLDEVRLRGRKRSMVG

FIGURE 1S

SEQ ID NO: 195_17000139801197_H, IRAKM_H
MAGNCGARGALSAHTLLFDLPPALLGELCAVLDSCDGALGWRGLAERLSSSWLDVRHIEK
YVDQGKSGTRELLWSWAQKNKTIGDLLQVLQEMGHRRAIHLITNYGAVLSPSEKSYQEGG
FPNILFKETANVTVDNVLIPEHNEKGVLLKSSISFQNIIEGTRNFHKDFLIGEGEIFEVY
RVEIQNLTYAVKLFKQEKKMQCKKHWKRFLSELEVLLLFHHPNILELAAYFTETEKFCLI
YPYMRNGTLFDRLQCVGDTAPLPWHIRIGILIGISKAIHYLHNVQPCSVICGSISSANIL
LDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSSSSKHLWYMPEEYIRQGKLSIKTDVYSF
GIVIMEVLTGCRVVLDDPKHIQLRDLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFC
LAGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRCPSPLFLENVPSIPVE
DDESQNNNLLPSDEGLRIDRMTQKTPFECSQSEVMFLSLDKKPESKRNEEACNMPSSSCE
ESWFPKYIVPSQDLRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE

SEQ ID NO: 196_AA840598_M IRAKM_M
MWKRFLSELEVLLLFRHPHILELAAYFTETEKLCLVYPYMSNGTLFDRLQCTNGTTPLSW
HVRISVLIGIAKAIQYLHNTQPCAVICGNVSSANILLDDQLQPKLTDFAAAHFRPNLEQQ
SSTINMTGGGRKHLWYMPEEYIRQGRLSVKTDVYSFGIVIMEVLTGCKVVLDDPKHVQLR
DLLMELMEKRGLDSCLSFLDRKIPPCPRNFSAKLFSLAGRCVATKAKLRPTMDEVLSSLE
STQPSLYFAEDPPTSLKSFRCPSPLFLDNVPSIPVEDDENQNNHSVPPKEVLGTDRVTQK
TPFECSQSEVTFLGLDRNRGNRGSEADCNVPSSSHEECWSPELVAPSQDLSPTVISLGSS
WEVPGHSYGSKPMEKRCSSGLFCSEHEQSKKQ

SEQ ID NO: 197_AA088547_H
MASAVRGSRPWPRLGLQLQFAALLLGTLSPQVHTLRPENLLLVSTLDGSLHALSKQTGDL
KWTLRDDPVIEGPMYVTEMAFLSDPADGSLYILGTQKQQGLMKLPFTIPELVHASPCRSS
DGVFYTGRKQDAWFVVDPESGETQMTLTTEGPSTPRLYIGRTQYTVTMHDPRAPALRWNT
TYRRYSAPPMDGSPGKYMSHLASCGMGLLLTVDPGSGTVLWTQDLGVPVMGVYTWHQDGL
RQLPHLTLARDTLHFLALRWGHIRLPASGPRDTATLFSTLDTQLLMTLYVGKDETGFYVS
KALVHTGVALVPRGLTLAPADGPTTDEVTLQVSGEREGSPSTAVRYPSGSVALPSQWLLI
GHHELPPVLHTTMLRVHPTLGSGTAETRPPENTQAPAFFLELLSLSREKLWDSELHPEEK
TPDSYLGLGPQDLLAASLTAVLLGGWILFVMRQVVEKQQETPLAPADFAHISQDAQSLHS
GASRRSQKRLQSPSKQAQPLDDPEAEQLTVVGKISFNPKDVLGRGAGGTFVFRGQFEGRA
VAVKRLLRECFGLVRREVQLLQESDRHPNVLRYFCTERGPQFHYIALELCRASLQEYVEN
PDLDRGGLEPEVVLQQLMSGLAHLHSLHIVHRDLKPGNILITGPDSQGLGRVVLSDFGLC
KKLPAGRCSFSLHSGIPGTEGWMAPELLQLLPPDSPTSAVDIFSAGCVFYYVLSGGSHPF
GDSLYRQANILTGAPCLAHLEEEVHDKVVARDLVGAMLSPLPQPRPSAPQVLAHPFFWSR
AKQLQFFQDVSDWLEKESEQEPLVRALEAGGCAVVRDNWHEHISMPLQTDLRKFRSYKGT
SVRDLLRAVRNKKHHYRELPVEVRQALGQVPDGFVQYFTNRFPRLLLHTHRAMRSCASES
LFLPYYPPDSEARRPCPGATGR

SEQ ID NO: 198_HGP_6644466
MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTGVNVYLMKRSPRGLSHSP
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGE
KSLNDLIEERYKASQDPFPAAIILKVALNMARGLKYLHQEKKLLHGDIKSSNVVIKGDFE
TIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEAVEENGVITDKADIFAFGLTLWEM
MTLSIPHINLSNDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIELFSVC
TNEDPKDRPSAAHIVEALETDV

SEQ ID NO: 199_AA449542_M
SPRGLSHSPWAVKKISLLCDDHYRTVYQKRLTDEAKILKNLNHPNIIGYRAFTEASDGSL
CLAMEYGGEKSLNDLIEERNKDSGSPFPAAVILRVALHMARGLKYLHQEKKLLHGDIKSS

FIGURE 1T

NVVIKGDFETIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEALEENGIITDKADVF
AFGLTLWEMMTLCIPHVNLPDDDVDEDATFDESDFDDEAYYAALGTRPSINMELDDSYQK
AIELFCVCTNEDPKDRPSAAHIVEALELDGQCCGLSESKH

SEQ ID NO: 200_5R57_10_2_M TESK2_M
LLDSDLYLPWTVRVKLAYGIAVGLSYLHFKGIFHRDLTSKV

SEQ ID NO: 201_AA232253_H
MSSLGASFVQIKFDDLQFFENCGGGSFGSVYRAKWISQDKEVAVKKLLKIEKEAEILSVL
SHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMDHIMTWATDVAKGMHY
LHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTTHMSLVGTFPWMAPEVIQS
LPVSETCDTYSYGVVLWEMLTREVPFKGLEGLQVAWLVVEKNERLTIPSSCPRSFAELLH
QCWEADAKKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAEWRCEIEATLERLKKLERD
LSFKEQELKERERRLKMWEQKLTEQSNTPLLPSFEIGAWTEDDVYCWVQQLVRKGDSSAE
MSVYASLFKENNITGKRLLLLEEEDLKDMGIVSKGHIIHFKSAIEKLTHDYINLFHFPPL
IKDSGGEPEENEEKIVNLELVFGFHLKPGTGPQDCKWKMYMEMDGDEIAITYIKDVTFNT
NLPDAEILKMTKPPFVMEKWIVGIAKSQTVECTVTYESDVRTPKSTKHVHLIQWSRTKPQ
DEVKAVQLAIQTLFTNSDGNPGSRSDSSADCQWLDTLRMRQIASNTSLQRSQSNPILGSP
FFSHFDGQDSYAAAVRRPQVPIKYQQITPVNQSRSSSPTQYGLTKNFSSLHLNSRDSGFS
SGNTDTSSERGRYSDRSRNKYGRGSISLNSSPRGRYSGKSQHSTPSRGRYPGKFYRVSQS
ALNPHQSPDFKRSPRDLHQPNTIPGMPLHPETDSRASEEDSKVSEGGWTKVEYRKKPHRP
SPAKTNKERARGDHRGWRNF

SEQ ID NO: 202_AI375137_H
MGNYKSRPTQTCTDEWKKKVSESYVITIERLEDDLQIKEKELTELRNIFGSDEAFSKVNL
NYRTENGLSLLHLCCICGGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL
LHSGADIQQVGYGGLTALHIATIAGHLEAADVLLQHGANVNIQDAVFFTPLHIAAYYGHE
QVTRLLLKFGADVNVSGEVGDRPLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVPLH
FCSRFGHHDIVKYLLQSDLEVQPHVVNIYGDTPLHLACYNGKFEVAKEIIQISGTESLTK
ENIFSETAFHSACTYGKSIDLVKFLLDQNVININHQGRDGHTGLHSACYHGHIRLVQFLL
DNGADMNLVACDPSRSSGEKDEQTCLMWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG
GDGSYVSVPSPLGKIKSMTKEKADILLLRAGLPSHFHLQLSEIEFHEIIGSGSFGKVYKG
RCRNKIVAIKRYRANTYCSKSDVDMFCREVSILCQLNHPCVIQFVGACLNDPSQFAIVTQ
YISGGSLFSLLHEQKRILDLQSKLIIAVDVAKGMEYLHNLTQPIIHRDLNSHNILLYEDG
HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT
GEIPFAHLKPAAAAADMAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE
ECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA
LSQSAGQYSSQGLSLEEMKRSLQYTPIDKYGYVSDPMSSMHFHSCRNSSSFEDSS

SEQ ID NO: 203_H97685_H
MESERSPLYRQLIDLGYLSSSHWNCGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRL
VDAAKALNLVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMNIANRKQEE
MKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEPVGTREIKCCIRQIQELIISRLNQA
VANKLISSVDYLRESFVGTLERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGS
SVTRMLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAKSICSQFRTRLNS
SHEAFAASLRQLEAGHSGRLEKTEDLWLRVRKDHAPRLARLSLESRSLQDVLLHRKPKLG
QELGRGQYGVVYLCDNWGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG
SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIALDVVEGIRFLHSQGLVH
RDIKLKNVLLDKQNRAKITDLGFCKPEAMMSGSIVGTPIHMAPELFTGKYDNSVDVYAFG

FIGURE 1U

ILFWYICSGSVKLPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDGDPLK
RPLLGIVQPMLQGIMNRLCKSNSEQPNRGLDDST

SEQ ID NO: 204_W20810_M
DVNLKASKASDVYSFGILVWAVLAGREAELVDKTSLIRETVCDRQSRPPLTELPPGSPET
PGLEKLKELMIHCWGSQSENRPSFQDCEPKTNEVYNLVKDKVDAAVSEVKHYLSQHRSSG
RNLSAREPSQRGTEMDCPRETMVSKMLDRLHLEEPSGPVPGKCPERQAQDTSVGPATPAR
TSSDPVAGTPQIPHTLPFRGTTPGPVFTETPGPHPQRNQGDGRHGTPWYPWTPPNPMTGP
PALVFNNCSEVQIGNYNSLVAPPRTTASSSAKYDQAQFGRGRGWQPFHK

SEQ ID NO: 205_AA744236_H
MGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYKRENEDKVNKAAKHLKTL
RHPCLLRFLSCTVEADGIHLVTERVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHL
THNNVCLSSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPPEEMSPEFTT
LPECHGHARDAFSFGTLVESLLTIILNEQVSADVLSSFQQTLHSTLLNPIPKCRPALCTLL
SHDFFRNDFLEVVNFLKSLTLKSEEEKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVF
AEPVAVKSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLFEVHEEHVRMVLLSH
IEAYVEHFTQEQLKKVILPQVLLGLRDTSDSIVAITLHSLAVLVSLLGPEVVVGGERTKI
FKRTAPSFTKNTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSENFPSSSKKSEEWPDWSE
PEEPENQTVNIQIWPREPCDDVKSQCTTLDVEESSWDDCEPSSLDTKVNPGGGITATKPV
TSGEQKPIPALLSLTEESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSELG
LGEEFTIQVKKKPVKDPEMDWFADMIPEIKPSAAFLILPELRTEMVPKKDDVSPVMQFSS
KFAAAEITEGEAEGWEEEGELNWEDNNW

SEQ ID NO: 206_AI052250_H
MESMLNKLKSTVTKVTADVTSAVMGIPVTREFDVGRHIASGCNGLAWKIFNGTKKSTKQE
VAVFVFDKKLIDKYQKFEKDQIIDSLKRGVQQLTRLRHPRLLTVQHPLEESRDCLAFCTE
PVFASLANVLGNWENLPSPISPDIKDYKLYDVETKYGLLQVSEGLSFLHSSVKMVHGNIT
PENIILNKSGAWKIMGFDFCVSSTNPSEQEPKFPCKEWDPNLPSLCLPNPEYLAPEYILS
VSCETASDMYSLGTVMYAVFNKGKPIFEVNKQDIYKSFSRQLDQLSRLGSSSLTNIPEEV
REHVKLLLNVTPTVRPDADQMTKIPFFDDVGAVTLQYFDTLFQRDNLQKSQFFKGLPKVL
PKLPKRVIVQRILPCLTSEFVNPDMVPFVLPNVLLIAEECTKEEYVKLILPELGPVFKQQ
EPIQILLIFLQKMDLLLTKTPPDEIKNSVLPMVYRALEAPSIQIQELCLNIIPTFANLID
YPSMKNALIPRIKNACYKHLPLRFV

SEQ ID NO: 207_AA278842_H
MWFFARDPVRDFPFELIPEPPEGGLPGPWALHRGRKKATGSPVSIFVYDVKPGAEEQTQV
AKAAFKRFKTLRHPNILAYIDGLETEKCLHVVTEAVTPLGIYLKARVEAGGLKELEISWG
LHQIVKALSFLVNDCSLIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE
LEQYDPPELADSSGRVVREKWSADMWRLGCLIWEVFNGPLPRAAALRNPGKIPKTLVPHY
CELVGANPKVRPNPARFLQNCRAPGGFMSNRFVETNLFLEEIQIKEPAEKQKFFQELSKS
LDAFPEDFCRHKVLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVKMFSS
TDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDTNPAIREQTVKSMLLLAPKLN
EANLNVELMKHFARLQAKDEQGPIRCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPF
APSRVAGVLGFAATHNLYSMNDCAQKILPVLCGLTVDPEKSVRDQAFKAIRSFLSKLESV
SEDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTGVSSLTSKLIRSHPTTAPTETNIPQ
RPTPEGVPAPAPTPVPATPTTSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVL
AQQDDWSTGGQVSRASQVSNSDHKSSKSPESDWSSWEAEGSWEQGWQEPSSQEPPPDGTR
LASEYNWGGPESSDKGDPFATLSARPSTQPRPDSWGEDNWEGLETDSRQVKAELARKKRE
ERRREMEAKRAERKVAKGPMKLGARKLD

FIGURE 1V

SEQ ID NO: 208_AA599286_H
MAFMEKPPAGKVLLDDTVPLTAAIEASQSLQSHTEYIIRVQGGISVENSWQIVRRYSDFD
LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD
PNNYSANYTEIALQQVSMFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLSW
ADLGPDKYLSDKDFQCLIKLLPSCLHPYIYRVTFATANESSALLIRMFNEKGTLKDLIYK
AKPKDPFLKKYCNPKKIQGLELQQIKTYGRQILEVLKFLHDKGFPYGHLHASNVMLDGDT
CRLLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP
PAPSMAVVAVLESTLSCEACKNGMPTISRLLQMPLFSDVLLTTSEKPQFKIPTKLKEALR
IAKECIEKRLIEEQKQIHQHRRLTRAQSHHGSEEERKKRKILARKKSKRSALENSEEHSA
KYSNSNNSAGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPAAPLPPASTEAPAQLS
SQAVNGMSRGALLSSIQNFQKGTLRKAKPVITVLRRSAEASCLHLEGKVLFYSYSPLPPN
YPLPGKVIAEPVQPQTVLFCRCSCKQLFERNNSLSRIKLGWHAKKKKKK

SEQ ID NO: 209_AA425725_H
MSASTGGGGDSGGSGGSSSSSQASCGPESSGSELALATPVPQMLQGLLGSDDEEQEDPKD
YCKGGYHPVKIGDVFNGRYHVVRKLGWGHFSTVWLCWDIQRKRFVALKVVKSAGHYTETA
VDEIKLLKCVRDSDPSDPKRETIVQLIDDFRISGVNGVHVCMVLEVLGHQLLKWIIKSNY
QGLPVPCVKSIVRQVLHGLDYLHTKCKIIHTDIKPENILLCVGDAYIRRLAAEATEWQQA
GAPPPSRSIVSTAPQEVLTGKLSKNKRKKMRRKRKQQKRLLEERLRDLQRLEAMEAATQA
EDSGLRLDGGSGSTSSSGFSGSLFSPASCSILSGSSNQRETGGLLSPSTPFGASNLLVNP
LEPQNADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEYGPPADIWSTACMAF
ELATGDYLFEPHSGEDYSRDEDHIAHIVELLGDIPPAFALSGRYSREFFNRRGELRHIHN
LKHWGLYEVLMEKYEWPLEQATQFSAFLLPMMEYIPEKRASAADCLQHPWLNP

SEQ ID NO: 210_SGK022_H
MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGGPSEFIQRFLPRELQ
IVRTLDHKNIIQVYEMLESADGKICLVMELAEGGDVFDCVLNGGPLPESRAKALFRQMVE
AIRYCHGCGVAHRDLKCENALLQGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEV
LQGIPHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSFPTHLSISADCQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 211_AA060026_M SGK022_M
MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKIIDKMGGPEEFIQRFLPRELQ
IVRTLDHKNIIQVYEMLESADGKIYLVMELAEGGDVFDCVLNGGPLPESRAKALFRQMVE
AIRYCHGCGVAHRDLKCENALLQGFNLKLTDFGFAKVLPKSRRELSQTFCGSTAYAAPEV
LQGIPHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSFPTHLGISTECQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 212_AA399669_H
MGKGDVLEAAPTTTAYHSLMDEYGYEVGKAIGHGSYGSVYEAFYTKQKVMVAVKIISKKK
ASDDYLNKFLPREIQQVMKVLRHKYLINFYRAIESTSRVYIILELAQGGDVLEWIQRYGA
CSEPLAGKWFSQLTLGIAYLHSKSIVHRDLKLENLLLDKWENVKISDFGFAKMVPSNQPV
GCSPXYRQVNCFSHLSQTYCGSFAYACPEILRGLPYNPFLSDTWSMGVILYTLVVAHLPF
DDTNLKKLLRETQKEVTFPANHTISQECKVQLLIACVAQWRKTQARPLSPLL

SEQ ID NO: 213_AA758539_H
MDDATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRRKTPTDFVERFLPRE
MDILATVNHGSIIKTYEIFETSDGRIYIIMELGVQGDLLEFIKCQGALHEDVARKMFRQL
SSAVKYCHDLDIVHRDLKCENLLLDKDFNIKLSDFGFSKRCLRDSNGRIILSKTFCGSAA

FIGURE 1W

YAAPEVLQSIPYQPKVYDIWSLGVILYIMVCGSMPYDDSDIRKMLRIQKEHRVDFPRSKN
LTCECKDLIYRMLQPDVSQRLHIDEILSHSWLQPPKPKATSSASFKREGEGKYRAECKLD
TKTGLRPDHRPDHKLGAKTQHRLLVVPENENRMEDRLAETSRAKDHHISGAEVGKAST

SEQ ID NO: 214_AA883975_H
MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKYKGTVAIKVVDRRRAPPDFVNKFLPRE
LSILRGVRHPHIVHVFEFIEVCNGKLYIVMEAAATDLLQAVQRNGRIPGVQARDLFAQIA
GAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGRQAHGYPDLSTTYCGSAAYASP
EVLLGIPYDPKKYDVWSMGVVLYVMVTGCMPFDDSDIAGLPRRQKRGVLYPEGLELSERC
KALIAELLQFSPSARPSAGQVARNCWLRAGDSG

SEQ ID NO: 215_AA905446_H
VGRQETGVRRWAFLICQPISPPLTSSEFIQRFLPRELQIVRTLDHKNIIQVYEMLESADG
KICLVMELAEGGDVFDCVLNGGPLPESRAKALFRQMVEAIRYCHGCGVAHRDLKCENALL
QGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEVLQGIPXKMLWQQQKGVSFPTHL
SISADCQDLLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 216_H29974_H
YSLLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVELALAEFWALTSLKRRHQNV
VQFEECVLQRNGLAQRMSHGNKSSQLYLRLVETSLKGERILGYAEEPCYLWFVMEFCEGG
DLNQYVLSRRPDPATNKSFMLQLTSAIAFLHKNHIVHRDLKPDNILITERSGTPILKVAD
FGLSKVCAGLAPRGKEGNQDNKNVNVNKYWLSSACGSDFYMAPEVWEGHYTAKADIFALG
IIIWAMIERITFIDSETKKELLGTYIKQGTEIVPVGEALLENPKMELHIPQKRRTSMSEG
IKQLLKDMLAANPQDRPDAFELETRMDQVTCAA

SEQ ID NO: 217_AA498104_M H29974_M
PLLLPPPPAAMETGKENGARRGTKSPERKRRSPVQRVLCEKLRPAAQAMDPAGAEVPGEA
FLARRRPDGGGGDVPARPRYSLLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVE
LALAEFWALTSLKRRHQNIVQFEECVLQRNGLAQRMSHGNKNSQLYLRLVETSLKGERIL
GYAEEPCYLWFVMEYCEGGDLNQYVLSRRPDPATNKSFMLQLTSAIAFLHKNHIVHRDLK
PDNILITERSGTPILKVADFGLSKVCAGLAPRGKEGNQDNKNVNVNKYWLSSACGSDFYM
APEVWEGHYTAKADIFALGIIIWAMIERITFIDSETKKELLGTYIKQGTEIVPVGEALLE
NPKMELHIPQKRRTSMSEGVKQLLKDMLAANPQDRPDAFELETRMDQVTCAA

SEQ ID NO: 218_AA215311_H
MVSSQPKYDLIREVGRGSYGVVYEAVIRKTSARVAVKKIRCHAPENVELALREFWALSSI
KSQHPNVIHLEECILQKDGMVQKMSHGSNSSLYLQLVETSLKGEIAFDPRSAYYLWFVMD
FCDGGDMNEYLLSRKPNRKTNTSFMLQLSSALAFLHKNQIIHRDLKPDNILISQTRLDTS
DLEPTLKVADFGLSKVCSASGQNPEEPVSVNKCFLSTACGTDFYMAPEVWEGHYTAKADI
FALGIIIWAMLERITFIDTETKKELLGSYVKQGTEIVPVGEALLENPKMELLIPVKKKSM
NGRMKQLIKEMLAANPQDRPDAFELELRLVQIAFKDSSWET

SEQ ID NO: 219_AA018361_H
MRAAFPAGGAGGSVEPPSARPAPQPAGTAARSEEAPARAQAAGMAGPGWGPPRLDGFILT
ERLGSGTYATVYKAYAKKDTREVVAIKCVAKKSLNKASVENLLTEIEILKGIRHPHIVQL
KDFQWDSDNIYLIMEFCAGGDLSRFIHTRRILPEKVARVFMQQLASALQFLHERNISHLD
LKPQNILLSSLEKPHLKLADFGFAQHMSPWDEKHVLRGSPLYMAPEMVCQRQYDARVDLW
SMGVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLSRDCRDLLQRLLERDPSR
RISFQDFFAHPWVDLEHMPSGESLGRATALVVQAVKKDQEGDSAAALSLYCKALDFFVPA

FIGURE 1X

LHYEVDAQRKEAIKAKVGQYVSRAEELKAIVSSSNQALLRQGTSARDLLREMARDKPRLL
AALEVASAAMAKEEAAGGEQDALDLYQHSLGELLLLLRSPRAGGGSCFTLRFRTSWPELN
T

SEQ ID NO: 220_AA311714_H
MENFILYEEIGRGSKTVVYKGRRKGTINFVAILCTDKCRRPEITNWVRLTREIKHKNIVT
FHEWYETSNHLWLVXENLPEDVVREFGIDLISGLHHLHKLGILFCDISPRKILLEGPGTL
KFSNFCLAKVEGENLEEFFALVAAEEGGGDNGENVLKKSMKSRVKGSPVYTAPEVVRGAD
FSISSDLWSLGCLLYEMFSGKPPFFSESVSELTEKILCEDPLPPIPKDSSRPKASSDFIN
LLDGLLQRDPQKRLTWTRLLQHSFWKKAFAGADQESSVEDLSLSRNTMECSGPQDSKELL
QNSQSRQAKGHKSGQPLGHSFRLENPTEFRPKSTLEGQLNESMFLLSSRPTPRTSTAVEV
SPGEDMTHCSPQKTSPLTKITSGHLSQQDLESQMRELIYTDSDLVVTPIIDNPKIMKQPP
VKFDAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMGASRAKLNLLCYLCVV
AGHQEVATRLLHSPLFQLLIQHLRIAPNWDIRAKVAHVIGLLASHTTELQENTPVVETTS
SIGIGILNCLVQHSTPVPRQCLVYV

SEQ ID NO: 221_SGK384_H
SLAHVLRARQILTEPEVRDYLRGLVSGLRYLHQRCILHR

SEQ ID NO: 222_AA210451_M SGK384_M
MGQQHGTRNGLTHRELPRGVGLLLAMALMNVALYLCLDQLFISPGRSTADSRRCPPGYFR
MGRMRNCSRWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALSRLTRLEMKEDFLH
GLQMLKSLQSEHVVTLVGYCEEDGTILTEYHPLGSLSNLEETLNLSKYQDVNTWQHRLQL
AMEYVSIINYLHHSPLGTRVMCDSNDLPKTLSQYLLTSNFSIVANDLDALPLVDHDSGVL
IKCGHRELHGDFVAPEQLWPYGEDTPFQDDLMPSYNEKVDIWKIPDVSSFLLGHVEGSDM
VRFHLFDIHKACKSQIPAERPTAQNVLDAYQRVFHSLRDTVMSQTKEML

SEQ ID NO: 223_SGK071_2_H
EVVAVQMMVECMDDHYASQALEELMPLLKLRHAHISVYQELFITWNGEISSLYLCLVMEF
NELSFQEVIEDKRKAKKIIDSEWMQNVLGQVLDALEYLHHLDIIHRNLKPSNIILISSDH
CKLQDLSSNVLMTDKAKWNIRAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIILDMTSC
SFMDGTEAMHLRKSLRQSPGSLKAVLKTMEEKQIPDVETFRNLLPLMLQIDPSDRITIKD
VVHITFLRGSFKSSCVSLTLHRQMVPASITDMLLEGNVASILGDAGDTKGERALKLLSMA
LASYCLVPEGSLFMPLALLHMHDQWLSCDQDRVPGKRDFASLGKLGKLLGPIPKGLPWPP
ELVEVVVTTMELHDRVLDVQLCACSLLLHLLGQALVHHPEAKAPCNQAITSTLLSALQSH
PEEEPLLVMVYSLLAITTTQESESLSEELQNAGLLEHILEHLNSSLESRDVCASGLGLLW
ALLLDDPILALQRPRKKRAPNHGKPGKPKNPASTQSIIVNKAPLEKVPDLISQVLATYPA
DGEMAEASCGVFWLLSLLGCIKEQQFEQVVALLLQSIRLCQDRALLVNNAYRGLASLVKV
SELAAFKVVVQEEGGSGLSLIKETYQLHRDDPEVVENVGMLLVHLASYEEILPELVSSSM
KALLQEIKERFTSSLVSDSSAFSKPGLPPGGSPQLGCTTSGGLE

SEQ ID NO: 224_AA118352_M SGK071_M
EEDPCQKSWMAPEALKFSFSTKSDIWSLGCIILDMATCSFLNDTEAMQLRKAIRHHPGSL
KPILKTMEEKQIPGTDVYYLLLPFMLHINPSDRLAIKDVMQVTFMSNSFKSSSVALNMQR
QKVPIFITDVLLEGNMANILGSWLCASFVNDSRHCDSGIGSQRLGFDFQSVSWTEHPLKD
VMQNFSSRPEVQLRAINKLLTMPEDQLGLPWPTELLEEVISIIKQHGRILDILLSTCSLL
LRVLGQALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISSQGQISEEL
EEEGLFQLAQENLEHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHP
EDVEIAEAGCAVLWLLSLLGCIKESQFEQVVVLLLRSIQLCPGRVLLVNNAFRGLASLAK

FIGURE 1Y

VSELVAFRIVVLEEGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGG
IKDLVQVIRGRFTSSLELISYADEILQVLEANAQPGLQEDQLEPPAGQEAPLQGEPLFRP

SEQ ID NO: 225_018653.9_H
GRGRGAGHARGLGRGPAGRRAEPPRSLSRPGPGPGSRAGPAGRGEGSDAAPAGGSGRGFL
RLLPAGLRPQRALRSGSEPPRPGQSPEPSPAPGAGRRGGRGELARQIRARYEEVQRYSRG
GPGPGAGRPERRRLMDLAPGGPGLPRPRPPWARPLSDGAPGWPPAPGPGSPGPGPRLGCA
ALRNVSGAQYMGSGYTKAVYRVRLPGGAAVALKAVDFSGHDLGSCVREFGVRRGCYRLAA
HKLLKEMVLLERLRHPNVLQLYGYCYQDSEDIPDTLTTITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKVTDLDDARVEETPCAGSTDCI
LEFPARNFTLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDSIVNATGE
LAWGVDETLAQLEKVLHLYRSGQYLQNSTASSSTEYQCIPDSTIPQEDYRCWPSYHHGSC
LLSVFNLAEAVDVCESHAQCRAFVVTNQTTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

SEQ ID NO: 226_AA396601_M
TRPGCAALRNVSGAQYVGSGYTKAVYRVRLPGGAAVALKAVDFSGHDLGSCVREFGARRG
CYRLAAHKLLKEMVLLERLRHPNVLQLYGYCYQDSEGIPDTLTTITELGAPVEMIQLLQT
SWEDRFRICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVNGELKVTDLDDARVEETPCT
SSADCTLEFPARNFSLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDSI
VNATGELAWGVDETLAQLETALHLFRSGQYLQNSTSSRAEYQRIPDSAITQEDYRCWPSY
HHGGCLLSVFNLAEAIDVCESHAQCRAFVVTNQTTWTGRKLVFFKTGWNQVVPDAGKTTY
VKAPG

SEQ ID NO: 227_VRK3_H
MISFCPDCGKSIQAAFKFCPYCGNSLPVEEHVGSQTFVNPHVSSFQGSKRGLNSSFETSP
KKVKWSSTVTSPRLSLFSDGDSSESEDTLSSSERSKGSGSRPPTPKSSPQKTRKSPQVTR
GSPQKTSCSPQKTRQSPQTLKRSRVTTSLEALPTGTVLTDKSGRQWKLKSFQTRDNQGIL
YEAAPTSTLTCDSGPQKQKFSLKLDAKDGRLFNEQNFFQRAAKPLQVNKWKKLYSTPLLA
IPTCMGFGVHQDKYRFLVLPSLGRSLQSALDVSPKHVLSERSVLQVACRLLDALEFLHEN
EYVHGNVTAENIFVDPEDQSQVTLAGYGFAFRYCPSGKHVAYVEGSRSPHEGDLEFISMD
LHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGPCGH
WIRPSETLQKYLKVVMALTYEEKPPYAMLRNNLEALLQDLRVSPYDPIGLPMVP

SEQ ID NO: 228_S71575_M VRK3_M
IPTCIGFGIHQDKYRFLVFPSLGRSLQSALDDNPKHVVSERCVLQVACRLLDALEYLHEN
EYVHGNLTAENVFVNPEDLSQVTLVGYGFTYRYCPGGKHVAYKEGSRSPHDGDLEFISMD
LHKGCGPSRRSDLQTLGYCMLKWLYGSLPWTNCLPNTEKITRQKQKYLDSPERLVGLCGR
WNKASETLREYLKVVMALNYEEKPPYATLRNSLEALLQDMRVSPYDPLDLQMVP

SEQ ID NO: 229_AA45427_H
MGHALCVCSRGTVIIDNKRYLFIQKLGEGGFSYVDLVEGLHDGHFYALKRILCHEQQDRE
EAQREADMHRLFNHPNILRLVAYCLRERGAKHEAWLLLPFFKRGTLWNEIERLKDKGNFL
TEDQILWLLLGICRGLEAIHAKGYAHRDLKPTNILLGDEGQPVLMDLGSMNQACIHVEGS
RQALTLQDWAAQRCTISYRAPELFSVQSHCVIDERTDVWSLGCVLYAMMFGEGPYDMVFQ
KGDSVALAVQNQLSIPQSPRHSSALRQLLNSMMTVDPHQRPHIPLLLSQLEALQPPAPGQ
HTTQI

SEQ ID NO: 230_H05721_H
MAVRQALGRGLQLGRALLLRFTGKPGRAYGLGRPGPAAGCVRGERPGWAAGPGAEPRRVG
LGLPNRLRFFRQSVAGLAARLQRQFVVRAWGCAGPCGRAVFLAFGLGLGLIEEKQAESRR

FIGURE 1Z

AVSACQEIQAIFTQKSKPGPDPLDTRRLQGFRLEEYLIGQSIGKGCSAAVYEATMPTLPQ
NLEVTKSTGLLPGRGPGTSAPGEGQERAPGAPAFPLAIKMMWNISAGSSSEAILNTMSQE
LVPASRVALAGEYGAVTYRKSKRGPKQLAPHPNIIRVLRAFTSSVPLLPGALVDYPDVLP
SRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNTPSPRLAAMMLLQLLEGVDHLVQQGIAH
RDLKSDNILVELDPDGCPWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVST
ARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFYGQGKAHLESRSYQEAQLPALPESVPP
DVRQLVRALLQREASKRPSARVAANVLHLSLWGEHILALKNLKLDKMVGWLLQQSAATLL
ANRLTEKCCVETKMKMLFLANLECETLCQAALLLCSWRAAL

SEQ ID NO: 231_AI086865_H
MEKYERIRVVGRGAFGIVHLCLRKADQKLVIIKQIPVEQMTKEERQAAQNECQVLKLLNH
PNVIEYYENFLEDKALMIAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALHHVH
THLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSTPCYISPELCEGKPYNQKSDIW
ALGCVLYELASLKRAFEAANLPALVLKIMSGTFAPISDRYSPELRQLVLSLLSLEPAQRP
PLSHIMAQPLCIRALLNLHTDGREVRGPQQHREQDHQCPLQRGIIMTFGSGSNGCLGHGS
LTDISQPTIVEALLGYEMVQQVEEALSFTLLGSAPLDQEPLLSIDLGTAHSAAVTGEEDL
GSGDVNRLPSWERGHLLAGVASSTDVSTFSEGDCKEPDKCCWRHKQCTGHIIYPFASDCV
RHSLHLHSVNHCNCNSRLKDSSEDSSSSRGAGPTCSHVIESPCFELTPEEEHVERFRYGW
CKSYRPVSVAVIHHPLYHECGADDLNXKKRKRRRRKSKPPIPTQVGPATASPDLGTSMAT
GTPDSTAPITIWRSESPTGKGQGSKVIKKVKKKKEKEKDKEEMDEKAKLKKKAKKGQLTK
KKSPVKLEPSPPDVSRSLSARQLARMSESSPESREELESEDSYNGRGQGELSSEDIVESS
SPRKRENTVQAKKTGAKPSQARKVNKRKSPPGSNPNLS

SEQ ID NO: 232_AA836348_H
MSVLGEYERHCDSINSDFGSESGGCGDSSPGPSASQGPRAGGGAAEQEELHYIPIRVLGR
GAFGEATLYRRTEDDSLVVWKEVDLTRLSEKERRDALNEIVILALLQHDNIIAYYNHFMD
NTTLLIELEYCNGGNLYDKILRQKDKLFEEEMVVWYLFQIVSAVSCIHKAGILHRDIKTL
NIFLTKANLIKLGDYGLAKKLNSEYSMAETLVGTPYYMSPELCQGVKYNFKSDIWAVGCV
IFELLTLKRTFDATNPLNLCVKIVQGIRAMEVDSSQYSLELIQMVHSCLDQDPEQRPTAD
ELLDRPLLRKRRRSSTVTEAPIAVVTSRTSEVYVWGGGKSTPQKLDVIKSGCSARQVCAG
NTHFAVVTVEKELYTWVNMQGGTKLHGQLGHGDKASYRQPKHVEKLQGKAIRQVSCGDDF
TVCVTDEGQLYAFGSDYYGCMGVDKVAGPEVLEPMQLNFFLSNPVEQVSCGDNHVVVLTR
NKEVYSWGCGEYGRLGLDSEEDYYTPQKVDVPKALIIVAVQCGCDGTFLLTQSGKVLACG
LNEFNKLGLNQCMSGIINHEAYHEVPYTTSFTLAKQLSFYKIRTIAPGKTHTAAIDERGR
LLTFGCNKCGQLGVGNYKKRLGINLLGGPLGGKQVIRVSCGDEFTIAATDEKVLNSKTIR
SNSSGLSIGTVFQSSSPGGGGGGGGEEEDSQQESETPDPSGGFRGTMEADRGMEGLISP
TEAMGNSNGASSSCPGWLRKELENAEFIPMPDSPSPLSAAFSESEKDTLPYEELQGLKVA
SEAPLEHKPQVEASVTELFAFESQLVTSAESCSNLCWEGNTTDSSCVCVQLSAGGG

SEQ ID NO: 233_R86668_H, MKK6_H
MNLLLSYRDVQDYSAIIELVETLQALPTCDVAEQHNVCFHYTFALNRRNRPGDRAKALSV
LLPLVQLEGSVAPDLYCMCGRIYKDMFFSSGFQDAGHREQAYHWYRKAFDVEPSLHSGIN
AAVLLIAAGQHFEDSKELRLIGMKLGCLLARKGCVEKMQYYWDVGFYLGAQILANDPTQV
VLAAEQLYKLNAPIWYLVSVMETFLLYQHFRPTPEPPGGPPRRAHFWLHFLLQSCQPFKT
ACAQGDQCLVLVLEMNKVLLPAKLEVRGTDPVSTVTLSLLEPETQDIPSSWTFPVASICG
VSASKRDERCCFLYALPPAQDVQLCFPSVGHCQWFCGLIQAWVTNPDSTAPAEEAEGAGE
MLEFDYEYTETGERLVLGKGTYGVVYAGRDRHTRVRIAIKEIPERDSRFSQPLHEEIALH
RRLRHKNIVRYLGSASQGGYLKIFMEEVPGGSLSSLLRSVWGPLKDNESTISFYTRQILQ
GLGYLHDNHIVHRDIKGDNVLINTFSGLLKISDFGTSKRLAGITPCTETFTGTLQYMAPE
IIDQGPRGYGKAADIWSLGCTVIEMATGRPPFHELGSPQAAMFQVGMYKVHPPMPSSLSA

FIGURE 1AA

EAQAFLLRTFEPDPRLRASAQTLLGDPFLQPGKRSRSPSSPRHAPRPSDAPSASPTPSAN
STTQSQTFPCPQAPSQHPPSPPKRCLSYGGTSQLRVPEEPAAEEPASPEESSGLSLLHQE
SKRRAMLAAVLEQELPALAENLHQEQKQEQGARLGRNHVEELLRCLGAHIHTPNRRQLAQ
ELRALQGRLRAQGLGPALLHRPLFAFPDAVKQILRKRQIRPHWMFVLDSLLSRAVRAALG
VLGPEVEKEAVSPRSEELSNEGDSQQSPGQQSPLPVEPEQGPAPLMVQLSLLRAETDRLR
EILAGKEREYQALVQRALQRLNEEARTYVLAPEPPTALSTDQGLVQWLQELNVDSGTIQM
LLNHSFTLHTLLTYATRDDLIYTRIRGGMVCRIWRAILAQRAGSTPVTSGP

SEQ ID NO: 234_PAK6_H
MFGKKKKKIEISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMVDPSCIT
PIQLAPMKTIVRGNKPCKETSINGLLEDFDNISVTRSNSLRKESPPTPDQGASSHGPGHA
EENGFITFSQYSSESDTTADYTTEKYREKSLYGDDLDPYYRGSHAAKQNGHVMKMKHGEA
YYSEVKPLKSDFARFSADYHSHLDSLSKPSEYSDLKWEYQRASSSSPLDYSFQFTPSRTA
GTSGCSKESLAYSESEWGPSLDDYDRRPKSSYLNQTSPQPTMRQRSRSGSGLQEPMMPFG
ASAFKTHPQGHSYNSYTYPRLSEPTMCIPKVDYDRAQMVLSPPLSGSDTYPRGPAKLPQS
QSKSGYSSSSHQYPSGYHKATLYHHPSLQSSSQYISTASYLSSLSLSSSTYPPPSWGSSS
DQQPSRVSHEQFRAALQLVVSPGDPREYLANFIKIGEGSTGIVCIATEKHTGKQVAVKKM
DLRKQQRRELLFNEVVIMRDYHHDNVVDMYSSYLVGDELWVVMEFLEGGALTDIVTHTRM
NEEQIATVCLSVLRALSYLHNQGVIHRDIKSDSILLTSDGRIKLSDFGFCAQVSKEVPKR
KSLVGTPYWMAPEVISRLPYGTEVDIWSLGIMVIEMIDGEPPYFNEPPLQAMRRIRDSLP
PRVKDLHKVSSVLRGFLDLMLVREPSQRATAQELLGHPFLKLAGPPSCIVPLMRQYRHH

SEQ ID NO: 235_SURTK106_H
MNDRNEIQMEAKLQSLTIIAQEILCRFFITLRRHARFLLTKLGRQGMARSGITHSCAVCI
LCGPSREGDSPVAMGMTRMLLECSLSDKLCVIQEKQYEVIIVPTLLVTIFLILLGVILWL
FIREQRTQQQRSGPQGIAPVPPPRDLSWEAGHGGNVALPLKETSVENFLGATTPALAKLQ
VPREQLSEVLEQICSGSCGPIFRANMNTGDPSKPKSVILKALKEPAGLHEVQDFLGRIQF
HQYLGKHKNLVQLEGCCTEKLPLYMVLEDVAQGDLLGFLWTCRRDVMTMDGLLYDLTEKQ
VYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT
IPLKWLAPERLLLRPASIRADVWSFGILLYEMVTLGAPPYPEVPPTSILEHLQRRKIMKR
PSSCTHTMYSIMKSCWRWREADRPSPRELRLRLEAAIKTADDEAVLQVPELVVPELYAAV
AGIRVESLFYNYSML

SEQ ID NO: 236_AA098024_M
LQEKHLFHGDVAARNILIQSDLTPKLCHLGLAYEVHAHGAISSARSSTIPLKWLAPERLL
LRPASIRGDIWSFGILLYEMVTLGAPPYPEVPPTSILQYLQRKKIMKRPSSCSHAMYNIM
KCCWRWSEDSRPLLVQLLQRLEAASRSADDKAVLQVPELVVPELYADVAGIRAESISYSF
SVL

SEQ ID NO: 237_SGK2ALPHA_H
MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDFDFLKVIGKGNYGKVLLAKRKSDGAF
YAVKVLQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE
LFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDFGL
CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSQDVS
QMYENILHQPLQIPGGRTVAACDLLQSLLHKDQRQRLGSKADFLEIKNHVFFSPINWDDL
YHKRLTPPFNPNVTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE
DDDILDC

FIGURE 1BB

SEQ ID NO: 238_CCRK_H
MDQYCILGRIGEGAHGIVFKAKHVETGEIIALKKVALRRLEDGFPNQALREIKALQEMED
NQYVVQLKAVFPHGGGFVLAFEFMLSDLAEVVRHAQRPLAQAQVKSYLQMLLKGVAFCHA
NNIVHRDLKPANLLISASGQLKIADFGLARVFSPDGSRLYTHQVATRSVGCIMGELLNGS
PLFPGKNDIEQLCYVLRILGTPNPQVWPELTELPDYNKISFKEQVPMPLEEVLPDVSPQA
LDLLGQFLLYPPHQRIAASKALLHQYFFTAPLPAHPSELPIPQRLGGPAPKAHPGPPHIH
DFHVDRPLEGVAVEPRADSALHPGGVRSWPWSRLPAPQDHSVHLFLCHLPGFTLQGLPMA
TVGPHHTLPLSPCEGWSRGRGHVPSQEYENIQSSRGDSWPVLGEPYLLCATDVPIRTVSS
AASQGLHMQNDDACLGAASPECCLLVKEKCRE

SEQ ID NO: 239_TESK2_H
MDRSKRNSIAGFPPRVERLEEFEGGGGGEGNVSQVGRVWPSSYRALISAFSRLTRLDDFT
CEKIGSGFFSEVFKVRHRASGQVMALKMNTLSSNRANMLKEVQLMNRLSHPNILRYINSG
NLEQLLDSNLHLPWTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNCLIKRDENGYSAVVA
DFGLAEKIPDVSMGSEKLAVVGSPFWMAPEVLRDEPYNEKADVFSYGIILCEIIARIQAD
PDYLPRTENFGLDYDAFQHMVGDCPPDFLQLTFNCCNMDPKLRPSFVEIGKTLEEILSRL
QEEEQERDRKLQPTARGLLEKAPGVKRLSSLDDKIPHKSPCPRRTIWLSRSQSDIFSRKP
PRTVSVLDPYYRPRDGAARTPKVNPFSARQDLMGGKIKFFDLPSKSVISLVFDLDAPGPG
TMPLADWQEPLAPPIRRWRSLPGSPEFLHQEACPFVGREESLSDGPPPRLSSLKYRVKEI
PPFRASALPAAQAHEAMDCSILQEENGFGSRPQGTSPCPAGASEEMEVEERPAGSTPATF
STSGIGLQTQGKQDG

FIGURE 2A

SEQ ID NO: 1_X69117_H BARK2_H
ATGGCGGACCTGGAGGCCGTGCTGGCCGATGTCAGTTACCTGATGGCCATGGAGAAGAGC
AAGGCGACCCCGGCCGCCCGCGCCAGCAAGAGGATCGTCCTGCCGGAGCCCAGTATCCGG
AGTGTGATGCAGAAGTACCTTGCAGAGAGAAATGAAATAACCTTTGACAAGATTTTCAAT
CAGAAAATTGGTTTCTTGCTATTTAAAGATTTTTGTTTGAATGAAATTAATGAAGCTGTA
CCTCAGGTGAAGTTTTATGAAGAGATAAAGGAATATGAAAAACTTGATAATGAGGAAGAC
CGCCTTTGCAGAAGTCGACAAATTTATGATGCCTACATCATGAAGGAACTTCTTTCCTGT
TCACATCCTTTCTCAAAGCAAGCTGTAGAACACGTACAAAGTCATTTATCCAAGAAACAA
GTGACATCAACTCTTTTTCAGCCATACATAGAAGAAATTTGTGAAAGCCTTCGAGGTGAC
ATTTTTCAAAAATTTATGGAAAGTGACAAGTTCACTAGATTTTGTCAGTGGAAAAACGTT
GAATTAAATATCCATTTGACCATGAATGAGTTCAGTGTGCATAGGATTATTGGACGAGGA
GGATTCGGGGAAGTTTATGGTTGCAGGAAAGCAGACACTGGAAAAATGTATGCAATGAAA
TGCTTAGATAAGAAGAGGATCAAAATGAAACAAGGAGAAACATTAGCTTTAAATGAAAGA
ATCATGTTGTCTCTTGTCAGCACAGGAGACTGTCCTTTCATTGTATGTATGACCTATGCC
TTCCATACCCCAGATAAACTCTGCTTCATCCTGGATCTGATGAACGGGGGCGATTTGCAC
TACCACCTTTCACAACACGGTGTGTTCTCTGAGAAGGAGATGCGGTTTTATGCCACTGAA
ATCATTCTGGGTCTGGAACACGTGCACAATCGGTTTGTTGTCTACAGAGATTTGAAGCCA
GCAAATATTCTCTTGGATGAACATGGACACGCAAGAATATCAGATCTTGGTCTTGCCTGC
GATTTTTCCAAAAAGAAGCCTCATGCGAGTGTTGGCACCCATGGGTACATGGCTCCCGAG
GTGCTGCAGAAGGGGACGGCCTATGACAGCAGTGCCGACTGGTTCTCCCTGGGCTGCATG
CTTTTCAAACTTCTGAGAGGTCACAGCCCTTTCAGACAACATAAAACCAAAGACAAGCAT
GAAATTGACCGAATGACACTCACCGTGAATGTGGAACTTCCAGACACCTTCTCTCCTGAA
CTGAAGTCCCTTTTGGAGGGCTTGCTTCAGCGAGACGTTAGCAAGCGGCTGGGCTGTCAC
GGAGGCGGCTCACAGGAAGTAAAAGAGCACAGCTTTTTCAAAGGTGTTGACTGGCAGCAT
GTCTACTTACAAAAGTACCCACCACCCTTGATTCCTCCCCGGGGAGAAGTCAATGCTGCT
GATGCCTTTGATATTGGCTCATTTGATGAAGAGGATACCAAAGGGATTAAGCTACTTGAT
TGCGACCAAGAACTCTACAAGAACTTCCCTTTGGTCATCTCTGAACGCTGGCAGCAAGAA
GTAACGGAAACAGTTTATGAAGCAGTAAATGCAGACACAGATAAAATCGAGGCCAGGAAG
AGAGCTAAAAATAAGCAACTTGGCCACGAAGAAGATTACGCTCTGGGGAAGGACTGTATT
ATGCACGGGTACATGCTGAAACTGGGAAACCCATTTCTGACTCAGTGGCAGCGTCGCTAT
TTTTACCTCTTTCCAAATAGACTTGAATGGAGAGGAGAGGGAGAGTCCCGGCAAAATTTA
CTGACAATGGAACAGATTCTCTCTGTGGAAGAAACTCAAATTAAAGACAAAAAATGCATT
TTGTTCAGAATAAAAGGAGGGAAACAATTTGTCTTGCAATGTGAGAGTGATCCAGAGTTT
GTGCAGTGGAAGAAAGAGTTGAACGAAACCTTCAAGGAGGCCCAGCGGCTATTGCGTCGT
GCCCCGAAGTTCCTCAACAAACCTCGGTCAGGTACTGTGGAGCTCCCAAAGCCATCCCTC
TGTCACAGGAACAGCAACGGCCTCTGA

SEQ ID NO: 2_AA144574_M BARK2_M
CTGCTTCGTAGTCTACAGAGACCTGAAGCCTGCGAACATCCTCCTAGATGAATATGGGCA
CGTGAGGATATCGGATCTCGGCCTTGCCTGTGATTTCTCCAAAAAGAAGCCTCATGCCAG
CGTGGGCACCCATGGGTACATGGCTCCCGAGGTGTTGCAGAAGGGAACGTGCTATGACAG
CAGCGCCGACTGGTTCTCCCTGGGCTGTATGCTCTTCAAACTTCTGCGGGGCCACAGCCC
CTTCAGGCAGCATAAAACCAAAGACAAGCATGAGATAGACCGAATGACCCTGACCGTGAA
CGTGCAGCTTCCAGATGCCTTCTCCCCTGAGCTGAGGTCCCTCTTAGAGGGTTTGCTCCA
GCGGGACGTGAGCCAGCGGCTGGGCTGCGGAGGAGGAGGGGCACGAGAGTTGAAGGAGCA
CATCTTCTTCAAGGGCATTGACTGGCAGCATGTGTACTTACGGAAGTACCCGCCACCCCT
AATCCCTCCTCGGGGAGAGGTCAACGCTGCAGATGCCTTCGATATCGGCTCCTTCGATGA
GGAAGACACCAAAGGCATTAAGCTGTTGGACTGTGACCAGGACCTCTATAAGAACTTCCC
ACTGGTGATCTCCGAGCGCTGGCAGCAAGAAGTGGTGGAGACCATCTATGACGCCGTCAA
TGCTGATACTGATAAAATCGAGGCCAGGAAGAAGGCTAAAAATAAGCAACTTGGTCAAGA

FIGURE 2B

GGAAGATTACGCTATGGGGAAGGACTGCATCATGCACGGGTACATGCTGAAGCTGGGGAA
CCCCTTTCTCACACAGTGGCAAAGACGCTATTTTTACCTGTTCCCCAACAGACTGGAGTG
GAGAGGAGAGGGCGAGTCTCGGCAAAGTCTACTGACCATGGAACAGATCATGTCTGTGGA
GGAGACCCAGATTAAAGACAGAAAGTGCATCTTACTCAGGATAAAGGGAGGGAAGCAATT
TGTCTTGCAATGTGAGAGTGACCCCGAGTTTGCACAGTGGCTGAAGGAGCTGACCTGCAC
CTTCAATGAGGCCCAGAGACTGCTGCGCCGTGCCCCCAAATTCCTCAACAAACCACGGGC
CGCCATCCTGGAGTTCTCCAAGCCACCACTGTGTCACAGAAATAGCAGCGGCCTCTGAAC
CACAGAGCAGCGGGGCCTGAAGGAGGGGCCCCAGCTCTTCAGCCCAGGAGTGGAACGAAG
CCACGGGGAACCGTGTGGGGCTAAGACACAGTGTTTCTGAGCACTGACGGGGCTGCTCCA
AGCCGAGGAGGCTCAGGACACCAGGGCGGCCTTCTGGGAGCTGGGACATCCTCGGGGCTG
TCCTATCCACACTCGAAATTACTGAAGAAGCAGAGGCATTCTGCTGTG

SEQ ID NO: 3_AA826850_H
GAAGAGGATGGGCTCGTCCATGTCGGCGGCCACCGCGCGGAGGCCGGTGTTTGACGACAA
GGAGGACGTGAACTTCGACCACTTCCAGATCCTTCGGGCCATTGGGAAGGGCAGCTTTGG
CAAGGTGTGCATTGTGCAGAAGCGGGACACGGAGAAGATGTACGCCATGAAGTACATGAA
CAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCCGGGAGCTGGAGATCCT
GCAGGAGATCGAGCACGTCTTCCTGGTGAACCTCTGGTACTCCTTCCAGGACGAGGAGGA
CATGTTCATGGTCGTGGACCTGCTACTGGGCGGGGACCTGCGCTACCACCTGCAGCAGAA
CGTGCAGTTCTCCGAGGACACGGTGAGGCTGTACATCTGCGAGATGGCACTGGCTCTGGA
CTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAACATTCTCCTGGA
TGAGAGAGGACATGCACACCTGACCGACTTCAACATTGCCACCATCATCAAGGACGGGGA
GCGGGCGACGGCATTAGCAGGCACCAAGCCGTACATGGCTCCGGAGATCTTCCAXTCTTT
TGTCAACGGCGGGACCGGCTACTCCTTCGAGGTGGACTGGTGGTCGGTGGGGGTGATGGC
CTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCGTGGAGTC
CCTGGTGCAGCTGTTCAGCACCGTGAGCGTCCAGTATGTCCCCACGTGGTCCAAGGAGAT
GGTGGCCTTGCTGCGGAAGCTCCTCACTGTGAACCCCGAGCACCGGCTCTCCAGCCTCCA
GGACGTGCAGGCAGCCCCGGCGCTGGCCGGCGTGCTGTGGGACCACCTGAGCGAGAAGAG
GGTGGAGCCGGGCTTCGTGCCCAACAAAGGCCGTCTGCACTGCGACCCCACCTTTGAGCT
GGAGGAGATGATCCTGGAGTCCAGGCCCCTGCACAAGAAGAAGAAGCGCCTGGCCAAGAA
CAAGTCCCGGGACAACAGCAGGGACAGCTCCCAGTCCGAGAATGACTATCTTCAAGACTG
CCTCGATGCCATCCAGCAAGACTTCGTGATTTTTAACAGAGAAAAGCTGAAGAGGAGCCA
GGACCTCCCGAGGGAGCCTCTCCCCGCCCCTGAGTCCAGGGATGCTGCGGAGCCTGTGGA
GGACGAGGCGGAACGCTCCGCCCTGCCCATGTGCGGCCCCATTTGCCCCTCGGCCGGGAG
CGGCTAGGCCGGGATGCCCGTGGTCCTCACCCCTTGAGCTGCTTTGGAGACTCGGCTGCC
AGAGGGAGGGCCATGGGCCGAGGCCTGGCATTCACGTTCCCACCCAGCCTGGCTGGCGGT
GCCCACAGTGCCCCGGACACATTTCACACCTCAGGCTCGTGGTGGTGCAGGGGACAAGAG
GCTGTGGGTGCAGGGGACACCTGTGGAGGGCATTTCCCGTGGCCCCCGAGACCCGCCTA
GATGGAGGAAGCGCTGCTGGGCGCCCTCTTACCGCTCACGGGGAGCTGGGGCCATGGATG
GGACAGGAGTCTTTGTCCCTGCTCAGCCCGGAGGCTGTGCACGGCCCTCGTCACAAGGTG
ACCCTTGCAGCACAGGCCGCGGGTGCCCCAGGCTCGGCTCAGTTCTTGGAGGTCAAGGGC
ATGGGTTGGGGTAGTGGGTGGGGAGGTGAATGTTTTCTAGAGATTCAAACTGCTCCAGCA
ATTTCTGTATAGTTTTCACCTCTGAGAATTACAATGTGAGAACCGCTC

SEQ ID NO: 4_AA960957_H
GTCCCACATCCCGCATCCGGCATCCCAGCGGCCGGGCATGTAGCAGCGGCAGCAACGGCG
GAATATGGGCGGGAACCACTCCCACAAGCCCCCCGTGTTTGACGAGAATGAGGAAGTCAA
CTTTGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCAT
CGTGCAGAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTG
CATCGAGAGGGATGAGGTTCGGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGA

FIGURE 2C

GCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTCATGGT
GGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTCAC
AGAGGGGACTGTGAAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAG
GTACCACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACA
TGTTCACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTC
CATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTACATGGACAGAGG
CCCCGGATACTCGTACCCTGTCGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCT
GCGGGGCTGGAGGCCGTACGAAATCCACTCGGTCACGCCCATCGATGAAATCCTCAACAT
GTTCAAGGTGGAGCGTGTCCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCT
GAGGAAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCTTCATGACATACAGAG
CGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGCACTGATGCCCGG
CTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCCACATTTGAGCTTGAAGAGATGAT
TCTAGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGA
TGGCACAAAGGACAGCTGCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCG
GGAGGAATTCATCATATTCAACAGAGAGAAGCTCAGGAGGCAGCAGGGACAGGGCAGCCA
GCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCTCCAGGACGGGTG
CAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCCACACTTG
TTGCTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCCACCCAGAGCCCCTCTTTGTGC
CCTGATGGTCCCTGTCTCACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGA
GCTGGGAAGCCTGGGTTCTGGTCCCATCTCCATGACTGATTCACGTGTGACCTCAGACAA
GTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTTAAACACTTCTGCC
CCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAAACCTT
TGATATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCC
ATTCCCCAAAGCAATCAAACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTTAGA
GGGCACTTCCGAAAAACACAGCCCTGACAGCAAAATAAAGGTCTGATATGTTGGCCCCTT
CTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTTCATGTGCATTCT
CTGGCAGGCCACAGTCCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCTCATTTAAGAAGACTATCCTTACCTTTT
AGTTTCAGCAGTCCTCACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCA
TTCAGATGAGAGTTGGGTCGCTGAGCATTGGTTACTCCTGCAGAGTGTAATCAGCACCCC
ATCCAACTGGCCCGAAAGCCCAGACCTGCAGCAGAACTCTCCAACTCTCTATCAGCTTTC
AGGGTTTTCTCTCCTGGGAAGGGTGTAAAATCAGCTTGTCAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAG
AAAGTTTATTTCAGGAGGAAAATGGGTTCACACAAAAAGCAAACTACATTCTGATCTGCT
CAGGGAGAAGCTTGCCTTTGAACTGGAAGATGTTGGGATGAGCAGGGAAAGCTTAGACTT
TGGAGTCAGGTTTGTGTTCAGAATCCAGCCCTGCTGGCTACTAACTAACTGGGAGACCTT
AGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCCTCATTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTG
GATGACTCATAGAATGGCCTTTTTTGTCAGCATAATCGTCATCATTATTTAGATACTTTC
TTCCTTCACTCACCCAGCAGGTCAGTTTTCTGTGCAAACAAACCTGTTTAGGATTCTTCC
AAATGTTCTTCCTGGGGTCTTTGATATTTGTTTGTTACATCCTGCTGAAGTTCGACTGTG
TTTTTATTTTTTCATCCAACTTCCATTTTTCACTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTCATCTCTTAGATTTCTTAAAAGACATTTTAATGTATGGTTAGGTTTTAT
ATTTTTATTTTTTAAAAAAGAAATAGTCAGTGTTTTCCTCCTTTCAACCGAGACTATTTC
TGGATTGTGTGCTCCTCGTCAGTTGACTTGTTTTGCACACTTTTCTTTACTTCATGTCCC
CATCAACAACCGTCCTGCTCCCCACCTCCCCCAGGAAATAAGGGGCCTGCTCCTCTCCCT
ACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTATTGGGCTGAGTTCACGA
ATTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCCTGGTTCTGTTCAAGT
TGGCATTTCTTGTTTGGAATAAACTATTTCTTGGACATTCCTTC

FIGURE 2D

SEQ ID NO: 5_TBK1_H
TCCTGAGTCTCGAGGAGGCCGCGGGAGCCCGCCGGCGGTGGCGCGGCGGAGACCCGGCTG
GTATAACAAGAGGATTGCCTGATCCAGCCAAGATGCAGAGCACTTCTAATCATCTGTGGC
TTTTATCTGATATTTTAGGCCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGA
AAACTGGTGATTTATTTGCTATCAAAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGG
ATGTTCAAATGAGAGAATTTGAAGTGTTGAAAAAACTCAATCACAAAAATATTGTCAAAT
TATTTGCTATTGAAGAGGAGACAACAACAAGACATAAAGTACTTATTATGGAATTTTGTC
CATGTGGGAGTTTATACACTGTTTTAGAAGAACCTTCTAATGCCTATGGACTACCAGAAT
CTGAATTCTTAATTGTTTTGCGAGATGTGGTGGGTGGAATGAATCATCTACGAGAGAATG
GTATAGTGCACCGTGATATCAAGCCAGGAAATATCATGCGTGTTATAGGGGAAGATGGAC
AGTCTGTGTACAAACTCACAGATTTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGT
TTGTTTCTCTGTATGGCACAGAAGAATATTTGCACCCTGATATGTATGAGAGAGCAGTGC
TAAGAAAAGATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAA
CATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGA
ATAAAGAAGTGATGTATAAAATAATTACAGGAAAGCCTTCTGGTGCAATATCTGGAGTAC
AGAAAGCAGAAAATGGACCAATTGACTGGAGTGGAGACATGCCTGTTTCTTGCAGTCTTT
CTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCTTGCAAACATCCTTGAAGCAGATCAGG
AAAAGTGTTGGGGTTTTGACCAGTTTTTTGCAGAAACTAGTGATATACTTCACCGAATGG
TAATTCATGTTTTTTCGCTACAACAAATGACAGCTCATAAGATTTATATTCATAGCTATA
ATACTGCTACTATATTTCATGAACTGGTATATAAACAAACCAAAATTATTTCTTCAAATC
AAGAACTTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACATT
TCCCTAAAACTACTGAGGAAAACCCTATATTTGTAGTAAGCCGGGAACCTCTGAATACCA
TAGGATTAATATATGAAAAAATTTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG
GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTGTGTTATGCCTGCAGAATTGCCA
GTACCTTACTGCTTTATCAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGAATTAA
TTAAAGATGATTACAATGAAACTGTTCACAAAAAGACAGAAGTTGTGATCACATTGGATT
TCTGTATCAGAAACATTGAAAAAACTGTGAAAGTATATGAAAAGTTGATGAAGATCAACC
TGGAAGCGGCAGAGTTAGGTGAAATTTCAGACATACACACCAAATTGTTGAGACTTTCCA
GTTCTCAGGGAACAATAGAAACCAGTCTTCAGGATATCGACAGCAGATTATCTCCAGGTG
GATCACTGGCAGACGCATGGGCACATCAAGAAGGCACTCATCCGAAAGACAGAAATGTAG
AAAAACTACAAGTCCTGTTAAATTGCATGACAGAGATTTACTATCAGTTCAAAAAAGACA
AAGCAGAACGTAGATTAGCTTATAATGAAGAACAAATCCACAAATTTGATAAGCAAAAAC
TGTATTACCATGCCACAAAAGCTATGACGCACTTTACAGATGAATGTGTTAAAAAGTATG
AGGCATTTTTGAATAAGTCAGAAGAATGGATAAGAAAGATGCTTCATCTTAGGAAACAGT
TATTATCGCTGACTAATCAGTGTTTTGATATTGAAGAAGAAGTATCAAAATATCAAGAAT
ATACTAATGAGTTACAAGAAACTCTGCCTCAGAAAATGTTTACAGCTTCCAGTGGAATCA
AACATACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACTCTTGGTA
TGAAGAAATTAAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGCTGAAAATAACCACA
TTTTAGAAAGGTTTGGCTCTTTAACCATGGATGGTGGCCTTCGCAACGTTGACTGTCTTT
AGCTTTCTAATAGAAGTTTAAGAAAAGTTTCCGTTTGCACAAGAAAATAACGCTTGGGCA
TTAAATGAATGCCTTTATAGATAGTCACTTGTTTCTACAATCCAGTATTTGATGTGGTCG
TGTAAATATGTACAATATTGTAAATACATAAAAAATATACAAATTTTTGGCTGCTGTGAA
GATGTAATTTTATCTTTTAACATTTATAATTATATGAGGAAATTTGACCTCAGTGATCAC
GAGAAGAAAGCCATGACCGACCAATATGTTGACATACTGATCCTCTACTCTGAGTGGGGC
TAAATAAGTTATTTTCTCTGACCGCCTACTGGAAATATTTTTAAGTGGAACCAAAATAGG
CATCCTTACAAATCAGGAAGACTGACTTGACACGTTTGTAAATGGTAGAACGGTGGCTAC
TGTGAGTGGGGAGCAGAACCGCACCACTGTTATACTGGGATAACAATTTTTTTGAGAAGG
ATAAAGTGGCATTATTTTATTTTACAAGGTGCCCAGATCCCAGTTATCCTTGTATCCATG
TAATTTCAGATGAATTATTAAGCAAACATTTTAAAGTGAATTCATTATTAAAAACTATTC
ATTTTTTTCCTTTGGCCATAAATGTGTAATTGTCATTAAAATTCTAAGGTCATTTCAACT

FIGURE 2E

GTTTTAAGCTGTATATTTCTTTAATTCTGCTTACTATTTCATGGAAAAAAATAAATTTCT
CAATTTTAAAAAA

SEQ ID NO: 6_AA305176_H
TGGCTGCTCGCGGAGGGGCAGTGTACGCGGGGCCGCTGTAGGCTGTCCAGCGATGGATCC
CACCGCGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGAGGGCGTGAATAG
GATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATTCAGCATAGTGAAGCCCATTAGCCG
GGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTGTATGCAGTAAAGGT
TGTTAAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCAAGCTGAGAGAGA
TGCACTGGCACTAAGCAAAAGCCCATTCATTGTCCATTTGTATTATTCACTGCAGTCTGC
AAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCTCTCCTACA
TATATATGGTTATTTTGATGAAGAGATGGCTGTGAAATATATTTCTGAAGTAGCACTGGC
TCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGACAATATGCT
TATTTCTAATGAGGGTCATATTAAACTGACGGATTTTGGCCTTTCAAAAGTTACTTTGAA
TAGAGATATTAATATGATGGATATCCTTACAACACCATCAATGGCAAAACCTAGACAAGA
TTATTCAAGAACCCCAGGACAAGTGTTATCGCTTATCAGCTCGTTGGGATTTAACACACC
AATTGCAGAAAAAAATCAAGACCCTGCAAACATCCTTTCAGCCTGTCTGTCTGAAACATC
ACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGACACTACGCCTTA
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GAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCCAGTGCCAG
TAGTCAATCCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAGCAGTCCCAAATG
GGAAAAAGATTGCCAGGTTTGAGGGACATTTATCTTAATGAAAATCAATTATGTATGTCA
AATGAATGTGAGAAATATTATACCTTTTCATATAAATTCCATAAAGAAATGAAATTGTTA
CATGAATGGCAGTCATAGTATTAATCAGAAATTCATTTTCCTGCACATTCTGTCAAATTC
TTTTGAAATATTTCATTTCTCATTCAATTGTGACATTGTTCTTACTTGATTATATAATGA
GATTCTTGCAGTAAATTGATAATAAATGCTTGGCTTCTGTGTATCTAGGTGGACCTCACT
TGTTTTTAGAAGTCCTTCCCATGATACAGACATTGGCTTGTTGGTTTTGTTTTATTTTGT
TTTTAACATATGTCATTTAAAAACTCATATTACCTCCTTTT

SEQ ID NO: 7_AA116841_M
CCACGCGTCCGATCCCATGGCCAGAAGGCGAAGAAAAGCTATCTGATAATGCTCAAAGTG
CAATGGACATGCTTTTAACCATTGATGATTCAAAGAGAGCTGGAATGAGAGAACTAAAAC
AGCATCCTCTCTTCAGTGAAGTGGACTGGGAAAATCTGCAGCATCAGACTATGCCTTTCG
TACCCCAACCAGACGACGAAACAGATACATCCTATTTTGAAGCCAGAAATAATGCTCAAC
ATCTGACCGTATCTGGGTTTAGTCTGTAGCACATGCGTGTCATTTTTATCTAACTTGTGA
TATAGAATTAAGTTTTACAGTAATATGCTACTTAATACTAGATTGGTCTAAATGGGATAA
AAGTCATTATTTTACCCAGACTGAACAGCTTTTAATTACTAAGTACAACAGTTTTTACAG
AATTAAAATACTATAAGCAATATAATCAGTAATTAATCTTTACCTTAGAACTGTATATAA
GCCATAATAGCTTTTTTCATCTTATTTATTCACTGCACTTTATGAAGAGCAAAGTATCAA
TAAACTAAAACACTACCACTCTAAATAGAGGGAGTGAGCCGT

SEQ ID NO: 8_AA256100_H
AGGGAGCTGACGGGCGCCCGGCCGGCTGCGGTCCGTGCGGAGGCTGAGCCGGCCGCGGGC
GCGACCGGAGGCAGTTTCCGTTACTATGGCAATGACGGCAGGGACTACAACAACCTTTCC
TATGAGCAACCATACCCGGGAAAGAGTGACTGTAGCCAAGCTCACATTGGAGAATTTTTA
TAGCAACCTAATTTTACAGCATGAAGAGAGAGAAACCAGGCAGAAGAAATTAGAAGTGGC
CATGGAAGAAGAAGGATTAGCAGATGAAGAGAAAAAGTTACGTCGATCACAACACGCTCG
CAAAGAAACAGAGTTCTTACGGCTCAAAAGGACCAGACTTGGCTTGGATGACTTTGAGTC
TCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTGCGGTTGGTCCAGAAGAAAGATAC
AGGCCATATCTATGCAATGAAGATATTGAGAAAGTCTGATATGCTTGAAAAAGAGCAGGT

FIGURE 2F

GGCCCATATCCGAGCAGAAAGAGATATTTTGGTAGAAGCAGATGGTGCCTGGGTGGTGAA
GATGTTTTACAGTTTTCAGGATAAGAGGAATCTTTATCTAATCATGGAATTTCTCCCTGG
AGGTGACATGATGACATTGCTAATGAAGAAAGACACCTTGACAGAAGAGGAAACACAGTT
CTACATTTCAGAGACTGTTCTGGCAATAGATGCGATCCACCAGTTGGGTTTCATCCATCG
GGATATTAAGCCAGACAACCTTTTATTGGATGCCAAGGGTCATGTAAAATTATCTGATTT
TGGTTTATGTACGGGATTAAAGAAAGCTCACAGGACTGAATTTTATAGAAATCTCACACA
CAACCCACCAAGTGACTTCTCATTTCAGAACATGAACTCAAAGAGGAAAGCAGAAACTTG
GAAGAAGAACAGGAGACAACTGGCATATTCCACAGTTGGGACACCAGATTACATTGCTCC
AGAAGTATTCATGCAGACTGGTTACAACAAATTGTGTGACTGGTGGTCTTTGGGAGTGAT
TATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATA
CAGAAAAGTGATGAACTGGAAAGAAACTCTGGTATTTCCTCCAGAGGTACCTATATCTGA
GAAAGCCAAGGACTTAATTCTCAGATTTTGTATTGATTCTGAAAACAGAATTGGAAATAG
TGGAGTAGAAGAAATAAAAGGTCATCCCTTTTTTGAAGGTGTCGACTGGGAGCACATAAG
GGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAAGCATTGATGATACTTCAAATTTTGA
TGACTTCCCTGAATCTGATATTTTACAACCAGTGCCAAATACCACAGAACCGGACTACAA
ATCCAAAGACTGGGTTTTTCTCAATTATACCTATAAAAGGTTTGAAGGGTTGACTCAACG
TGGCTCTATCCCCACCTACATGAAAGCTGGGAAGTTATGAATGAAGATAACATTCACCCA
TAACCAAGAGAACTCAGGTAGCTGCATCACCAGGCTTGCTTGGCGTAGATAACAATACAC
TGAAATACTCCTGAAGATGGTGGTGCTTATTGACTACAAGAGGAAATTCTACAGGATTAG
GATTTCTAAGACTACTATAGGAATTGGTTGGCAGTGCCAGCTGGCTCTTTTTTTTAATAT
TTTATTATTTTTGTTAACTTTATTATATGAAGGTACTGGAATAAAAGGAACAGACATCCC
TTTCTAACTGCACTGCCTACATGCGTATTAAGGTCCATTCTGCCTGTGTGTGCTGTGGCT
TTGAACTGTAACACCTCTAATCAATTCAGGAGAAACACATATCATTTAAAGCAACATAGG
CTAACCTGTAGGTAACACTGCAGTATTGATGTTTTACTGCAAATCTTATGGGTCTAGATA
ATCAGTAAAAGCCATCTTCCATAGTTGGTGTTAGAACATTGCCCTATTGGTTTGGACATC
TGTAGAATATATATGAAGACAATTTCTGTAATGGTTTTAAGAGATTTAAAAAGAAATTCA
CTGGTTCTTTACAAAATAGAATTTATCATCAAGTTATTACACAAACTTCACAGTAAGGAG
TGACAAGTTTATAATAAGGAAGACAAAGTTTAACACCTTCACTCAAGCACTCCACTAATA
TATTTACGTTGCATTCAGAAATACTGATGACCTTCATATACGTAGTCTGTATACTCATAG
GGAGATGTACTGTATTATATAACATGTAAAGTTGATTTTCTTGTGACAAGAGAACTTCTT
TTTTTAACAAGAGGACATGGCATTATTTTAATTTGATTATGGTGAGTTGAATTTAAGACA
TGACCATGAAGGCTGCTTGTAGAATTAGTGTATTTTTATTAAACTATTTTTTTAAATGTC
AAACTTCTATCATGTAAATGGACTTATAGAGAACAAAAAGCTATTTACTTTGGTTTTCTA
GAAAGTTGTTACATATCATGGCTGGTTAACTTTTATTTCTTTTGATGAAAATTTTTCCTT
TGATAGTACTTGTATTATTGTGCCATTATTTTCTTATGCTCCAAATGTACCAAAGATCTT
GAACAGAGTGGATGTTCACAACTGAGTAGAATTTTCCTTTCCTGTGGGCATGCTGTATTC
AGACCTGACAGATCTTTGATAGAGGTCAGCTTATTAAAGGGCAATATTGTTCTTGTTTAG
CTACATCACTGTGGTGAATATAGATGGAATTAAGGAAGTAAATGCAGGCCAGGGGGTTGT
GATGAGAGGATAGGGGAGATAATATCAGCATCAAATTCTTTGGGTATCTCTCTAAGAATT
AAATAATCTTTTCTAGCTTAATATTTTAATTCTAATTCAAACAACTCTGAGGTTTTGGTT
TCATTAGTAATAGTTGAGGAATAATATACTAGCAAAGAATGGCCTAATGTTTGTCATAAC
TGTTAATGGATGAAATTTTTTAAAGATACAACCATGATAACCATTATAAATGATCTATGA
TCAAAATCTAAAGTGATGAATTATTTGTAGGAATGTCTTCCTAATGGGGAAGAATTGCAT
AGGAGCATTATGCAAATCTACACAAGCTTTTATAAATGTTGCTGCTGGGTAGCTCCACAG
TGTTTCATAAGGCCATCCTGTTTCCCCCAACTCCCCCATTTTTGGTTTGTTTCTTTTTAA
ATATTTGTTGAGTACTTACGTGTTTATCTAACAGTTCACTTCCATTTTTCTAGTCTGGAT
TTTTTGAGTATTTAGGAAAGAGAGCTATTAAAAACTCTGGGGATTTCTCAATGTGACTAA
CTCTAATTTTTCTAATTATAACTGCCTTTAATTAACATAATATTAACTTTTGCTGAGGTT
TATGAGATTTTCTCACCCCACATCGCTCCCCTTTTTTTAAAAAGGACTGTTTTGCTAGTG
TGATAATGAATAGGTAAGATATGAGATAATTGCAACATTGTCCTAGTTCTAGTATGGTAA

FIGURE 2G

CTATTCTTGAAATGGTATTGAAAAATACCGTTAATTCAAATTGACAGAGATTGATAAAAA
GAAACTGATTTACCTAAGTTTACTTTTAATTGCATAATAGAGCATTTTTTGTTTTGAGT
TCCCTCATTCTTATTACCAGAAAGAGCTTGCAAATAGTTTTACTTTCTTGGCACTGGAAG
GGTAGTTCTGGAAAGCTACTTTGTTGAGAGTCTCATTCTTCCCTGGAGTTAATAGAGTGA
TTCACAATCTTTGGGGTTTTCTCCTCATCAAAAGCATTTCTTAAGTGCCTATCTAAAAGC
AATTAAAGACTGTGTCTGCCCTTTAGAAGCTAAGAATTTGATTCATGATGCAAATTAACT
AGATAATTTGCAAAGTACCCTTGAGATTGAATTTTCTCTATTATATATTTCCCATATTTC
AGGTGAATAATTTAATTTAAATGACAAAACCCTATCTAGTCAACTGGGCATAATGACATT
TTCTTTAAATTAGACTCTATTTTGAATTAAAAGAGTTTTATTATAAACCGTGTGTTTTTG
GTTTTTCTAAGTATATAGAAAGCTTGTATAATTCAGATTTATCAATTTCCTGATTTAATG
TAGACTTTGACTTTTTTATTAAAAACCTTTGTATTAAAGCAAGTTATGTTATTTTTCTTT
TATGCATTTATTACTAACATAGCTTTAAATCTTTAAATGTATTGAAGCATTGTGCTGTCT
GAAAATAAGGAATTGCTTATAAACCAGCCACTTCTGAATACAATATGTAGCTGATTTAAT
AAGCTAGTTAGTGAATGGAAAATAAGTGTGGAGTATTAAAAATGTTCTTTGGTTGGTAAG
GCCTAAGATAGGGTTTCATTTATTTCTATACTTTTTCTGTTTTTTAAACACCTGCATATT
TTTATGTAAATCTCTAAATTTAAAATATTTTAAGTACATTTATTTTTGGTGTTTTATTGT
ATAAAACCTTAGACAATCAATCAGTCAGTCTTTACTGACAGGAGCAGCAGCTATCTGTCT
TTTGCTGATCTACAAATAAATGAATTGAGAATTTAGTCCATAGAGGTCCCTGGCTACCAA
ACACATTCTCCTTTGAATTGTTAAAATTCAGAACATTCAAAATAACTGTTTTGCTACAAC
CCATGATTATTTTCCTGTTGTGTTTATTTAAATTTACTTTCTCTTTAGAAGTGCACTTAT
TTCTGAAAAATCTTAATGAAACAAACGCTTAGAACAAATATAAATATGAGACACTTGGGA
CTACTAGAGATATTTTAGATTTTTATGAAAAAAATGTGAGGGGATATTGCTGCTTTAAAA
AGGAATAAAGTAATAAAAATATATCTCAGCTATTTTTTTAAAGCAATATAATTCAGCAAT
TGTCTAGAAAAGTAATCATGAGGCTACTGAGTTTGGTGTTCAGTTACTGAGTTTCAAAAA
TGTTTTGGTGGCATGAGGACAAAATTTCATTGAAGGTAAGATAAGAATAAAAACTATGTT
TAC

SEQ ID NO: 9_AA210825_H
CACGAGGGCTACTGGCGCCTGGCGACCCTCCCTGCCCCCCACCCAACCCCGCTCCGGCAA
CGCCCCCTTCCTCACGGCTCCCGACCGAACTTTTCTCCAACTTCTGCGACTCGTGAGATT
CCCTTCTACCCACTCCGGCCCTCGGGACCCCTCTGCCCATCCCCTGGCCGGTCGGGTCCC
TGCGAACCCCTTTATCTCTGGAATCCACTCGGTCCCCGACTCAGAGACTCCTGCCCTCCA
CCCCCAAGGACCCCGCCATCCTCAGGTCCCCTCCGCCTGCCAGATCTTTTCTCGGATCCC
CGCTCTCCCACCACCTGCTCACGAGATCCCGCGGATCTAGAACCCAGGGTCCCCCGGGGC
CCCCCGGCGGGTCCCGGGTGGGCTCCAGGCGGGCGGTCCCCGGCCTCCCCCCATGGCCAC
CGCCCCCTCATTATCCCGCCGGGCTCCCTGGCTCTCCCGGGCCGGGGTCTCCTCCGCCCC
CCGGCGGCCTAGAGCTGCAGTCGCCGCCACCGCTACTGCCCCAGATCCCGGCCCCGGGTT
CCGGGGTCTCCTTTCACATCCAGATCGGGCTGACCCGCGAGTTCGTGCTGTTGCCCGCCG
CCTCCGAGCTGGCTCATGTGAAGCAGCTGGCCTGTTCCATCGTGGACCAGAAGTTCCCTG
AGTGTGGCTTCTACGGCCTTTACGACAAGATCCTGCTTTTCAAACATGACCCCACGTCGG
CCAACCTCCTGCAGCTGGTGCGCTCGTCCGGAGACATCCAGGAGGGCGACCTGGTGGAGG
TGGTGCTGTCGGCCTCGGCCACCTTCGAGGACTTCCAGATCCGCCCGCACGCCCTCACGG
TGCACTCCTATCGGGCGCCTGCCTTCTGTGATCACTGCGGGGAGATGCTCTTCGGCCTAG
TGCGCCAGGGCCTCAAGTGCGATGGCTGCGGGCTGAACTACCACAAGCGCTGTGCCTTCA
GCATCCCCAACAACTGTAGTGGGGCCCGCAAACGGCGCCTGTCATCCACGTCTCTGGCCA
GTGGCCACTCGGTGCGCCTCGGCACCTCCGAGTCCCTGCCCTGCACGGCTGAAGAGCTGA
GCCGTAGCACCACCGAACTCCTGCCTCGCCGTCCCCCGTCATCCTCTTCCTCCTCTTCTG
CCTCATCGTATACGGGCCGCCCCATTGAGCTGGACAAGATGCTGCTCTCCAAGGTCAAGG
TGCCGCACACCTTCCTCATCCACAGCTATACACGGCCCACCGTTTGCCAGGCTTGCAAGA
AACTCCTCAAGGGCCTCTTCCGGCAGGGCCTGCAATGCAAAGACTGCAAGTTTAACTGTC

FIGURE 2H

ACAAACGCTGCGCCACCCGCGTCCCTAATGACTGCCTGGGGGAGGCCCTTATCAATGGAG
ATGTGCCGATGGAGGAGGCCACCGATTTCAGCGAGGCTGACAAGAGCGCCCTCATGGATG
AGTCAGAGGACTCCGGTGTCATCCCTGGCTCCCACTCAGAGAATGCGCTCCACGCCAGTG
AGGAGGAGGAAGGCGAGGGAGGCAAGGCCCAGAGCTCCCTGGGGTACATCCCCCTAATGA
GGGTGGTGCAATCGGTGCGACACACGACGCGGAAATCCAGCACCACGCTGCGGAGGGTT
GGGTGGTTCATTACAGCAACAAGGACACGCTGAGAAAGCGGCACTATTGGCGCCTGGACT
GCAAGTGTATCACGCTCTTCCAGAACAACACGACCAACAGATACTATAAGGAAATTCCGC
TGTCAGAAATCCTCACGGTGGAGTCCGCCCAGAACTTCAGCCTTGTGCCGCCGGGCACCA
ACCCACACTGCTTTGAGATCGTCACTGCCAATGCCACCTACTTCGTGGGCGAGATGCCTG
GCGGGACTCCGGGTGGGCCAAGTGGGCAGGGGGCTGAGGCCGCCCGGGGGCTGGNNGAGA
CAGCCATCCGCCAGGCCCTGATGCCCGTCATCCTTCAGGACGCACCCAGCGCCCCAGGCC
ACGCGCCCCACAGACAAGCTTCTCTGAGCATCTCTGTGTCCAACAGTCAGATCCAAGAGA
ATGTGGACATTGCCACTGTCTACCAGATCTTCCCTGACGAAGTGCTGGGCTCAGGGCAGT
TTGGAGTGGTCTATGGAGGAAAACACCGGAAGACAGGCCGGGACGTGGCAGTTAAGGTCA
TTGACAAACTGCGCTTCCCTACCAAGCAGGAGAGCCAGCTCCGGAATGAAGTGGCCATTC
TGCAGAGCCTGCGGCATCCCGGGATCGTGAACCTGGAGTGCATGTTCGAGACGCCTGAGA
AAGTGTTTGTGGTGATGGAGAAGCTGCATGGGGACATGTTGGAGATGATCCTGTCCAGTG
AGAAGGGCCGGCTGCCTGAGCGCCTCACCAAGTTCCTCATCACCCAGATCCTGGTGGCTT
TGAGACACCTTCACTTCAAGAACATTGTCCACTGTGACTTGAAACCAGAAAACGTGTTGC
TGGCATCAGCAGACCCATTTCCTCAGGTGAAGCTGTGTGACTTTGGCTTTGCTCGCATCA
TCGGCGAGAAGTCGTTCCGCCGCTCAGTGGTGGGCACGCCGGCCTACCTGGCACCCGAGG
TGCTGCTCAACCAGGGCTACAACCGCTCGCTGGACATGTGGTCAGTGGGCGTGATCATGT
ACGTCAGCCTCAGCGGCACCTTCCCTTTCAACGAGGATGAGGACATCAATGACCAGATCC
AGAACGCCGCCTTCATGTACCCGGCCAGCCCCTGGAGCCACATCTCAGCTGGAGCCATTG
ACCTCATCAACAACCTGCTGCAGGTGAAGATGCGCAAACGCTACAGCGTGGACAAATCTC
TCAGCCACCCCTGGTTACAGGAGTACCAGACGTGGCTGGACCTCCGAGAGCTGGAGGGGA
AGATGGGAGAGCGATACATCACGCATGAGAGTGACGACGCGCGCTGGGAGCAGTTTGCAG
CAGAGCATCCGCTGCCTGGGTCTGGGCTGCCCACGGACAGGGATCTCGGTGGGGCCTGTC
CACCACAGGACCACGACATGCAGGGGCTGGCGGAGCGCATCAGTGTTCTCTGAGGTCCTG
TGCCCTCGTCCAGCTGCTGCCCTCCACAGCGGTTCTTCACAGGATCCCAGCAATGAACTG
TTCTAGGGAAAGTGGCTTCCTGCCCAAACTGGATGGGACACGTGGGGAGTGGGGTGGGG
GAGCTATTTCCAAGGCCCCTCCCTGTTTCCCCAGCAATTAAAACGGACTCATCTCTGGCC
CCATGGCCTTGATCTCAGCAAAA

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ATTCAATTCATAATTGTTGGTGCAAAAGATTTGCTTGCTATGGATTCAAATGGTCTTTCT
GATCCTTACATCAAAATCACAAATCTTTCTCAAAAAACGAAAGTGATTAAGAAAACTTTG
ACTCCAACTTGGAATGAAACTTTTTTTGTGCATTTTCCAGAAAAAACAACCCTTGAATTA
GAATGTTGGGACCACGATACTTTTTCAGATGATTTTATTGGCAAGGCTTCCATTTCTTTG
GCAGAGATTCCAGCTTTGGCAGAAGTTGATATGTGGATAGATATGAAAACGAAAAAAGGA
GAATTTGCAGGAAAA

SEQ ID NO: 11_AA316804_H
ATGTCTGCAAATAATTCCCCTCCATCAGCCCAGAAGTCTGTATTACCCACAGCTATTCCT
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TCTAATGGAAGCTTCAGTGCACCATCACTCACCAACTCCAGAGGCTCAGTGCATACAGTT
TCATTTCTACTGCAAATTGGCCTCACACGGGAGAGTGTTACCATTGAAGCCCAGGAACTG
TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT
GGATTCTTTGGCATGTATGACAAAATTCTTCTCTTTCGCCATGACATGAACTCAGAAAAC
ATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGGTT

FIGURE 2I

CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTCGTCCACATACTCTCTATGTACAT
TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT
CAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAAACGATGTGCCTTCAAGATT
CCAAATAACTGTAGTGGAGTAAGAAAGAGACGTCTGTCAAATGTATCTTTACCAGGACCC
GGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTTCCCAGTGAAGAGTCA
CATGTCCACCAGGAACCAAGTAAGAGAATTCCTTCTTGGAGTGGTCGCCCAATCTGGATG
GAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCTGTTCACTCTTACACC
CGTCCCACGATATGTCAGTACTGCAAGCGGTTACTGAAAGGCCTCTTTCGCCAAGGAATG
CAGTGTAAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCAAAAGTACCAAGAGAC
TGCCTTGGAGAGGTTACTTTCAATGGAGAACCTTCCAGTCTGGGAACAGATACAGATATA
CCAATGGATATTGACAATAATGACATAAATAGTGATAGTAGTCGGGGTTTGGATGACACA
GAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTG
GAAAGAGATGAAGAAGCCGTTAAAACAATCAGTCCATCAACAAGCAATAATATTCCGCTA
ATGAGGGTTGTACAATCCATCAAGCACACAAAGAGGAAGAGCAGCACAATGGTGAAGGAA
GGGTGGATGGTCCATTACACCAGCAGGGATAACCTGAGAAAGAGGCATTATTGGAGACTT
GACAGCAAATGTCTAACATTATTTCAGAATGAATCTGGATCAAAGTATTATAAGGAAATT
CCACTTTCAGAAATTCTCCGCATATCTTCACCACGAGATTTCACAAACATTTCACAAGGC
AGCAATCCACACTGTTTTGAAATCATTACTGATACTATGGTATACTTCGTTGGTGAGAAC
AATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTTGGACTTGATGTAGCA
CAGAGCTGGGAAAAAGCAATTCGCCAAGCCCTCATGCCTGTTACTCCTCAAGCAAGTGTT
TGCACTTCTCCAGGGCAAGGGAAAGATCACAAAGATTTGTCTACAAGTATCTCTGTATCT
AATTGTCAGATTCAGGAGAATGTGGATATCAGTACTGTTTACCAGATCTTTGCAGATGAG
GTGCTTGGTTCAGGCCAGTTTGGCATCGTTTATGGAGGAAAACATAGAAAGACTGGGAGG
GATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAACAAGAAAGTCAACTC
CGTAATGAAGTGGCTATTTTACAGAATTTGCACCATCCTGGGATTGTAAACCTGGAATGT
ATGTTTGAAACCCCAGAACGAGTCTTTGTAGTAATGGAAAAGCTGCATGGAGATATGTTG
GAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATTACTAAATTCATGGTC
ACACAGATACTTGTTGCTTTGAGGAATCTGCATTTTAAGAATATTGTGCACTGTGATTTA
AAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCCTCAGGTGAAGCTGTGTGAC
TTTGGATTTGCACGCATCATTGGTGAAAAGTCATTCAGGAGATCTGTGGTAGGAACTCCA
GCATACTTAGCCCCTGAAGTTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG
TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCCTTTTAATGAGGATGAA
GATATAAATGACCAAATCCAAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAGAA
ATTTCTGGTGAAGCAATTGATCTGATAAACAATCTGCTTCAAGTGAAGATGAGAAAACGT
TACAGTGTTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC
CTTAGAGAATTTGAAACTCGCATTGGAGAACGTTACATTACACATGAAAGTGATGATGCT
CGCTGGGAAATACATGCATACACACATAACCTTGTATACCCAAAGCACTTCATTATGGCT
CCTAATCCAGATGATATGGAAGAAGATCCTTAA

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ATGGAGGAGGGGGCGCCGCGGCAGCCTGGGCCGAGCCAGTGGCCCCCAGAGGATGAGAAG
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CGGCGCGTGGCCACAGACCGCCGCCACTTGGGCCATGTGCAGCAGCTGCTGCGGTCCTCC
AACCGCCGCCTGGAGCAGCTGCATGGCGAGCTGCGGGAGCTGCACGCCCGAATCCTGCTG
CCCGGCCCTGGGCCTGGCCCAGCTGAGCCTGTGGCCTCAGGACCCCGGCCGTGGGCAGAG
CAGCTCAGGGCTCGGCACCTAGAGGCTCTCCGGAGGCAGCTGCATGTGGAGCTGAAGGTG
AAACAGGGGGCTGAGAACATGACCCACACGTGCGCCAGTGGCACCCCCAAGGAGAGGAAG
CTCCTTGCAGCTGCCCAGCAGATGCTGCGGGACAGCCAGCTGAAGGTGGCCCTGCTGCGG
ATGAAGATCAGCAGCCTGGAGGCCAGTGGGTCCCCGGAGCCAGGGCCTGAGCTACTGGCG
GAGGAGCTACAGCATCGACTGCACGTTGAGGCAGCGGTGGCTGAGGGCGCCAAGAACGTG

FIGURE 2J

GTGAAACTGCTTAGTAGCCGGAGAACACAGGACCGCAAGGCACTGGCTGAGGCCCAGGCC
CAGCTACAGGAGTCCTCTCAGAAACTGGACCTCCTGCGCCTGGCCTTGGAGCAGCTGCTG
GAGCAACTGCCTCCTGCCCACCCTTTGCGCAGCAGAGTGACCCGAGAGTTGCGGGCTGCG
GTGCCTGGATACCCCCAGCCTTCAGGGACACCTGTGAAGCCCACCGCCCTAACAGGGACA
CTGCAGGTCCGCCTCCTGGGCTGTGAACAGTTGCTGACAGCCGTGCCTGGGCGCTCCCCA
GCGGCCGCACTGGCCAGCAGCCCCTCCGAGGGCTGGCTTCGGACCAAGGCCAAGCACCAG
CGTGGCCGAGGCGAGCTTGCCAGTGAGGTGCTGGCTGTGCTAAAGGTGGACAACCGTGTT
GTGGGGCAGACGGGCTGGGGGCAGGTGGCCGAACAGTCCTGGGACCAGACCTTTGTCATC
CCACTGGAGCGAGCCCGTGAGCTGGAGATTGGGGTACACTGGCGGGACTGGCGGCAGCTA
TGTGGCGTGGCCTTCCTGAGACTTGAAGACTTCCTGGACAATGCCTGTCACCAACTGTCC
CTCAGCCTGGTACCGCAGGGACTGCTTTTTGCCCAGGTGACCTTCTGCGATCCTGTCATT
GAGAGGCGGCCCCGGCTGCAGAGGCAGGAACGCATCTTCTCTAAACGCAGAGGCCAGGAC
TTCCTGAGGCGTTCGCAGATGAACCTCGGCATGGCGGCCTGGGGGCGCCTCGTCATGAAC
CTGCTGCCCCCCTGCAGCTCCCCGAGCACAATCAGCCCCCCTAAAGGATGCCCTCGGACC
CCAACAACACTGCGAGAGGCCTCTGACCCTGCCACTCCCAGTAATTTCCTGCCCAAGAAG
ACCCCCTTGGGTGAAGAGATGACACCCCCACCCAAGCCCCCACGCCTCTACCTCCCCCAG
GAGCCAACATCCGAGGAGACTCCGCGCACCAAACGTCCCCATATGGAGCCTAGGACTCGA
CGTGGGCCATCTCCACCAGCCTCCCCCACCAGGAAACCCCCTCGGCTTCAGGACTTCCGC
TGCTTAGCTGTGCTGGGCCGGGGACACTTTGGGAAGGTCCTCCTGGTCCAGTTCAAGGGG
ACAGGGAAATACTACGCCATCAAAGCACTGAAGAAGCAGGAGGTGCTCAGCCGGGACGAG
ATAGAGAGCCTGTACTGCGAGAAGCGGATCCTGGAGGCTGTGGGCTGCACAGGGCACCCT
TTCCTGCTCTCCCTCCTTGTCTGCTTCCAGACCTCCAGCCATGCCCGCTTTGTGACTGAG
TTTGTGCCTGGTGGTGACCTCATGATGCAGATCCACGAGGATGTCTTCCCCGAGCCCCAG
GCCCGCTTCTACGTGGCTTGTGTTGTCCTGGGGCTGCAGTTCTTACACGAGAAGAAGATC
ATTTACAGGGACCTGAAGTTGGATAACCTTCTGCTGGATGCCCAGGGATTCCTGAAGATC
GCAGACTTTGGACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGT
GGCACCCCGGAGTTCCTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACACAGGCCGTC
GACTGGTGGGCGCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCA
GGGGACACAGAGGAAGAGGTGTTTGACTGCATCGTCAACATGGACGCCCCCTACCCCGGC
TTTCTGTCGGTGCAAGGGCTTGAGTTCATTCAGAAGCTCCTCCAGAAGTGCCCGGAGAAG
CGCCTCGGGGCAGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACC
ACCAACTGGCAAGCCCTGCTCGCCCGCACCATCCAGCCCCCCTTCGTGCCTACCCTGTGT
GGCCCTGCGGACCTGCGCTACTTTGAGGGCGAGTTCACAGGGCTGCCGCCTGCCCTGACC
CCACCTGCACCCCACAGCCTCCTCACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGAC
TTTGTGTCAGAGCGATTCCTGGAACCCTGA

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GCTGAAGTGGGATAACCTTCTGCTGGATGCCCAGGGATTCCTGAAGATCGCAGACTTTGG
ACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGTGGCACCCCGGA
GTTCCTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACACGGGCTGTGGACTGGTGGGG
GCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCAGGGGACACAGA
GGAAGAGGTGTTTGACTGCATCGTCAACATGGACGCCCCCTACCCCGGCTTTCTGTCGGT
GCAAGGGCTTGAGTTCATTCAGAAGCTCCTCCAGAAGTGCCCGGAGAAGCGCCTCGGGGC
GGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACCACCAACTGGCA
AGCCCTGCTCGCCCGCACCATCCAGCCCCCCTTTGTGCCTACCCTGTGTGGCCCTGCGGA
CCTGCGCTACTTTGAGGGCGAGTTCACAGGGCTGCCGCCTGCCCTGACCCCACCTGCACC
CCACAGCCTCCTCACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGACTTTGTGTCAGA
GCGATTCCTGGAACCCTGAGGGCATCTCCTGGCACCTCTGTCCCCTTCCCCCACAGACTG
TTAGAGCCTCTGCTCGTTCACCCGTGCGCCCTGCCTGGAGGTCCAGGCCTTGCTGGGTAC
TTCTGAGCCCTTGGGATTCAAAGTGGCAGCCATGGGGCCACTGTTGTGGGCTTTGCTCAG

FIGURE 2K

TGTCACTGGGCAAAGTGTGTCCCTTCCCCCTCCAGCTCGCCCTCTTCTACCTCCCAGCGA
GACCTGGCCCAGAAAGGGTGCCGCAGCAAGGAGTGATATGGTTTGTCTTTTTAAGACTGG
ACTTGCTTTATATTAAATTTGTAAAAGTG

SEQ ID NO: 14_H19102_H
GGTGGCAACATCCGGGGTCCCTGGGCCCGAGGCTGGAAGAGCCTCTGGACAGGTTTGGGA
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CAGTTCATCAACCTCTTTCTACCAGAGTTTCCCATTAGGCCCATTAGGGGGCAGCAGCAG
CTGAAGATTTTAGGCCTCGTGGCTAAAGGCTCCTTTGGAACTGTCCTCAAGGTGCTAGAT
TGCACCCAGAAAGCTGTATTTGCAGTGAAGGTGGTGCCCAAGGTAAAGGTCCTACAGAGG
GATACCGTGAGGCAGTGCAAAGAGGAGGTTAGCATCCAGCGACAGATCAACCATCCCTTT
GTACACAGCTTGGGGGACAGCTGGCAGGGAAAACGGCACCTTTTCATTATGTGTAGCTAC
TGCAGCACAGATCTGTACTCCCTTTGGTCGGCTGTTGGCTGCTTTCCTGAGGCTTCCATC
CGTCTCTTTGCTGCCGAGTTGGTGCTGGTACTGTGTTATCTCCATGACTTGGGCATCATG
CATCGAGATGTGAAGATGGAGAATATTCTTCTAGATGAACGAGGCCATCTGAAACTGACA
GACTTTGGTCTGTCCCGCCACGTGCCCCAGGGAGCTCAAGCCTACACTATCTGTGGCACT
CTTCAGTACATGGCCCCAGAGGTCCTAAGTGGAGGACCTTACAACCATGCTGCTGATTGG
TGGTCCCTGGGTGTCTTGCTTTTCTCTCTGGCGACTGGAAAGTTTCCAGTGGCTGCAGAG
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CTACGTTATCTGCATCACTTCCAGGTCCACCCTTTCTTTCGGGGTGTGGCCTTCGACCCA
GAGCTCCTACAGAAGCAGCCAGTGAACTTTGTCACGGAGACACAAGCTACCCAGCCCAGT
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CCTATCCCTGCTTGA

SEQ ID NO: 15_AA476563_H
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GACACCATTAGCAGGGGCTCAGATGACTCAGTGCCAGTTATTTCGTTTAAAGATGCTGCT
TTTGATGATGTCAGTGGTACTGATGAAGGAAGACCTGATCTTCTTGTAAATTTACCTGGT
GAATTGGAGTCAACAAGAGAAGCTGCAGCAATGGGACCTACTAAGTTTACACAAACTAAT
ATAGGGATAATAGAAAATAAACTCTTGGAAGCCCCTGATGTTTTATGCCTCAGGCTTAGT
ACTGAACAATGCCAAGCACATGAGGAGAAAGGCATAGAGGAACTGAGTGATCCCTCTGGG
CCCAAATCCTATAGTATAACAGAGAAACACTATGCACAGGAGGATCCCAGGATGTTATTT
GTAGCAGCTGTTGATCATAGTAGTTCAGGAGATATGTCTTTGTTACCCAGCTCAGATCCT
AAGTTTCAAGGACTTGGAGTGGTTGAGTCAGCAGTAACTGCAAACAACACAGAAGAAAGC
TTATTCCGTATTTGTAGTCCACTCTCAGGTGCTAATGAATATATTGCAAGCACAGACACT
TTAAAAACAGAAGAAGTATTGCTGTTTACAGATCAGACTGATGATTTGGCTAAAGAGGAA
CCAACTTCTTTATTCCAGAGAGACTCTGAGACTAAGGGTGAAAGTGGTTTAGTGCTAGAA
GGAGACAAGGAAATACATCAGATTTTTGAGGACCTTGATAAAAAATTAGCACTAGCCTCC
AGGTTTTACATCCCAGAGGGCTGCATTCAAAGATGGGCAGCTGAAATGGTGGTAGCCCTT
GATGCTTTACATAGAGAGGGAATTGTGTGCCGCGATTTGAACCCAAACAACATCTTATTG
AATGATAGAGGACACATTCAGCTAACGTATTTTAGCAGGTGGAGTGAGGTTGAAGATTCC
TGTGACAGCGATGCCATAGAGAGAATGTACTGTGCCCCAGAGGTTGGAGCAATCACTGAA
GAAACTGAAGCCTGTGATTGGTGGAGTTTGGGTGCTGTCCTCTTTGAACTTCTCACTGGC
AAGACTCTGGTTGAATGCCATCCAGCAGGAATAAATACTCACACTACTTTGAACATGCCA
GAATGTGTCTCTGAAGAGGCTCGCTCACTCATTCAACAGCTCTTGCAGTTCAATCCTCTG

FIGURE 2L

GAACGACTTGGTGCTGGAGTTGCTGGTGTTGAAGATATCAAATCTCATCCATTTTTTACC
CCTGTGGATTGGGCAGAACTGATGAGATGA

SEQ ID NO: 16_AA626690_H
ATGCTACCATTCGCTCCTCAGGACGAGCCCTGGGACCGAGAAATGGAAGTGTTCAGCGGC
GGCGGCGCGAGCAGCGGCGAGGTAAATGGTCTTAAAATGGTTGATGAGCCAATGGAAGAG
GGAGAAGCAGATTCTTGTCATGATGAAGGAGTTGTTAAAGAAATCCCTATTACTCATCAT
GTTAAGGAAGGCTATGAGAAAGCAGATCCTGCACAGTTTGAGTTGCTCAAGGTTCTTGGT
CAGGGGTCATTTGGAAAGGTTTTTCTTGTTAGAAAGAAGACCGGTCCTGATGCTGGGCAG
CTCTATGCAATGAAGGTGTTAAAAAAAGCCTCTTTAAAAGTTCGAGACAGAGTTCGGACA
AAGATGGAGAGGGATATACTGGTGGAAGTAAATCATCCATTTATTGTCAAATTGCACTAT
GCCTTTCAGACTGAAGGGAAACTGTACTTAATACTGGATTTTCTCAGGGGAGGAGATGTT
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GAACTGGCCCTTGCTTTGGATCATCTGCACCAATTAGGAATTGTTTATAGAGACCTGAAG
CCAGAAAACATTTTGCTTGATGAAATAGGACATATCAAATTAACAGATTTTGGACTCAGC
AAGGAGTCAGTAGATCAAGAAAAGAAGGCTTACTCATTTTGTGGTACAGTAGAGTATATG
GCTCCTGAAGTAGTAAATAGGAGAGGCCATTCCCAGAGTGCTGATTGGTGGTCATATGGT
GTTCTTATGTTTGAAATGCTTACTGGTACTCTGCCATTTCAAGGTAAAGACAGAAATGAG
ACCATGAATATGATATTAAAAGCAAAACTTGGAATGCCTCAATTTCTTAGTGCTGAAGCA
CAAAGTCTTCTAAGGATGTTATTCAAAAGGAATCCAGCAAATAGATTGGGATCAGAAGGA
GTTGAAGAAATCAAAAGACATCTGTTTTTTGCAAATATTGACTGGGATAAATTATATAAA
AGAGAAGTTCAACCTCCTTTCAAACCTGCTTCTGGAAAACCAGATGATACTTTTTGTTTT
GATCCTGAATTTACTGCAAAAACACCTAAAGATTCTCCCGGTTTGCCAGCCAGTGCAAAT
GCTCATCAGCTCTTCAAAGGATTCAGCTTTGTTGCAACTTCTATTGCAGAAGAATATAAA
ATCACTCCTATCACAAGTGCAAATGTATTACCAATTGTTCAGATAAATGGAAATGCTGCA
CAATTTGGTGAAGTATATGAATTGAAGGAGGATATTGGTGTTGGCTCCTACTCTGTTTGC
AAGCGATGCATACATGCAACTACCAACATGGAATTTGCAGTGAAGATCATTGACAAAAGT
AAGCGAGACCCTTCAGAAGAGATTGAAATATTGATGCGCTATGGACAACATCCCAACATT
ATTACTTTGAAGGATGTCTTTGATGATGGTAGATATGTTTACCTTGTTACGGATTTAATG
AAAGGAGGAGAGTTACTTGACCGTATTCTCAAACAAAAATGTTTCTCGGAACGGGAGGCT
AGTGATATACTATATGTAATAAGTAAGACAGTTGACTATCTTCATTGTCAAGGAGTTGTT
CATCGTGATCTTAAACCTAGTAATATTTTATACATGGATGAATCAGCCAGTGCAGATTCA
ATCAGGATATGTGATTTTGGGTTTGCAAAACAACTTCGAGGAGAAAATGGACTTCTCTTA
ACTCCATGCTACACTGCAAACTTTGTTGCACCTGAGGTTCTTATGCAACAGGGATATGAT
GCTGCTTGTGATATCTGGAGTTTAGGAGTCCTTTTTTACACAATGTTGGCTGGCTACACT
CCATTTGCTAATGGCCCCAATGATACTCCTGAAGAGATACTGCTGCGTATAGGCAATGGA
AAATTCTCTTTGAGTGGTGGAAACTGGGACAATATTTCAGACGGAGCAAAGGATTTGCTT
TCCCATATGCTTCATATGGACCCACATCAGCGGTATACTGCTGAACAAATATTAAAGCAC
TCATGGATAACTCACAGAGACCAGTTGCCAAATGATCAGCCAAAGAGAAATGATGTGTCA
CATGTTGTTAAGGGAGCAATGGTTGCAACATACTCTGCCCTGACTCACAAGACCTTTCAA
CCAGTCCTAGAGCCTGTAGCTGCTTCAAGCTTAGCCCAGCGACGGAGCATGAAAAAGCGA
ACATCAACTGGCCTGTAA

SEQ ID NO: 17_AA215680_H
ATGAGCCTGGTGGCCTGTGAGTGCCTGCCCAGCCCCGGCCTGGAGCCTGAGCCTTGCTCA
CGAGCACGGTCCCAAGCTCACGTGTACCTGGAGCAGATTCGCAACAGGGTGGCTCTGGGA
GTGCCTGACATGACAAAACGTGACTATCTGGTGGATGCGGCCACGCAGATCCGGCTGGCC
CTGGAGCGCGATGTTAGTGAGGACTATGAGGCGGCCTTCAACCACTATCAGAATGGCGTG
GACGTGCTGCTCCGTGGCATACACGTTGACCCCAACAAGGAGCGACGTGAGGCTGTGAAG
CTGAAAATTACCAAATACCTGCGGCGGGCAGAGGAGATCTTCAACTGCCACCTGCAGCGG

FIGURE 2M

CCGCTGAGCAGTGGAGCCAGCCCCAGCGCGGGTTTCAGCAGCCTGAGGCTCCGGCCCATT
CGCACGCTGAGCTCTGCCGTGGAGCAGCTGAGGGGCTGCAGGGTGGTCGGGGTCATCGAG
AAGGTGCAGCTGGTCCAGGACCCGGCAACCGGAGGGACCTTTGTGGTGAAGAGCCTACCC
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ACGAAGCTGCTCAGGTACTTTGTGAGCGAGGACTCCATCTTCCTGCACCTGGAGCATGTG
CAAGGAGGCACTCTCTGGTCCCACCTGCTCTCCCAGGCGCACTCCCGACATTCTGGGCTC
AGCTCTGGCTCTACCCAGGAGAGGATGAAGGCTCAGCTCAACCCCCACCTCAACCTCCTG
ACCCCAGCGAGGCTTCCCTCAGGCCATGCCCCTGGCCAGGACAGAATCGCCCTGGAGCCT
CCTAGGACTTCTCCGAACCTTCTCCTAGCTGGGGAGGCCCCATCCACCAGACCCCAGAGG
GAGGCTGAAGGTGAACCCACAGCCAGGACCAGCACCTCTGGCTCCTCGGACCTTCCAAAG
GCCCCAGGTGGCCACCTGCACCTTCAAGCTAGGAGGGCTGGCCAGAACTCAGACGCTGGG
CCCCCTCGGGGGCTCACTTGGGTTCCTGAGGGGGCCGGCCCGGTGCTAGGGGGCTGTGGC
CGAGGCATGGATCAGAGCTGCCTGTCAGCAGATGGGGCCGGCCGGGGCTGTGGCAGGGCC
ACCTGGAGTGTGAGAGAGGAGCAGGTGAAGCAGTGGGCGGCAGAGATGCTGGTAGCGCTG
GAGGCGCTGCACGAGCAGGGGGTGCTGTGCCGGGACCTCCACCCCGGGAACCTGCTCCTG
GACCAGGCAGGTCACATCCGGCTCACATATTTGGCCAGTGGTCAGAGGTGGAGCCCCAG
TGCTGCGGGGAGGCCGTGGACAATCTCTACAGCGCCCCAGAGGTGGGTGGGATTTCCGAG
CTGACGGAAGCCTGTGACTGGTGGAGCTTTGGGTCTCTACTGTATGAACTGCTGACGGGA
ATGGCACTGTCCCAGAGCCACCCTTCAGGAATCCAGGCCCACACCCAGCTCCAGCTGCCC
GAGTGGCTCAGTCGCCCAGCGGCCTCTCTGCTGACTGAGCTGCTGCAGTTCGAGCCTACC
CGGCGCCTGGGCATGGGAGAAGGTGGTGTCAGCAAACTCAAGTCCCATCCCTTTTTCAGT
ACCATCCAATGGAGCAAGCTGGTGGGGTAA

SEQ ID NO: 18_SGK_H
ATGACGGTGAAAACTGAGGCTGCTAAGGGCACCCTCACTTACTCCAGGATGAGGGGCATG
GTGGCAATTCTCATCGCTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTCAG
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TCCCAACCTCAGGAGCCTGAGCTTATGAATGCCAACCCTTCTCCTCCACCAAGTCCTTCT
CAGCAAATCAACCTTGGCCCGTCGTCCAATCCTCATGCTAAACCATCTGACTTTCACTTC
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GAAGTGTTCTATGCAGTCAAAGTTTTACAGAAGAAAGCAATCCTGAAAAAGAAAGAGGAG
AAGCATATTATGTCGGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCCTTTCCTGGTG
GGCCTTCACTTCTCTTTCCAGACTGCTGACAAATTGTACTTTGTCCTAGACTACATTAAT
GGTGGAGAGTTGTTCTACCATCTCCAGAGGGAACGCTGCTTCCTGGAACCACGGGCTCGT
TTCTATGCTGCTGAAATAGCCAGTGCCTTGGGCTACCTGCATTCACTGAACATCGTTTAT
AGAGACTTAAAACCAGAGAATATTTTGCTAGATTCACAGGGACACATTGTCCTTACTGAT
TTCGGACTCTGCAAGGAGAACATTGAACACAACAGCACAACATCCACCTTCTGTGGCACG
CCGGAGTATCTCGCACCTGAGGTGCTTCATAAGCAGCCTTATGACAGGACTGTGGACTGG
TGGTGCCTGGGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCCGCCTTTTTATAGCCGA
AACACAGCTGAAATGTACGACAACATTCTGAACAAGCCTCTCCAGCTGAAACCAAATATT
ACAAATTCCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAGGACAGGACAAAGCGGCTC
GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGTCTTCTTCTCCTTAATTAACTGG
GATGATCTCATTAATAAGAAGATTACTCCCCCTTTTAACCCAAATGTGAGTGGGCCCAAC
GAGCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCCAACTCCATTGGCAAG
TCCCCTGACAGCGTCCTCGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCCTAGGC
TTTTCCTATGCGCCTCCCACGGACTCTTTCCTCTGA

SEQ ID NO: 19_AA107515_M
CGGGTCGACCCACGCGTCCGCCGGTTTCACTGCTCCCCTCAGTCTCTTTTGGGCTCTTTC
CGGGCATCGGGACGATGACCGTCAAAGCCGAGGCTGCTCGAAGCACCCTTACCTACTCCA

FIGURE 2N

GAATGAGGGGAATGGTAGCGATTCTCATCGCTTTTATGAAACAGAGAAGGATGGGCCTGA
ACGATTTTATTCAGAAGATTGCCAGCAACACCTATGCATGCAAACACGCTGAAGTTCAGT
CCATTTTGAAAATGTCCCATCCTCAGGAGCCGGAGCTTATGAACGCTAACCCCTCTCCTC
CGCCAAGTCCCTCTCAACAAATCAACCTGGGTCCGTCCTCCAACCCTCACGCCAAACCCT
CCGACTTTCACTTCTTGAAAGTGATCGGAAAGGGCAGTTTTGGAAAGGTTCTTCTGGCTA
GGCACAAGGCAGAAGAAGTATTCTATGCAGTCAAAGTTTTACAGAAGAAAGCCATCCTGA
AGAAGAAAGAGGAGAAGCATATTATGTCAGAGCGGAATGTTCTGTTGAAGAATGTGAAGC
ACCCTTTCCTGGTGGGCCTTCACTTCTCATTCCAGACCGCTGACAAGCTCTACTTTGTCC
TGGACTACATTAATGGTGGAGAGCTGTTCTACCATCTCCAGAGGGAGCGCTGCTTCCTGG
AACCACGGGCTCGATTCTACGCAGCTGAAATAGCCAGTGCCCTGGGCTATCTGCACTCCC
TAAACATCGTTTATAGAGACTTAAAACCTGAGAATATTCTCCTAGACTCCCAGGGGCACA
TCGTCCTCACTGACNTATTTCAGCTGCGTAGAATCGAGCATAACGGGACAACATCTACCT
TCTGTGGCACGCCTGAGTATCTGGCTCCTGAGGTCCTCCATAAGCAGCCGTATGACCGGA
CGGTGGACTGGTGGTGTCTTGGGGCTGTCCTGTATGAGATGCTCTACGGCCTGCCCCCGT
TTTATAGCCGGAACACGGCTGAGATGTACGACAATATTCTGAACAAGCCTCTCCAGTTGA
AACCAAATATTACAAACTCGGCAAGGCACCTCCTGGAAGGCCTCCTGCAGAAGGACCGGA
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GTGGGCCCAGTGACCTTCGGCACTTCGATCCCGAGTTTACCGAGGAGCCGGTCCCCAGCT
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CCTTCCTCGGCTTCTCCTATGCACCTCCTGTGGATTCCTTCCTCTGAGTGCTCCCGGGAT
GGTTCTGAAGGACTTCCTCAGCGTTTCCTAAAGTGTTTTCGTTAGCCTTTGGTGGAGTTG
CCAGCTGACAGAACATTTTAAAAGAATTTGCACACCTGGAAGCTTGGCAGTCTCGCCTGC
CCGGCGTGGCGCGACGCAGCGCGCGCTGCTTGATGGGAGCTTTCCGAAGAGCACACCCTC
CTCTCAATGAGCTTGTGAGGTCTTCTTTTCTTCTCTTCCTTCCAACGTGGTGCTAGCTCC
AGGCGAGCGAGCGTGAGAGTGCCGCCTGAGACAGACACCTTGGTCTCAGTTAGAAGGAAG
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ATGTGCCTTTTCTGAGATCGTGTTAGCTCCAAAGCTTTTTCCTATCGCAGAGTGTTCAGT
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GTGGCGTGAGTGTGCTATGCCTGATCACAGACGGTTTTGTTGTGAGCATCAATGTGACAC
TTGCAGGACACTACAATGTGGGACATTGTTTGTTTCTTCCACATTTGGAAGATAAATTTA
TGTGTAGACTGTTTTGTAAGATATAGTTAATAACTAAAACCTATTGAAACGGTCTTGCAA
TGACGAGCATTCAGATGCTTAAGGAAAGCATTGCTGCTACAAATATTTCTATTTTTAGAA
AGGGTTTTTATGGACCAATGCCCCAGTTGTCAGTCAAAGCCGTTGGTGTTTTCATTGTTT
AAAATGTCACCTATAAAACGGGCATTATTTATGTTTTTTTTCCCTTTGTTCATATTCTTT
TGCATTCCTGATTATTGTATGTATCGTGTAAAGGAAGTCTGTACATTGGGTTATAACACT
AGATATTTAAACTTACAGGCTTATTTGTAAACCATCATTTTAATGTACTGTAATTAACAT
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CAATTTTGGTTTGCAATAAAATCTTGAAAACT

SEQ ID NO: 20_AA109508_M
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AGGTGTAGAGCCTGAAGACACCACATCCACATTCTGTGGTACCCCTGAGTACTTGGCACC
TGAAGTGCTTCGGAAAGAGCCTTATGATCGAGCAGTGGACTGGTGGTGCTTGGGGGCAGT
CCTCTACGAGATGCTCCATGGCCTGCCGCCCTTCTACAGCCAAGATGTATCCCAGATGTA
TGAGAACATTCTGCACCAGCCGCTACAGATCCCCGGAGGCCGGACAGTGGCCGCCTGTGA
CCTCCTGCAAAGCCTTCTCCACAAGGACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTT
TCTTGAGATTAAGAACCATGTATTCTTCAGCCCCATAAACTGGGATGACCTGTACCACAA

FIGURE 2O

GAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTGA
CCCAGAGTTCACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGC
CAGCAGCTCTGGGGCCTCAAGTGCATTCCTGGGATTTTCTTATGCGCCAGAGGATGATGA
CATCTTGGATTGCTAGAAGAGAAGGACCTGTGAAACTACTGAGGCCAGCTGGTATTAGTA
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CAGGTTTATTTTTTCCAGCACATAAAAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAG
GACAGGTCATCAGATACTCAGAGGCTGTATCTCTGCCCTGCCAACCTTGACAAATGGCTT
CCAATGTTAGGTTTGCTACAAGATGGTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAG
GGAAGGGAAAATGGAGGAAAGGGGAGAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAA
AAGCTCCACCCAATGACTTCTGCTTCCATCTCACTAACCACCCACCCCTACCTGGAATGG
AGGCTGGGAGATGTGGCTTATTTGCTGGGTACGTGACTATCCCTAATAACAAAGGGGTTC
TGACACTAAGACATTAGGGGAGAATGTTGGGTAGGCAGCCAGCACTCTTTTACCAGAGGG
CCTCCTGGTGTTTGGATTTTGATCTCAATGTGTAAAATGACAGAGATGTAACAAGCTCAT
AGGGTATCAATATCTCTTATTGTTCT

SEQ ID NO: 21_AA887783_H
CGGATGCATTTNTTGGTGTGCTCTTGAGGGATTAAATGCAAAGAGATCACACCATGGACT
ACAAGGAAAGCTGCCCAAGTGTAAGNATTCCCAGCTCCGATGAACACAGAGAGAAAAAGA
AGAGGTTTACTGTTTATAAAGTTCTGGTTTCAGTGGGAAGAAGTGAATGGTTTGTCTTCA
GGAGATATGCAGAGTTTGATAAACTTTATAACACTTTAAAAAAACAGTTTCCTGCTANGG
CCCTGAAGATTCCTGCCAAGAGAATATTTGGTGATAATTTTGATCCAGATTTTATTAAAC
AAAGACGAGCAGGACTAAACGAATTCATTCAGAACCTAGTTAGGTATCCAGAACTTTATA
ACCATCCAGATGTCAGAGCATTCCTTCAAATGGACAGTCCAAAACACCAGTCAGATCCAT
CTGAAGATGAGGATGAAAGAAGTTCTCAGAAGCTACACTCTACCTCACAGAACATCAACC
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CCTTCCAAACAACTGAAAAGCTTTATTTTGTTCTGGATTTTGTTAATGGAGGGGAGGGAC
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GTTTGAGGCCAGGAGTGAGTCTTACAGCCTGGTCCATTCTGGAAGAACTCCTAGAAAAAG
ACAGGCAAAATCGACTTGGTGCCAAGGAAGACTTTCTTGAAATTCAGAATCATCCTTTTT
TTGAATCACTCAGCTGGGCTGACCTTGTACAAAAGAAGATTCCACCACCATTTAATCCTA
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TATGAAAAAATGTATTTTCTTCTATGTGCAAGAAAAATAGGGCATTTCAAAGAGCTGTTT
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TCTTAGCATTAACCTATTTTTAAAGAAACCTTTTTTGCTATTGACTGTTTTTTCCCTCTA
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GCAATTGGTACATGGTTGTTTAAGAAGAAACCGTATTTTTCCATGATAAATCACTGTTTG
AAATATTTGGTTCATGGTATGATCGAAATGTAAAAGCATAATTAACACATTGGCTGCTAG
TTAACAATTGGAATAACTTTATTCTGCAGATCATTTAAGAAGTAACAGGCCGGGCGCGGT
GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACCTGAGGTCA

FIGURE 2P

GGAGTTGGAGACCAGCCTGACCAACATGGACAAACCCCGTCTCTACTAAAAATACAAAAT
TGGCAGGGTGTGGTGGCACATGCCTATAATCCCAGCTACTTGGGAGGCTAAGGCAGGAGA
ATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCATTGCACTCCTG
CCTGGGCAACAAGAGTGAAACTCCATCTCC

SEQ ID NO: 22_R47805_H
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CTGGACGCCCAGCAGCCCTGCTACCTGCTCTACCGCCTCGACTCACAGAATGCTCAGGGC
TTCGAATGGCTCTTCCTCGCCTGGTCGCCTGATAACTCCCCCGTGCGGCTGAAGATGCTG
TACGCGGCCACGCGGGCCACAGTGAAAAAGGAGTTTGGAGGTGGCCACATCAAGGATGAG
CTCTTCGGGACTGTGAAGGATGACCTCTCTTTTGCTGGGTACCAGAAACACCTGTCGTCC
TGTGCGGCACCTGCCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAAC
GAGGTGAAGACAGAGATCAGTGTGGAAAGCAAGCACCAGACCCTGCAGGGCCTCGCCTTC
CCCCTGCAGCCTGAGGCCCAGCGGGCACTCCAGCAGCTCAAGCAGAAAATGGTCAACTAC
ATCCAGATGAAGCTGGACCTAGAGCGGGAAACCATTGAGCTGGTGCACACAGAGCCCACG
GATGTGGCCCAGCTGCCCTCCCGGGTGCCCCGAGATGCTGCCCGCTACCACTTCTTCCTC
TACAAGCACACCCATGAGGGCGACCCCCTTGAGTCTGTAGTGTTCATCTACTCCATGCCG
GGGTACAAGTGCAGCATCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCCTCCTC
GACTCCGTGGAGCAGGACTTCCATCTGGAGATCGCCAAGAAAATTGAGATTGGCGATGGG
GCAGAGCTGACGGCAGAGTTCCTCTACGACGAGGTGCACCCCAAGCAACACGCCTTCAAG
CAGGCCTTCGCCAAGCCCAAGGGCCCAGGGGGCAAGCGGGGCCATAAGCGCCTCATCCGC
GGCCCGGGTGAAAATGGGGATGACAGCTAG

SEQ ID NO: 23_H60215_H
CCACGCGTCCGGCGCCGCAGCCATGGAGGGAGGCGGCGGCGGCGGCGGCGGCGGCTCGGG
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CGGGAGGGAGAGCCGAGCAGCCCCGGCTCTGGGCTACGGACTATGGGCGAATAGCTCTGA
CCACCCGGCGAAGTGCACACACCCAGAAGCTATGTCCTTCGGCAGTAAAAGTTTTACAGC
ACAATATATGTGCTCTGCTCTCCTCCCGCAATCCTGCTCCAAGAGATCTTAAGCTGGAGG
CACCAGGTCTGAATTCCAGACTCCTCCCCACCACCCACACTTCACCTCCAACTGGAGCAT
GACCACAGACCCATTCAGGGAGGCTGGCGGACTCTTCATCCTGGACAGTCCCTTACTGTA
TGTCAAAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCGGCCA
GGGCCAAGGCTCTAGGAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTCA
TCCTTGGTCCCCGTCTGGGCAACTCACCGGTGCCAAGCATAGTGCAGTGTTTGGCGAGGA
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AAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCGAGTACTCAC
TGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACC
GCACCTGTGAAATCGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGC
GCATCTGCCTCGTCCTGGACTGCCTCTGTGCTCATGACTTCAGCGATAAGACCGCTGACC
TCATCAACCTGCAGCACTACGTCATCAAGGAGAAGAGGCTCAGCGAGAGGGAGACTGTGG
TAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGCACA
GAGACCTGAAGCTGGGGAACATGGTGCTCAACAAGAGGACACATCGGATAACCATCACCA
ACTTCTGCCTCGGGAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGA
GCCCTGCCTACATCAGTCCCGACGTGCTCAGCGGCCGGCCGTACCGTGGCAAGCCCAGTG
ACATGTGGGCCCTGGGCGTGGTGCTCTTCACCATGCTGTATGGCCAGTTCCCCTTCTACG
ACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGAGG
ATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCCTTGACCCCC
AGCAGCGCCTGGCCGCCGCCGACGTCCTGGAGGCCCTCAGTGCCATCATTGCATCATGGC

FIGURE 2Q

AGTCCCTGTCATCTCTGAGTGGGCCTTTGCAAGTGGTTCCTGACATTGATGACCAAATGA
GCAATGCGGATAGCTCCCAGGAGGCGAAGGTGACGGAGGAGTGCTCCCAGTACGAGTTTG
AGAACTACATGCGTCAGCAGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACACCC
GGAGCTGGGTACCCAAGCGGCAGTTCGGCAGCGCACCACCGGTGCGACGGCTGGGCCACG
ACGCACAGCCCATGACCTCCTTGGACACGGCCATCCTGGCGCAGCGCTACCTGCGGAAAT
AACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCG
TGGCTGTCAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGC
AGGGACAGGGACAGCCCAGGTCACACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTT
TGGGATGATTGCTCGATTGTTTGGTTTTTAAATCTGAGAAGCCTAGATAACTAATCTGCT
TTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTCTCTGGACTGAGC
AAGAGGGAGGAGGGAGCCTGCTCACCCCACTCCAGGGCCTTCCCCAGCGGCCACCAACTG
ACCTGGGGCGCTGCTCCCCACAGTCCAAATAAGCTGAAAGTGCAGCTCGCTGCAGGCCCC
AGAGCGAGCTTCCCCTCCTCCCTGCTCTCCCAGGCCCCTGCCACAGCCTCTTTCCGTCCC
TCTCTTTCTGATCCAGGCCCCTCAGTCCAAGCTTTGGAAAACCTTCACCTCATCTTAAAC
CAAACTCAAATATATTTATTTTTTTACCAT

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GCCGCGATGGCCAGCACCAGGAGTATCGAGCTGGAGCACTTTGAGGAACGGGACAAAAGG
CCGCGGCCGGGGTCGCGGAGAGGGGCCCCCAGCTCCTCCGGGGGCAGCAGCAGCTCGGGC
CCCAAGGGGAACGGGCTCATCCCCAGTCCGGCGCACAGTGCCCACTGCAGCTTCTACCGC
ACGCGGACCCTGCAGGCCCTCAGCTCGGAGAAGAAGGCCAAGAAGGCGCGCTTCTACCGG
AACGGGGACCGCTACTTCAAGGGCCTGGTGTTTGCCATCTCCAGCGACCGCTTCCGGTCC
TTCGATGCGCTCCTCATAGAGCTCACCCGCTCCCTGTCGGACAACGTGAACCTGCCCCAG
GGTGTCCGCACTATCTACACCATCGACGGCAGCCGGAAGGTCACCAGCCTGGACGAGCTG
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AAAAATATTAATCCAAACTGGTCTGTGAACATCAAGGGTGGGACATCCCGAGCGCTGGCT
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AAGACTGCTCATTCCTTTGAACAAGTCTTAACAGATATCACCGAAGCCATTAAACNAGCC
TCAGGAGTCGTCAAGAGGCTCTGCACCCTGGATGGAAAGCAGGTGAGAGTTACGTGTGTG
CATCTGCCAGACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTT
CGTTATGCCCAAGATGACTTTGTCCTGGATCATAGTGAATGTCGTGTCCTGAAGTCATCT
TATTCTCGATCCTCAGCTGTTAAGTATTCTGGATCCAAAAGCCCTGGGCCCTCTCGACGC
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CGTTGCATAAGTCCTGAAGGTGTGAATGGAAACAGATGCTCTGAATCATCAACTCTTCTT
GAGAAATACAAAATTGGAAAGGTCATTGGTGATGGCAATTTTGCAGTAGTCAAAGAGTGT
ATAGACAGGTCCACTGGAAAGGAGTTTGCCCTAAAGATTATAGACAAAGCCAAATGTTGT
GGAAAGGAACACCTGATTGAGAATGAAGTGTCAATACTGCGCCGAGTGAAACATCCCAAT
ATCATTATGCTGGTCGAGGAGATGGAAACAGCAACTGAGCTCTTTCTGGTGATGGAATTG
GTCAAAGGTGGAGATCTCTTTGATGCAATTACTTCGTCGACCAAGTACACTGAGAGAGAT
GGCAGTGCCATGGTGTACAACTTAGCCAATGCCCTCAGGTATCTCCATGGCCTCAGCATC
GTGCACAGAGACATCAAACCAGAGAATCTCTTGGTGTGTGAATATCCTGATGGAACCAAG
TCTTTGAAACTGGGAGACTTTGGGCTTGCGACTGTGGTAGAAGGCCCTTTATACACAGTC
TGTGGCACACCCACTTATGTGGCTCCARAAATCATTGCTGAAACTGGCTATGGCCTGAAG
GTGGACATTTGGGCAGCTGGTGTGATCACATACATACTTCTCTGTGGATTCCCACCATTC
CGAAGTGAGAACAATCTCCAGGAAGATCTCTTCGACCAGATCTTGGCTGGGAAGCTGGAG
TTTCCGGCCCCCTACTGGGATAACATCACGGACTCTGCCAAGGAATTAATCAGTCAAATG
CTTCAGGTAAATGTTGAAGCTCGGTGTACCGCGGGACAAATCCTGAGTCACCCCTGGGTG
TCAGATGATGCCTCCCAGGAGAATAACATGCAAGCTGAGGTGACAGGTAAACTAAAACAG
CACTTTAATAATGCGCTCCCCAAACAGAACAGCACTACCACCGGGGTCTCCGTCATCATG

FIGURE 2R

GTGAGTGGAAGGCGGCAGGTCTGGCCTGACTGCGGAGCCGGCCTTGAAGTTTTTGAATTA
GGTAGCCGGGAGCTGCCCTCACATGGAAGTTGGTGCCTTCCGTAGTCCTATTTCATATGA
AGATTGGCTTGGCATGTGGAGGGCACTCATTCGGCAACTCCCAGGCTTTGGGCACTGTGT
GGAGGGGCTTGTGTAGGGACCAGCAGGCCTGGTGTGAGGGGTCCAGGCGTCAAGGAGCTC
CTGGCTGGGCCCTCTGGGCAGCTGCTTCCACTCTTGTCTCTGCCTTCTCATCTAGAGAGA
CTCCCAAGCCCTGGAGGGGTGTGTTGTGTTAGGAATTAACTCCCTGCCTACCCCAAGGCC
TCAGAAATAGATTATTAGAGATGTGAATTATTCTTTGAGACTTGGGATAAGAAACAGCCA
AAGCTAAACATATTTCAGTTTTAAAAAATCAGTGTTTTATAAAACACAGTTTGGGGCTTT
TAAAGGTACATAATCAAGGAAAAAAATATATATTCATTTTTCAGGGTTGGTAACATTTTA
TGAGATGTCAGTGACAACGATGGCCTTATTTTTTTCAGCCTTTTCTTCTTCCAAAATGTT
TCTTAAGGCAACTCTCCTAAATACATAAACACAACAAATTAAAATGAAAAGTGACATGAG
AGTAAATGAATCAAAAGGAAAAAACATTGAACCAGAGGTGAGGGCAGCACACCCGCAGCA
GCTGTCCAGGCCTGAGCCAATGCAACCCTGGGCGGGAAGGCCAGCTCACCGTGAGCAGGT
AGAAGCCAGCCAGCCACCCAGGCAGGGACCTTGGTTCTCCCCACACACTCCCAGGAGCAG
GGAACAGGGGTGGAGTGGCCTTTCCCAGAGCTGGAGTTGGCTGCAGCAGCTTTCGAATCA
GACCTGCCAAGGTGATGGGCGTCTGAGTTTCACATCTGGGCCCCCCGTGACCCCACTGAG
TCCTGACAGCTAAGGATGGGCCACCTCCACAGCTCCGTCACTCGTACTTGGGACAGGCCT
CTCATCCTCTGGGAAGGTCCTCCTTGTTTCCTACCCAACTAGAAGGGAAACAGTGGCATA
TTCTCATGGTACATGGTTGTCTGAAAGCCTTACCTAGGAAGACGCAGGGTCTAGATAGAA
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CCTGAAGGTGTGAATGGAAACCGGTGCTCCGAGTCGTTCCCCCTTCTGGAGAAATACAGA
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ACTGGAAAAGAGTTTGCATTAAAGATTATAGACAAAGCCAAATGCTGTGGAAAGGAGCAT
CTGATTGAGAACGAAGTGTCAATCCTGCGCCGAGTGAAGCACCCCAACATCATCATGTTG
GTTGAAGAGATGGAAACAGCAACTGACCTCTTTCTAGTGATGGAACTGGTCAAAGGTGGA
GATCTCTTTGATGCGATTACCTCTTCAACCAAGTACACTGAGAGAGATGGAAGCGCCATG
GTGTACAACCTAGCCAATGCCCTCCGGTACCTGCACAGCCTCAGCATCGTCCACAGGGAC
ATCAAGCCTGAGAATCTGCTGGTGTGCGAATACCCAGATGGAACCAAGTCTTTGAAGCTG
GGAGACTTTGGGCTGGCGACGGTGGTTGAAGGCCCGTTGTACACGGTCTGTGGCACGCCA
ACTTATGTGGCACCAGAGATCATAGCTGAAACAGGTTATGGCCTGAAGGTGGATGTTTGG
GCAGCTGGTGTGATTACATACATACTTCTCTGTGGATTCCCACCATTCCGGAGTGAGAAC
AATCTCCAGGAAGATCTCTTTGACCAGATCTTGGCTGGAAAGCTGGAATTCCCAGCCCCC
TACTGGGACAACATTACAGACTCTCCTTGTGTGTGTTTAGGAAATGCTTATGAAGCTGG
CCCGTGGGCTTCCCAGTGGGACGTGCAGCAGTTCTTGGCAGAGCAGGGCCAGCTCTGCTG
TGTCATCTCCAGGGTCTCCCATCACCTCTGCTCTTTGCCATGGCAGGTCTGCTGAGACCC
CGCGGGGACGGGGGCATGGTGCTCCCTGATTGGCCTGTGACCAACCTTCTGGAAGGCTGC
TGGCAGTTTTCCCTGTTTTCCACCACCCCACTCTTTTTAATAATTGTATATAACTGTACT
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TGCCTTTTCCAGGTATCCCCAACCTGCAATAAACTCTTCCCTCTTCAG

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GCTGTGCAGGCCCCACTGGCTGTGCGTGCCCTCTACACACCTTGTCATGGCCACCCTGTC
ACCAACCTGGCAGACTTGAAGAACAGAGGGCAGTATGTGGCCGCTGGATTTGAACGATTC

FIGURE 2S

CACAAGCTCCCCCCTTACCAGGCTTTTTGTCTCAGTGTGTTCAGGAATGGGGACCTGGTA
AGTCCCCCATTTAGTCTGAAGCTGTCCCAGGCTGCCAGCCAGGACTGGGAAACTGTGTTG
AAGCTCCTGACTGAGAAGGTCAAGTTGCAGAGTGGGGCTGTGAGACTCTGCACCCTAGAG
GGGCTCCCACTGTCAGCAGGGAAGGAGCTGGTAACTGGCCATTACTATGTGGCTGTCGGA
GAGGATGAGTTCAAGGACCTTCCCTATCCAGCTCTGTCCACAAGAGGGCTCCTGGCAGCA
GGCAATGAAGCCCACCTGAGGAGTGGAGTGGGACTGTCGCTGGTTCCCCCAAGCCTCTT
GGAAGGAAGGCTAAGAAGGAGACATGCCTAATCGTGACCCTGACCCTGAAATACCAGCAG
TCAGAAACAAGCAGAGACGGGCAATCATTCCCATCAGGAGTTATAGGAGTATATGGAGCT
CCCCACCGAAGGAAGGAGACAGCGGGGGCCCTGGAAGTAGCAGATGATGAAGACACTCAG
ACAGAGGAGCCCTTGGATCAGAGGGCAGCACAGATAGTGGAACAGGTTACTTGTCTGCAA
GACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTTCGTTATGCC
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CCCATGGGCATCATTGCCGCCAATGTGGAAAAGCATTATGAGACTGGCCGGGTCATTGGG
GATGGGAACTTTGCTGTCGTGAAGGAGTGCAGACACCGCGAGACCAGGCAGGCCTATGCG
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GACATGGAAATCTACCTGATCCTGGAGTACGTGCAGGGAGGAGACCTTTTTGACGCCATC
ATAGAAAGTGTGAAGTTCCCGGAGCCCGATGCTGCCCTCATGATCATGGACTTATGCAAA
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TTGGTTCAGCGAAATGAGGACAAATCTACTACCTTGAAATTGGCTGATTTTGGACTTGCA
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ATTCTTTCTGAGAAAGGTTATGGACTGGAGGTGGACATGTGGGCTGCTGGCGTGATCCTC
TATATCCTGCTGTGTGGCTTTCCCCCATTCCGCAGCCCTGAXXGAGGGGACCAGGACGAG
CTCTTTAACATCATCCAGCTGGGCCACTTTGAGTTCCTCCCCCCTTACTGGGACAATATC
TCTGATGCTGCTAAAGATCTGGTGAGCCGGTTGCTGGTGGTAGACCCCAAAAAGCGCTAC
ACAGCTCATCAGGTTCTTCAGCACCCCTGGATCGAAACAGCTGGCAAGACCAATACAGTG
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GTTGTGGAGCAGGTATCATAGTCACCACCTTGGGAATCTGTCCAGCCCCCAGTTCTGCTC
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ATTGGTGAATCAGAGGGAGAGACACTGAGTATATTTTAAAGCATATTAAAAAAATTAAGT
CAATGTTAAATGTCACAACATATTTTTAGATTTGTATATTTAAAGCCTTTAATACATTTT
TGGGGGGTAAGCATTGTCATCAGTGAGGAATTTTGGTAATAATGATGTGTTTTGCTTCCC
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GTGCAGACCTTTGAGCAGCTCCTATCAGACATCTCCGAAGCCTTGGGCTTCCCACGCTGG
AAGAACGACCGTGTGCGGAAGCTGTTCACCCTCAAGGGCAGGGAGGTGAAGAGTGTGTCT
GACTTCTTCCGGGAGGGTGATGCTTTCATAGCTATGGGCAAAGAGCCGCTGACATTGAAG
AGTATCCAGTTGGCCATGGAGGAGCTGTATCCTAAGAACCGGGCTCTTGCCCTGGCCCCT
CACAGTAGAGTCCCCTCCCCAAGGCTGAGAAGCAGACTTCCCAGCAAGCTTCTGAAAGGA

FIGURE 2T

AGTCACCGCTGTGGGGAGGCAGGAAGCTATAGCGCGGAAATGGAGAGTAAGGCAGTCTCT
AGGCATCAGGGCAAGACTTCCACAGTGCTGGCCCCAGAAGACAAGGCGAGGGCCCAGAAG
TGGGTAAGAGGGAAACAGGAGTCAGAACCTGGTGGCCCGCCTTCACCCGGGGCAGCCACT
CAGGAGGAGACTCATGCAAGTGGAGAGAAACATCTGGGGGTGGAGATCGAAAAGACCTCC
GGGGAGATTGTCAGATGTGAGAAGTGTAAGAGAGAAAGAGAGCTGCAGTTGGGCCTGCAG
AGGGAGCCGTGCCCGCTGGGAACCAGTGAGCTGGACCTGGGGAGAGCTCAGAAGAGGGAT
TCCGAGAAGTTGGTGAGGACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT
GGAGAGGAAGGGTGGAAGGGTGACAGCCATCGGGGCAGTCCCAGGGACCCCCCTCAGGAA
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AGTTATCCTCAGGGGGCACCCAAGGCCCAGAAGGACTTCGTGGAAGGGCCACCAGCTGTA
GAGGAGGGGCCGATAGACATGAGGAGAGAGGACCGGCACACATGCAGGAGCAAGCATGCC
GCCTGGCTCCGGAGAGAGCAGCAGGCCGAACCCCCACAGCTCCCCAGAACCCGAGGGGAG
GAGAAGCAAGCAGAGCACGAGAAGAAGCCAGGCGGCTTAGGAGAGAGGAGGGCGCCAGAG
AAGGAGTCTAAGAGGAAGCTAGAAGAGAAGAGGCCAGAACGACCCAGTGGCCGGAAGCCG
AGGCCCAAGGGCATCATCTCAGCGGATGTGGAGAAGCACTATGACATAGGTGGGGTCATT
GGGGATGGCAACTTTGCCACCGTGAAGGAATGCAGGCACCGAGAGACCAAGCAGGCTTAC
GCCATGAAGATGATTGACAAGTCCCAGCTGAAGGGTAAGGAGGACATTGTCGACAGTGAG
ATTTTAATCATCCAGAGTCTCTCTCATCCCAACATTGTGAAACTGCATGAGGTCTACGAA
ACGGAGGCGGAGATCTACCTGATCATGGAGTATGTGCAGGGAGGGGACCTTTTTGATGCC
ATCGTTGAAAATGTGAAGTTTCCAGAGCCCGAGGCTGCAGTTATGATCACAGACTTGTGT
AAGGCCTTCGTCCACATGCACGACAAGAATATCGTCCACCGGGACGTGAAACCAGAAAAC
CTCCTGGTTCAGCGAAATGAAGACAAGTCTATCACCTTGAAGCTGGCTGATTTTGGCTTG
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GAAATTCTTTCTGAGAAAGGTTACGGCCTGGAGGTGGACATGTGGGCGGCAGGTGTGATC
CTATACATCCTCTTGTGTGGCTTCCCCCCTTTCCGAAGTCCTGAGAGGGACCAAGACGAG
CTCTTCAACATCATCCAAGTGGGCCAGTTTGAGTTCCTCTCTCCTTACTGGGACAACATT
TCTGATGCTGCCAAAGATCTGGTGAGAAATTTGCTGGAGGTGGACCCTAAGAAGCGGTAC
ACGGCCGAACAGGTCCTACAGCATCCCTGGATTGAGATGGTTGGGCATACCAACACAGGG
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GGGGGCAGTCCCGGGAGAACCTGCGGCGGCCGGAGCGGTAAAAATAAGTGACTAAAGAAG
CAGACCTGGGAATCACCTAACATGTCGAGGAGGAGATTTGATTGCCGAAGTATTTCAGGC
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GCAGGTGGAGAAATTTTCAGCCTGTGTTTACCTGAGTTGGCTGAAATGGTTTCTGAAAAT
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ATTGTACACCTTGATTTAAAGCCACAGAATATATTACTGAGCAGCATATACCCTCTCGGG
GACATTAAAATAGTAGATTTTGGAATGTCTCGAAAAATAGGGCATGCGTGTGAACTTCGG
GAAATCATGGGAACACCAGAATATTTAGCTCCAGAAATCCTGAACTATGATCCCATTACC
ACAGCAACAGATATGTGGAATATTGGTATAATAGCATATATGTTGTTAACTCACACATCA
CCATTTGTGGGAGAAGATAATCAAGAAACATACCTCAATATTTCTCAAGTTAATGTAGAT
TATTCGGAAGAAACTTTTTCATCAGTTTCACAGCTGGCCACAGACTTTATTCAGAGCCTT

FIGURE 2U

TTAGTAAAAAATCCAGAGAAAAGACCAACAGCAGAGATATGCCTTTCTCATTCTTGGCTA
CAGCAGTGGGACTTTGAAAACTTGTTTCACCCTGAAGAAACTTCCAGTTCCTCTCAAACT
CAGGATCATTCTGTAAGGTCCTCTGAAGACAAGACTTCTAAATCCTCCTGTAATGGAACC
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TTTCGTTTCGATGACTCATTACCCAATCCCCATGAACTTGTTTCAGATTTGCTCTGTTAG
CACTTTTTTCTTTGACTCATTTGGACTGAATTTGAAATTTTATATCCACTCCAGTGAGAT
TATGATTTGTAGCTTCATATATGACATGTTTATATTGTAAATGCACTTTTCCATGGAATA
ATTTAGGGAAGTGTTTTAATGTTAAATTACTAGTTGCTAGCATGTTATGATTTCATATCC
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GTGAAAG

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GAGTGCGAGGTAAAAGTCTGCCTAGAGAAGCAGGTCTGGCAGTCATCAACATGTCTCGGA
GGAGATTCGATTGCCGAAGTGTCTCAGGCTTGCTAACTACAACCCCTCAAACGCCGATTA
AAACAGAGAATTTTAATAATTTCTATACTCTTACCCCAAAAGAACTTGGGAGAGGAAAAT
TTGCTGTGGTTAGACAATGTATATCAAAATCAACTGGACAAGAGTATGCTGCCAAATCCC
TGAAAAAGAGGAGAAGAGGGCAGGATTGCCGGGCGGAAATTCTGCATGAGATAGCTGTGC
TGGAGCTGGCCAGGTCTTGTCCCCACGTGATTAATCTGCATGAGGTCTACGAAAATGCAA
CGGAAATCATTTTGGTGTTAGAATATGCTGCGGGTGGAGAAATTTTCAACCTGTGTTTAC
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AAGGAGTTCATTATCTACATCAGAATAACATTGTTCACCTTGATTTAAAGCCACAGAATA
TACTTTTGAGCAGTATATACCCACTCGGGGACATAAAAATTGTAGATTTTGGAATGTCTC
GAAAAATTGGGAATGCAAGTGAGCTTCGGGAAATCATGGGAACACCTGAATACTTAGCTC
CAGAAATCCTCAACTATGATCCCATTACCACAGCAACAGATATGTGGAATATTGGCATAA
TAGCGTATATGTTGTTAACTCATACATCACCATTTGTAGGAGAAGATAATCAAGAAACAT
ATCTGAATATTTCTCAAGTGAATGTAGATTATTCAGAAGAAATGTTTTCATCAGTTTCAC
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CGGAAATTTGAAATCTCTGGTGTGAGATTGTGTTTGTAGCTTCATATATTATGTTTATAT
TATAAATGCACTTCTGCTTAGAAGAACTTAAGGAACAGTTTAAATGCTAGGCTTCTGTTG
GCTAGCATATCATTTCTTGTCCTGAAATTGTTTTGCAGAGGAAAATATTTAAGTATATGA
CAAAAAATGTAAATTGTGTTTAAGAGAACACATGCAACTGAAAGAACTCAAGTTCAGTCA
GACTTATAAAATGGGTTATATTATGGTTAGTAAAAGTTGAAAAAAAAATGAAAACAGGAAT
TTAGTAGGTTCTAAGGTAAGCCCTATACCATAACTCTATTACAGAGAATCTGTTTGGGGA
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TGCAAACCGAGTCAAAACTCGACATCATTTCCAGCTCATGTATTTTGTACGTGCATCATA
TATCAGATCTAATAAGATCTGGAAGATGGATATGCAAATAAGAGGCCTTTGTCTTCTAGA
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TTCATAAAGGGAAATGTTAAGTTCTGGCAGCTGACTTAGTGTTGGATGTCTCCTAAGTCT
CAGGATAGAAGCCCATCATTAGAGCATAGGCACTTCAGGAATTCTTGTGTGAAATTCTAG
TGAGTGAGGAGGTGTGACATGCAGCTATCTTTGGGCTCCTTTTGTGTGTGTTCTGCTGGA
CACAACACATGGGAGTGTTCAGTGTTGTCCGTGGTCAATATCTATGTTCAGTCCTGATGG

FIGURE 2V

GAGGGGCCTAGGGACTGCTTTGGAGATTTCCCACTGGTGTCCATTTTAAGGTCTGTAATA
ATGTCATGTTAAGATAACAGATCTCATAAATATGCTACTCTATCAGACTCCGTTGCCAAA
ACAAATTAAAAGCCTGTGTATTGAAGTGGGTGTTAGTCTAACAACCTGTAAATTCTTGAA
ATTGTTACTAAAATTCCAAATTCTTTAGATAACTTTAAACTATTTAAATTGAGCATTGCT
GTCTTTGTTTGATTAAAGGTTGAGTTCCTTTATATCTGTTATTTTTAAAGGAAAAGTTGT
TTGCCTTTTGTATATGTGTGTGCATATGTGTATGTGTACAGGTATATGTATATATGTATT
GATAGATAAAATACAGCCTTTAAACAACTTC

SEQ ID NO: 31_H01248_H, DRAK1_H
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CTGTGCCCGGGCCGGGAGCTGGGCAGGGGGAAATTTGCAGTGGTGAGAAAATGTATAAAG
AAAGATTCTGGGAAAGAATTTGCTGCAAAGTTCATGAGAAAAAGAAGAAAAGGCCAAGAT
TGTCGGATGGAAATAATTCATGAGATTGCTGTACTTGAACTAGCACAAGACAATCCTTGG
GTCATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTAGTTCTGGAATAT
GCTGCTGGGGGTGAAATCTTTGACCAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAA
AAAGATGTTCAAAGACTTATGCGACAGATTTTAGAAGGTGTTCACTTTTTACACACTCGT
GATGTAGTTCATCTTGATTTGAAGCCTCAGAATATTCTGTTGACAAGTGAATCTCCATTG
GGTGACATTAAGATTGTTGATTTTGGCCTTTCAAGAATATTGAAGAACAGTGAAGAGCTC
CGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATTCTTAGTTATGATCCTATA
AGCATGGCAACAGATATGTGGAGCATTGGAGTGTTAACATATGTCATGCTTACAGGAATA
TCACCTTTCTTAGGCAATGATAAACAAGAAACATTCTTAAACATCTCACAGATGAATTTA
AGTTATTCTGAGGAAGAATTTGATGTTTTGTCTGAGTCGGCTGTTGATTTCATCAGGACA
CTTTTAGTTAAGAAACCTGAAGATCGAGCCACTGCTGAAGAATGTCTAAAGCACCCCTGG
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AATGCCCTCCAAGAAGGTCATTCTGTGCCTGAAATTAATTCGGATACCGACAAATCAGAA
ACCGAGGAATCCATTGTAACCGAAGAGTTAATTGTAGTTACTTCATATACTCTAGGACAA
TGCAGACAGTCTGAAAAAGAGAAAATGGAGCAAAAGGCCATTTCCAAACGATTTAAATTT
GAGGAACCTTTGCTACAAGAAATTCCAGGAGAATTTATCTACTGA

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CGGGGCTGCCGGGGCCGGGACTGGGGGAGCCGGGCCCGCGGGCCGCCTGCTGCCTCCGCC
CGCGCCGGGGTCCCCAGCCGCCCCCGCTGCCGTGTCCCCTGCGGCCGGCCAGCCGCGTCC
CCCAGCCCCGGCCTCCCGCGGACCCATGCCCGCCCGTATCGGCTACTACGAGATCGACCG
CACCATCGGCAAGGGCAACTTCGCGGTGGTCAAGCGGGCCACGCACCTCGTCACCAAGGC
CAAGGTTGCTATCAAGATCATAGATAAGACCCAGCTGGATGAAGAAAACTTGAAGAAGAT
TTTCCGGGAAGTTCAAATTATGAAGATGCTTTGCCACCCCCATATCATCAGGCTCTACCA
GGTTATGGAGACAGAACGGATGATTTATCTGGTGACAGAATATGCTAGTGGAGGGGAAAT
ATTTGACCACCTGGTGGCCCATGGTAGAATGGCAGAAAAGGAGGCACGTCGGAAGTTCAA
ACAGATCGTCACAGCTGTCTATTTTTGTCACTGTCGGAACATTGTTCATCGTGATTTAAA
AGCTGAAAATTTACTTCTGGATGCCAATCTGAATATCAAAATAGCAGATTTTGGTTTCAG
TAACCTCTTCACTCCTGGGCAGCTGCTGAAGACCTGGTGTGGCAGCCCTCCCTATGCTGC
ACCTGAACTCTTTGAAGGAAAAGAATATGATGGGCCCAAAGTGGACATCTGGAGCCTTGG
AGTTGTCCTCTACGTGCTTGTGTGCGGTGCCCTGCCATTTGATGGAAGCACACTGCAGAA
TCTGCGGGCCCGCGTGCTGAGTGGAAAGTTCCGCATCCCATTTTTTATGTCCACAGAATG
TGAGCATTTGATCCGCCATATGTTGGTGTTAGATCCCAATAAGCGCCTCTCCATGGAGCA
GATCTGCAAGCACAAGTGGATGAAGCTAGGGGACGCCGATCCCAACTTTGACAGGTTAAT
AGCTGAATGCCAACAACTAAAGGAAGAAAGACAGGTGGACCCCCTGAATGAGGATGTCCT
CTTGGCCATGGAGGACATGGGACTGGACAAAGAACAGACACTGCAGTCATTAAGATCAGA

FIGURE 2W

TGCCTATGATCACTATAGTGCAATCTACAGCCTGCTGTGTGATCGACATAAGAGACATAA
AACCCTGCGTCTCGGAGCACTTCCTAGCATGCCCCGAGCCCTGGCCTTTCAAGCACCAGT
CAATATCCAGGCGGAGCAGGCAGGTACTGCTATGAACATCAGCGTTCCCCAGGTGCAGCT
GATCAACCCAGAGAACCAAATTGTGGAGCCGGATGGACACTGAATTTGGACAGTGATGA
GGGTGAAGAGCCTTCCCCTGAAGCATTGGTGCGCTATTTGTCAATGAGGAGGCACACAGT
GGGTGTGGCTGACCCACGCACGGAAGTTATGGAAGATCTGCAGAAGCTCCTACCTGGCTT
TCCTGGAGTCAACCCCCAGGCTCCATTCCTGCAGGTGGCCCCTAATGTGAACTTCATGCA
CAACCTGTTGCCTATGCAAAACTTGCAACCAACCGGGCAACTTGAGTACAAGGAGCAGTC
TCTCCTACAGCCGCCCACGCTACAGCTGTTGAATGGAATGGGCCCCCTTGGCCGGAGGGC
ATCAGATGGAGGAGCCAACATCCAACTGCATGCCCAGCAGCTGCTGAAGCGCCCACGGGG
ACCCTCTCCGCTTGTCACCATGACACCAGCAGTGCCAGCAGTTACCCCTGTGGACGAGGA
GAGCTCAGACGGGGAGCCAGACCAGGAAGCTGTGCAGAGGTACTTGGCAAATAGGTCCAA
AAGACATACACTGGCCATGACCAACCCTACAGCTGAGATCCCACCGGACCTACAACGGCA
GCTAGGACAGCAGCCTTTCCGTTCCCGGGTCTGGCCTCCTCACCTGGTACCTGATCAGCA
TCGCTCTACCTACAAGGACTCCAACACTCTGCACCTCCCTACGGAGCGTTTCTCCCCTGT
GCGCCGGTTCTCAGATGGGGCTGCGAGCATCCAGGCCTTCAAAGCTCACCTGGAAAAAT
GGGCAACAACAGCAGCATCAAACAGCTGCAGCAGGAGTGTGAGCAGCTGCAGAAGATGTA
CGGGGGGCAGATTGATGAAAGAACCCTGGAGAAGACCCAGCAGCAGCATATGTTATACCA
GCAGGAGCAGCACCATCAAATTCTCCAGCAACAAATTCAAGACTCTATCTGTCCTCCTCA
GCCATCTCCACCTCTTCAGGCTGCATGTGAAAATCAGCCAGCCCTCCTTACCCATCAGCT
CCAGAGGTTAAGGATTCAGCCTTCAAGCCCACCCCCCAACCACCCCAACAACCATCTCTT
CAGGCAGCCCAGTAATAGTCCTCCCCCCATGAGCAGTGCCATGATCCAGCCTCACGGGGC
TGCATCTTCTTCCCAGTTTCAAGGCTTACCTTCCCGCAGTGCAATCTTTCAGCAGCAACC
TGAGAACTGTTCCTCTCCTCCCAACGTGGCACTAACCTGCTTGGGTATGCAGCAGCCTGC
TCAGTCACAGCAGGTCACCATCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC
AGGCACAGCTGCAGGCTCCAGTGGGCGCGGCATCTCCATCAGCCCCAGTGCTGGTCAGAT
GCAGATGCAGCACCGTACCAACCTGATGGCCACCCTCAGCTATGGGCACCGTCCCTTGTC
CAAGCAGCTGAGTGCTGACAGTGCAGAGGCTCACAGCTTGAACGTGAATCGGTTCTCCCC
TGCTAACTACGACCAGGCGCATTTACACCCCCATCTGTTTTCGGACCAGTCCCGGGGTTC
CCCCAGCAGCTACAGCCCTTCAACAGGAGTGGGGTTCTCTCCAACCCAAGCCCTGAAAGT
CCCTCCACTTGACCAATTCCCCACCTTCCCTCCCAGTGCACATCAGCAGCCGCCACACTA
TACCACGTCGGCACTACAGCAGGCCCTGCTGTCTCCCACGCCGCCAGACTATACAAGACA
CCAGCAGGTACCCCACATCCTTCAAGGACTGCTTTCTCCCCGGCATTCGCTCACCGGCCA
CTCGGACATCCGGCTGCCCCCAACAGAGTTTGCACAGCTCATTAAAAGGCAGCAGCAACA
ACGGCAGCAGCAGCAGCAACAGCAGCAACAGCAAGAATACCAGGAACTGTTCAGGCACAT
GAACCAAGGGGATGCGGGGAGTCTGGCTCCCAGCCTTGGGGGACAGAGCATGACAGAGCG
CCAGGCTTTATCTTATCAAAATGCTGACTCTTATCACCATCACACCAGCCCCCAGCATCT
GCTACAAATCAGGGCACAAGAATGTGTCTCACAGGCTTCCTCACCCACCCCGCCCCACGG
GTATGCTCACCAGCCGGCACTGATGCATTCAGAGAGCATGGAGGAGGACTGCTCGTGTGA
GGGGGCCAAGGATGGCTTCCAAGACAGTAAGAGTTCAAGTACATTGACCAAAGGTTGCCA
TGACAGCCCTCTGCTCTTGAGTACCGGTGGACCTGGGGACCCTGAATCTTTGCTAGGAAC
TGTGAGTCATGCCCAAGAATTGGGGATACATCCCTATGGTCATCAGCCAACTGCTGCATT
CAGTAAAAATAAGGTGCCCAGCAGAGAGCCTGTCATAGGGAACTGCATGGATAGAAGTTC
TCCAGGACAAGCAGTGGAGCTGCCGGATCACAATGGGCTCGGGTACCCAGCACGCCCCTC
CGTCCATGAGCACCACAGGCCCCGGGCCCTCCAGAGACACCACACGATCCAGAACAGCGA
CGATGCTTATGTACAGCTGGATAACTTGCCAGGAATGAGTCTCGTGGCTGGGAAAGCACT
TAGCTCTGCCCGGATGTCGGATGCAGTTCTCAGTCAGTCTTCGCTCATGGGCAGCCAGCA
GTTTCAGGATGGGGAAAATGAGGAATGTGGGGCAAGCCTGGGAGGTCATGAGCACCCAGA
CCTGAGTGATGGCAGCCAGCATTTAAACTCCTCTTGCTATCCATCTACGTGTATTACAGA
CATTCTGCTCAGCTACAAGCACCCCGAAGTCTCCTTCAGCATGGAGCAGGCAGGCGTGTA

FIGURE 2X

ACAAGAAACAGAGAGTTTTGTGTACAGCTTGGGAATGAAAAGGTTGATTGTAAACCCACA
GTATCTAGCAGCGTTGTGCCAAATTGCCCTTGTGTTTCTCTCCACCCAAAATATCACAGC
TGCTTTCCTCACATTTGGTTCATCCGTGTGCTGTTCTTTTGGGTTCTGAGAGGGTTTTGC
CATGTTTGCTTGTATGACCAAGTCACCAAGGAAATAAACAGGAAGGAAATCCATGTTCTC
C

SEQ ID NO: 33_2R22-5-11_H
CTGGGCCGCTGCCGGTCAGGTCGGCCGCCCCTGACAGCTCCGGGAGCCTCAAGCGCGACA
GGGCGCCCTCACCTCGGGACATCCACACACCGACCGCTCCTGCTCCAGAGGCAACAACCC
AGCGCGCCTAGCCTGGCGCCGTGCAGCGAAGCCCAAGAGCTGGCCTCGCCACGAAGGTTG
AACCAGCCAAATTTTCGAGACAGCTCACGGCTTAGAGGAAGGTTCATCTAAATAAAGGCC
GGCTAAAGTGACATTGCAGGGATTAAATCCTTCTTTGGCTGCCTGTGTGACCAGAAGGCT
TATTTGCAAGTTTCTTCTTTCCTGGGGTCCAGATTATTAGGTCTCCAGCGCCCTGCAGCT
TGACAGAAAGAGAAGCATGAAATGAAGGTCAGAGATGAGATCCCGCAGCAGGGACGTGGG
GGCCTCCCAGGGGCATTTACGCACCAGAGTGCAAGATTCTCTGGCCATCAAGGGAAATAG
CAAACAGAAGCCTTTGTCCTGGGGCACAGCCACCTACCACAAAGCATCAGACTCCACGTC
TGGCCAGAAAGTTCCTGGAGTCCCATCAGGCCAGTGGGTATGTAACATGTGCCTAATTGT
ACAGCTAGAGCCTGCAAGTTCAACGTGAGGGAAGGTGGGAAATGTCTTGAGTGAGGCGAG
CAGCTCCTGGCTGGGCTGGGCAGACTCAGCTACCACGTTCACTGCCTTCCTCTCACTAAA
GCCGAGAGGGAGGCTGCTCAGCTCTCAGGAAAACTCTTTTGAACCCTGGGCACCTGCTGT
CCTCAGTTGGCATCTCCCACCCTCTGAGCCTCTTCTGCTCCTGCACAACCTGCCTCTTCG
CTGAGATGGAGACGTGAGCCCCCGTGGACGATGACTGCAGTGTATATGAATGGAGGTGGC
CTGGTGAACCCCCACTATGCCCGGTGGGATCGGCGCGACAGTGTAGAAAGTGGCTGTCAG
ACCGAGAGTAGCAAGGAGGGTGAGGAGGGACAGCCCCGCCAGCTGACGCCCTTCGAGAAA
CTGACACAGGACATGTCCCAGGATGAGAAGGTGGTGAGGGAGATCACGCTGGGGAAACGG
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CCAGAAAGCAAGCTCATCTTCTCCCAGATTGTGTCTGCCGTGAAGCACATGCATGAAAAC
CAAATTATTCATAGAGATCTGAAAGCAGAAAATGTATTCTATACCAGTAATACTTGTGTG
AAGGTGGGCGATTTTGGATTCAGCACAGTAAGCAAAAAAGGTGAAATGCTGAACACTTTC
TGTGGGTCTCCTCCCTACGCTGCGCCTGAACTCTTCCGGGACGAGCACTACATCGGCATT
TACGTGGATATCTGGGCCTTGGGGGTGCTTTTGTACTTCATGGTGACTGGCACCATGCCA
TTTCGGGCAGAAACCGTGGCCAAACTAAAAAAGAGCATCCTCGAGGGCACATACAGTGTA
CCGCCGCACGTGTCAGAGCCCTGCCACCGACTCATCCGAGGAGTCCTTCAGCAGATCCCC
ACGGAGAGGTACGGAATCGACTGCATCATGAATGATGAATGGATGCAAGGGGTGCCATAC
CCTACACCTTTGGAACCTTTCCAACTGGATCCCAAACATTTGTCGGAAACCAGCACTCTC
AAGGAAGAAGAAAATGAGGTCAAAAGCACTTTAGAACATTTGGGCATTACAGAAGAGCAT
ATTCGAAATAACCAAGGGAGAGATGCTCGCAGCTCAATCACAGGGGTCTATAGAATTATT
TTACATAGAGTCCAAAGGAAGAAGGCTTTGGAAAGTGTCCCAGTCATGATGCTACCAGAC
CCTAAAGAAAGAGACCTCAAAAAAGGGTCCCGTGTCTACAGAGGGATAAGACACACATCC
AAATTTTGCTCGATTTTATAAATTGCACTAGACTGCTTGTAACTAACCAAGATGATTGTT
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AAACTTAAATTTGAGATATGCAAAAAAAAAA

SEQ ID NO: 34_R31237_1_H, AAC33487
ATGTCCACTAGGACCCCATTGCCAACGGTGAATGAACGAGACACTGAAAACCACACGTCA
CATGGAGATGGGCGTCAAGAAGTTACCTCTCGTACCAGCCGCTCAGGAGCTCGGTGTAGA

FIGURE 2Y

AACTCTATAGCCTCCTGTGCAGATGAACAACCTCACATCGGAAACTACAGACTGTTGAAA
ACAATCGGCAAGGGGAATTTTGCAAAAGTAAAATTGGCAAGACATATCCTTACAGGCAGA
GAGGTTGCAATAAAAATAATTGACAAAACTCAGTTGAATCCAACAAGTCTACAAAAGCTC
TTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATCCCAATATAGTGAAGTTATTCGAA
GTCATTGAAACTGAAAAAACACTCTACCTAATCATGGAATATGCAAGTGGAGGTGAAGTA
TTTGACTATTTGGTTGCACATGGCAGGATGAAGGAAAAAGAAGCAAGATCTAAATTTAGA
CAGATTGTGTCTGCAGTTCAATACTGCCATCAGAAACGGATCGTACATCGAGACCTCAAG
GCTGAAAATCTATTGTTAGATGCCGATATGAACATTAAAATAGCAGATTTCGGTTTTAGC
AATGAATTTACTGTTGGCGGTAAACTCGACACGTTTTGTGGCAGTCCTCCATACGCAGCA
CCTGAGCTCTTCCAGGGCAAGAAATATGACGGGCCAGAAGTGGATGTGTGGAGTCTGGGG
GTCATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGGGCAAAACCTAAAGGAA
CTGAGAGAGAGAGTATTAAGAGGGAAATACAGAATTCCCTTCTACATGTCTACAGACTGT
GAAAACCTTCTCAAACGTTTCCTGGTGCTAAATCCAATTAAACGCGGCACTCTAGAGCAA
ATCATGAAGGACAGGTGGATCAATGCAGGGCATGAAGAAGATGAACTCAAACCATTTGTT
GAACCAGAGCTAGACATCTCAGACCAAAAAAGAATAGATATTATGGTGGGAATGGGATAT
TCACAAGAAGAAATTCAAGAATCTCTTAGTAAGATGAAATACGATGAAATCACAGCTACA
TATTTGTTATTGGGGAGAAAATCTTCAGAGCTGGATGCTAGTGATTCCAGTTCTAGCAGC
AATCTTTCACTTGCTAAGGTTAGGCCGAGCAGTGATCTCAACAACAGTACTGGCCAGTCT
CCTCACCACAAAGTGCAGAGAAGTGTTTCTTCAAGCCAAAAGCAAAGACGCTACAGTGAC
CATGCTGGACCAGCTATTCCTTCTGTTGTGGCGTATCCGAAAAGGAGTCAGACAAGCACT
GCAGATGGTGACCTCAAAGAAGATGGAATTTCCTCCCGGAAATCAAGTGGCAGTGCTGTT
GGAGGAAAGGGAATTGCTCCAGCCAGTCCCATGCTTGGGAATGCAAGTAATCCTAATAAG
GCGGATATTCCTGAACGCAAGAAAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT
GGAATGACACGACGAAATACTTATGTTTGCAGTGAGAGAACTACAGCTGATAGACACTCA
GTGATTCAGAATGGCAAAGAAAACAGCACTATTCCTGATCAGAGAACTCCAGTTGCTTCA
ACACACAGTATCAGTAGTGCAGCCACCCCAGATCGAATCCGCTTCCCAAGAGGCACTGCC
AGTCGTAGCACTTTCCACGGCCAGCCCCGGGAACGGCGAACCGCAACATATAATGGCCCT
CCTGCCTCTCCCAGCCTGTCCCATGAAGCCACACCATTGTCCCAGACTCGAAGCCGAGGC
TCCACTAATCTCTTTAGTAAATTAACTTCAAAACTCACAAGGAGTCGCAATGTATCTGCT
GAGCAAAAAGATGAAAACAAAGAAGCAAAGCCTCGATCCCTACGCTTCACCTGGAGCATG
AAAACCACTAGTTCAATGGATCCCGGGGACATGATGCGGGAAATCCGCAAAGTGTTGGAC
GCCAATAACTGCGACTATGAGCAGAGGGAGCGCTTCTTGCTCTTCTGCGTCCACGGAGAT
GGGCACGCGGAGAACCTCGTGCAGTGGGAAATGGAAGTGTGCAAGCTGCCAAGACTGTCT
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ATCATTGATAAGACCCAGCTGAACCCCAGTAGCTTGCAGAAGCTGTTCAGAGAAGTCCGA
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TCGCACGGCCGCATGAAGGAGAAGGAGGCTCGAGCCAAGTTCCGGCAGATCGTGTCAGCC
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GGCTCCAAGCTGGACACCTTCTGTGGGAGCCCCCCATACGCCGCCCCAGAGCTGTTCCAG
GGCAAGAAGTATGATGGGCCAGAGGTGGACATCTGGAGCCTGGGTGTCATCCTGTACACG
CTGGTCAGCGGCTCCCTGCCCTTCGATGGGCACAACCTCAAGGAGCTGCGGGAGCGAGTC
CTCAGAGGAAAGTACCGGGTCCCCTTCTACATGTCTACAGACTGCGAGAGCATTCTGCGG

FIGURE 2Z

AGATTTCTGGTGCTGAACCCCGCAAAACGCTGTACTCTGGAGCAAATCATGAAAGACAAA
TGGATCAACATCGGCTATGAGGGTGAGGAGCTGAAGCCAGACACGGAGCTCAAAGAAGAG
CGGATGCCGGGTCGGAAAGCGAGCTGCAGTGCAGTGGGCAGTGGAAGTCGAGGCTTGCCC
CCCTCCAGCCCCATGGTCAGCAGTGCCCACAACCCCAATAAGGCAGAGATCCCTGAGCGG
CGGAAGGACAGCACTAGCACCCCTAACAACCTCCCCCCCAGCATGATGACCCGAAGAAAC
ACCTATGTGTGCACAGAGCGACCAGGATCTGAACGCCCGTCCTTGTTGCCAAATGGCAAA
GAAAATAGCTCCGGTACCTCGCGGGTGCCCCCTGCCTCGCCTTCCAGTCATAGCCTGGCT
CCCCCGTCAGGCGAGCGGAGCCGCCTGGCTCGGGGCTCCACCATCCGCAGCACCTTCCAT
GGGGGCCAGGTCCGAGACCGGCGGGCAGGGAGCGGGAGTGGCGGGGGTGTGCAGAATGGA
CCCCCAGCCTCACCCACGCTTGCCCACGAGGCCGCACCCCTGCCCTCCGGGCGGCCTCGC
CCCACCACCAACCTCTTCACCAAGCTGACCTCCAAACTGACCCGAAGGGTCACAGACGAA
CCTGAGAGAATCGGGGGACCTGAGGTCACAAGTTGCCATCTACCTTGGGATAAAACGGAA
ACCGCCCCCAGGCTGCTCCGATTCCCCTGGAGTGTGAAGCTGACCAGCTCGCGACCTTCC
TGAGGCCCTGATGGCTGCCCTGCGACAGGCCACA

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GTAGCCGGCTTGGCGTGACCGTCGCCTGATCCAGTTGTTAGAGGTGGAAGCTTGGCAGTT
GGCCTCCCTTCTTCCCATGGAGGTCGGGGGCTTAACAGTCTTTGAAGAGGACCAGAGATG
CCTTTCCCAGAGCCTCCCCTTGCCAGTGTCAGCAGAGGGCCCAGCTGCACAGACCACTGC
TGAGCCCAGCAGGTCGTTTTCCTCAGCCCACAGACACCTGAGCAGAAGGAATGGGCTTTC
CAGACTCTGCCAGAGCAGGACGGCGCTCTCTGAAGACAGATGGAGCTCCTATTGTCTATC
ATCACTGGCTGCCCAGAATATTTGTACAAGTAAACTGCACTGCCCTGCTGCCCCTGAGCA
CACGGACCCGTCCGAACCGCGGGGCAGTGTGTCCTGCTGCTCCCTGCTGCGGGGACTGTC
CTCAGGGTGGTCCTCACCTCTGCTTCCGGCCCCTGTGTGCAACCCTAACAAGGCCATCTT
CACGGTGGATGCCAAGACCACAGAGATCCTCGTTGCTAACGACAAAGCTTGCGGGCTCCT
GGGGTACAGCAGCCAGGACCTGATTGGCCAGAAGCTCACGCAGTTCTTTCTGAGGTCAGA
TTCTGATGTGGTGGAGGCCCTCAGCGAGGAGCACATGGAGGCCGACGGCCACGCTGCGGT
GGTGTTTGGCACGGTGGTGGACATCATCACCCGTAGTGGGGAGAAGATTCCAGTGTCTGT
GTGGATGAAGAGGATGCGGCAGGAGCGCCGCCTATGCTGCGTGGTGGTCCTGGAGCCCGT
GGAGAGGGTCTCGACCTGGGTCGCTTTCCAGAGCGATGGCACCATCACGTCATGTGACAG
TCTCTTTGCTCATCTTCACGGGTACGTGTCTGGGGAGGACGTGGCTGGGCAGCATATCAC
AGACCTGATCCCTTCTGTGCAGCTCCCTCCTTCTGGCCAGCACATCCCAAAGAATCTCAA
GATTCAGAGGTCTGTTGGAAGAGCCAGGGACGGTACCACCTTCCCTCTGAGCTTAAAGCT
GAAATCCCAACCCAGCAGCGAGGAGGCGACCACCGGTGAGGCGGCCCCTGTGAGCGGCTA
CCGGGCATCTGTCTGGGTGTTCTGCACCATCAGTGGCCTCATCACCCTCCTGCCGGATGG
GACCATCCACGGCATCAACCACAGCTTCGCGCTGACACTGTTTGGTTACGGAAAGACGGA
GCTCCTGGGCAAGAATATCACTTTCCTGATTCCTGGTTTCTACAGCTACATGGACCTTGC
GTACAACAGCTCATTACAGCTCCCAGACCTGGCCAGCTGCCTGGACGTCGGCAATGAGAG
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GGATCCAAGGATTAATGTCGTGCTTGCTGGTGGCCACGTTGTGCCCCGAGATGAGATCCG
GAAGCTGATGGAAAGCCAAGACATCTTCACCGGGACTCAGACTGAGCTGATTGCTGGAGG
CCAGCTCCTTTCCTGCCTCTCACCTCAGCCTGCTCCAGGGGTGGACAATGTCCCAGAAGG
AAGCCTGCCAGTGCACGGTGAACAGGCGCTGCCCAAGGACCAGCAAATCACTGCCTTGGG
GAGAGAGGAACCTGTGGCAATAGAGAGCCCCGGACAGGATCTTCTGGGAGAAAGCAGGTC
TGAACCAGTGGATGTGAAGCCATTTGCTTCCTGCGAAGATTCTGAAGCTCCAGTCCCAGC
TGAGGATGGGGGCAGTGATGCTGGCATGTGTGGCCTGTGTCAGAAGGCCCAGCTAGAGCG
GATGGGAGTCAGTGGTCCCAGCGGTTCAGACCTTTGGGCTGGGGCTGCCGTGGCCAAGCC
CCAGGCCAAGGGTCAGCTGGCGGGGGGCAGCCTCCTGATGCACTGCCCTTGCTATGGGAG
TGAATGGGGCTTGTGGTGGCGAAGCCAGGACTTGGCCCCCAGCCCCTCTGGGATGGCAGG
CCTCTCGTTTGGGACACCTACTCTAGATGAGCCGTGGCTGGGAGTGGAAAACGACCGAGA

FIGURE 2AA

AGAGCTGCAGACCTGCTTGATTAAGGAGCAGCTGTCCCAGTTGAGCCTTGCAGGAGCCCT
GGATGTCCCCCACGCCGAACTCGTTCCGACAGAGTGCCAGGCTGTCACCGCTCCTGTGTC
GTCCTGCGATCTGGGAGGCAGAGACCTGTGCGGTGGCTGCACGGGCAGCTCCTCAGCCTG
CTATGCCTTGGCCACGGACCTCCCTGGGGGCCTGGAAGCAGTGGAGGCCCAGGAGGTTGA
TGTGAATTCGTTTTCCTGGAACCTCAAGGAACTCTTTTTCAGTGACCAGACAGACCAAAC
GTCATCAAATTGTTCCTGTGCTACGTCTGAACTCAGAGAGACACCCTCTTCCTTGGCAGT
GGGCTCCGATCCAGATGTAGGCAGTCTCCAGGAACAGGGGTCGTGTGTCCTGGATGACAG
GGAGCTGTTACTACTGACCGGCACCTGTGTTGACCTTGGCCAAGGCCGACGGTTCCGGGA
GAGCTGTGTGGGACATGATCCAACAGAACCGCTTGAGGTTTGTTTGGTGTCCTCTGAGCA
TTATGCAGCAAGCGACAGAGAAAGCCCAGGACACGTTCCTTCCACGTTGGATGCTGGCCC
TGAGGACACGTGCCCATCAGCAGAGGAGCCAAGGCTGAACGTCCAGGTCACCTCCACGCC
CGTGATCGTGATGCGCGGGGCTGCTGGCCTGCAGCGGGAGATCCAGGAGGGTGCCTACTC
CGGGAGCTGCTACCATCGAGATGGCTTACGGCTGAGTATACAGTTTGAGGTGAGGCGGGT
GGAGCTCCAGGGCCCCACACCTCTGTTCTGCTGCTGGCTGGTGAAAGACCTCCTCCACAG
CCAACGCGACTCAGCCGCCAGGACCCGCCTGTTCCTTGCCAGCCTGCCCGGCTCCACCCA
CTCTACCGCTGCTGAGCTCACCGGACCCAGCCTGGTGGAAGTGCTCAGAGCCAGACCCTG
GTTTGAGGAGCCCCCCAAGGCTGTGGAACTGGAGGGGTTGGCGGCCTGTGAGGGCGAGTA
CTCCCAAAAGTACAGTACCATGAGCCCGCTGGGCAGTGGGGCCTTCGGCTTCGTGTGGAC
TGCTGTGGACAAGGGAAAAAACAAGGAGGTGGTGGTGAAGTTTATTAAGAAGGAGAAGGT
CTTGGAGGATTGTTGGATTGAGGATCCCAAACTTGGGAAAGTTACTTTAGAGATCGCAAT
TCTATCCAGGGTGGAGCACGCCAATATCATCAAGGTATTGGATATATTTGAAAACCAAGG
GTTCTTCCAGCTTGTGATGGAGAAGCACGGCTCCGGCCTAGACCTCTTCGCTTTCATCGA
CCGCCACCCCAGGCTGGATGAGCCCCTGGCGAGCTACATCTTCCGACAAGTGAGAGCAGG
CCAGAGCCGTCTAGTGTCAGCAGTGGGATACCTGCGCTTGAAGGACATCATCCACCGTGA
CATCAAGGATGAGAACATCGTGATCGCTGAGGACTTCACAATCAAGCTGATAGACTTTGG
CTCGGCCGCCTACTTGGAAAGGGGAAAATTATTTTATACTTTTTGTGGGACCATCGAGTA
CTGTGCACCGGAAGTTCTCATGGGGAATCCCTACAGAGGGCCGGAGCTGGAGATGTGGTC
TCTGGGAGTCACTCTGTACACGCTGGTCTTTGAGGAGAACCCCTTCTGTGAGCTGGAGGA
GACCGTGGAGGCTGCCATACACCCGCCATACCTGGTGTCCAAAGAACTCATGAGCCTTGT
GTCTGGGCTGCTGCAGCCAGTCCCTGAGAGACGCACCACCTTGGAGAAGCTGGTGACAGA
CCCGTGGGTAACACAGCCTGTGAATCTTGCTGACTATACATGGGAAGAGGTGTTTCGAGT
AAACAAGCCAGAAAGTGGAGTTCTGTCCGCTGCGAGCCTGGAGATGGGGAACAGGAGCCT
GAGTGATGTGGCCCAGGCTCAGGAGCTTTGTGGGGGCCCCGTTCCAGGCGAGGCTCCTAA
TGGCCAAGGCTGTTTGCATCCCGGGGATCCCCGTCTGCTGACCAGCTAAACACCAATTTC
TTCCTGCTTTTCTCCACTTGGTTTGGAAAATCACACAGTTTTCAGGCTCCATCTGTTTG

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CCACGCGTCCGCATCCCTGCTTGGATGAGCCCCTGGCGAGTTTCATCTTTCGACAACTAG
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ACATTGTGATTGCTGAGGACTTCACAATTAAGCTGATAGATTTTGGCTCAGCTGCCTACT
TAGAGAGGGGCAAACTATTTTATACCTTTTGTGGAACAATCGAATACTGTGCACCTGAGG
TTCTCATTGGAAATCCCTACAGAGGGCCAGAGCTGGAGATGTGGTCTCTGGGGGTCACCC
TGTACACGCTCATCTTCGAGGAGAATCCCTTCTGTGAGGTGGAGGAGACCATGGAGGCAG
TTATTCATCCCCCATTCCTGGTTTCCCAAGAACTTATGAGTCTTCTGTCTGGACTGCTGC
AGCCTTGCCCTGAGCAGCGGACCACTTTGGAGAAGCTGATCAGGGACCCCTGGGTGACAC
AGCCTGTGAACCTTGCTAGCTATACTTGGGAAGAGGTGTGTAGGACCAACCAGCCAGAAA
GTGGCCTGCTGTCAGCTGCAAGTCTGGAGATTGGGAGTAGGAGTCCAAGTGAAATGGCTC
AGAGAGAGGGTCTCTGTGGGCCTCCTGCTCCCAGGGAGACTCGTGGTGACCAGCACTGCT
TGCATCTTAAGGACCCCTCTTTGCCAGTCAGCTGAGCAAGCTCTCCTGCTCTTTGGTTTG
GGCAGTTGTATGGATTTCAGGGCTTTCTACCTGGAGAAAGGAAGTTGTGAAGGATTGGGA

FIGURE 2BB

TGACTTCTGCTTCTAGATTCCTATGCAAATGCTACAAGAGCCTGCGATGCTAGTTTTCTT
AGGTTTATGATATAGACTTGTAATTCATGTTTTTTATAACCTTGAAAATCATTCTAATG
TTCAGTTATACTGTACTATTAAAGGGCTTTAAGTTGTAAGCCTCAGAAAGACACAAGGAG
TGTTTAAGTTCTCTATTTTTGTTGTTTGTTTTTGCTTGTAAGTTTTTGAGACAGGATCTC
ACCATGTAACTTTGGCTGGCCTGGAACTCAACTATGTAGACCAGGTAGACCTTAAACTGA
CAGATCTGCCTGCGCTTGCCTCCCAAGCATTAGGACTGATGGTGTGTGTCACCATGCCCA
GTTCTTCCTGGTTTTGTGTGTAGGTTTCTTTCCCACTGACTTGGTACATGTGACATGTGA
CAGATGTATGGAGTCTATAGAAGTGGCCAGACAAAAATGGCCAGAATATTTATTTATTTT
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AGATAAACTTGGTTTTCTATTTCTTTTTGT

SEQ ID NO: 38_AA785735_H
GGCACGAGGCGCGCCTGGCTGGGCCCTGCGGAGGANGGGAAGGAGCGAAGGAGCGAAGGA
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CTCCTGTCCGCCGTGTCTAGCAGCGGGGCCCAGCATGGTCATGGCGGATGGCCCGAGGCA
CTTGCAGCGCGGGCCGGTCCGGGTGGGGTTCTACGACATCGAGGGCACGCTGGGCAAGGG
CAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGGATCACCAAGACGGAGGTGGCAATAAA
AATAATCGATAAGTCTCAGCTGGATGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACA
AATAATGAAAATGTTAGACCACCCTCACATAATCAAACTTTATCAGGTAATGGAGACCAA
AAGTATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAATTTTTGACTATCTTGC
TAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATTCTGGCAAATCCTGTCTGC
TGTTGATTATTGTCATGGTCGGAAGATTGTGCACCGTGACCTCAAAGCTGAAAATCTCCT
GCTGGATAACAACATGAATATCAAAATAGCAGATTTCGGTTTTGGAAATTTCTTTAAAAG
TGGTGAACTGCTGGCAACATGGTGTGGCAGCCCCCCTTATGCAGCCCCAGAAGTCTTTGA
AGGGCAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCTTTATGT
CCTTGTCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAATTTTGAGGCAGAGGGT
TCTGGAAGGAAGATTCCGGATTCCGTATTTCATGTCAGAAGATTGCGAGCACCTTATCCG
AAGGATGTTGGTCCTAGACCCATCCAAACGGCTAACCATAGCCCAAATCAAGGAGCATAA
ATGGATGCTCATAGAAGTTCCTGTCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAA
TGAGCCATCCATCGGGGAGTTTAATGAGCAGGTTCTGCGACTGATGCACAGCCTTGGAAT
AGATCAGCAGAAARCCATTGAGTCTTTGCAGAACAAGAGCTATAACCACTTTGCTGCCAT
TTATTTCTTGTTGGTGGAGCGCCTGAAATCACATCGGAGCAGTTTCCCAGTGGAGCAGAG
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GACTGTGGGGCTCCCAGTGACCATGCATTCACCGAACATGAGGCTGCTGCGATCTGCCCT
CCTCCCCCAGGCATCCAACGTGGAGGCCTTTTCATTTCCAGCATCTGGCTGTCAGGCGGA
AGCTGCATTCATGGAAGAAGAGTGTGTGGACACTCCAAAGGTCAATGGCTGTCTGCTTGA
CCCTGTGCCTCCTGTCCTGGTGCGGAAGGGATGCCAGTCACTGCCCAGCAACATGATGGA
GACCTCCATTGACGAAGGGCTGGAGACAGAAGGAGAGGCCGAGGAAGACCCCGCTCATGC
CTTTGAGGCATTTCAGTCCACACGCAGCGGGCAGAGACGGCACACTCTGTCAGAAGTGAC
CAATCAACTGGTCGTGATGCCTGGGGCAGGGAAAATTTTCTCCATGAATGACAGCCCCTC
CCTTGACAGTGTGGACTCTGAGTATGATATGGGGTCTGTTCAGAGGGACCTGAACTTTCT
GGAAGACAACCCTTCCCTTAAGGACATCATGTTAGCCAATCAGCCTTCACCCCGCATGAC
ATCTCCCTTCATAAGCCTGAGACCTACCAACCCAGCCATGCAGGCTCTGAGCTCCCAGAA
ACGAGAGGTCCACAACAGGTCTCCAGTGAGCTTCAGAGAGGGCCGCAGAGCATCAGATAC
CTCCCTCACCCAGGGAATTGTAGCATTTAGACAACATCTTCAGAATCTGGCTAGAACCAA
AGGAATTCTAGAGTTGAACAAAGTGCAGTTGTTGTATGAACAAATAGGACCGGAGGCAGA
CCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAGGACCTTGCTAGCAGCTGCCCTCAGGA
AGAAGTTTCTCAGCAGCAGGAAAGCGTCTCCACTCTCCCTGCCAGCGTGCATCCCCAGCT
GTCCCCACGGCAGAGCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCCAGCCT
TCTGTCAAAGGCCCAGAACACCTGTCAGCTTTATTGCAAAGAACCACCGCGGAGCCTTGA

FIGURE 2CC

GCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTCTTCAGAAGCAGTCTCA
ACTGCAGGCCTATTTTAATCAGATGCAGATAGCAGAGAGCTCCTACCCACAGCCAAGTCA
GCAGCTGCCCCTTCCCCGCCAGGAGACTCCACCGCCTTCTCAGCAGGCCCCACCGTTCAG
CCTGACCCAGCCCCTGAGCCCCGTCCTGGAGCCTTCCTCCGAGCAGATGCAATACAGCCC
TTTCCTCAGCCAGTACCAAGAGATGCAGCTTCAGCCCCTGCCCTCCACTTCCGGTCCCCG
GGCTGCTCCTCCTCTGCCCACGCAGCTACAGCAGCAGCAGCCGCCACCGCCACCACCCCC
TCCACCACCACGACAGCCAGGAGCTGCCCCAGCCCCCTTACAGTTCTCCTATCAGACTTG
TGAGCTGCCAAGCGCTGCTTCCCCTGCGCCAGACTATCCCACTCCCTGTCAGTATCCTGT
GGATGGAGCCCAGCAGAGCGACCTAACGGGGCCAGACTGTCCCAGAAGCCCAGGACTGCA
AGAGGCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTTTGATTG
TGAAATGCTAGACGCTGTGGATCCACAACACAACGGGTATGTCCTGGTGAATTAGTCTCA
GCACAGGAATTGAGGTGGGTCAGGTGAAGGAAGAGTGTATGTTCCTATTTTTATTCCAGC
CTTTTAAATTTAAAGCTTATTTCTTGCCCTCTCCCTAACGGGGAGAAATCGAGCCACCC
AACTGGAATCAGAGGGTCTGGCTGGGGTGGATGTTGCTTCCTCCTGGTTCTGCCCCACCA
CAAAGTTTTCTGTGGCAAGTGCTGGAACATAGTTGTAGGCTGAGGCAGGAGAATGGCGTG
AACCCGGGAGGCGGAGCTTGCAGTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGGGCG
ACTGAGCAAGACTCCACCTCAAAAAAAAAAAAAAAGGACAAGAGCAGTATCATCTGCCTC
TGTTTCTAAACTGGACAAAGAGATTTTCTTAAAGTTTCTATCATCTCCCTTCTGACAGGT
TCTACAGTGTGGTCTGAAGCACCTGTAATGTCAGAGCCCTTGTCTGGCCCTTGGTGGCAG
GTGAACGAAAGCAGTGGAGCCTCTCACCTTCCAGTAGCCTCTCACATTCTTATTTTACCA
TTTTTGTCCTAATTAAGGTAGCCTAGCTGATTCTAGAAGACAGCCATCCTACGTGCACCC
CCACCTTGTGTCCACATCTTCTCCAGGCAGGTTTCAACCTATCAGCAGACTCAGGCACAC
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TGTGATGGGTTCTGCCCAGATACTCTGCTCGCCCACCCACAAGGGAGCAATAGCTTATAT
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AGCTGGGGAGATACTGTCCTTATTTTTCACAGCTGAAGAAACCAAAGCTTTGGGAAGTTT
GTGACTTCTCTGAGATCACAGCTGGTGATAGAAGGAGCTGGGACACGCGCTTGGGTTGAC
TGGCTTCTGGTTTTGGTTCTCTGGCTTCTAGTGCTGGAAGAAGCCCTCTCTTTCCCTTCT
CTTTCCTCAGTAGCATCTGACTCTTTTCATAAGCAAACAGCTGTATAAACAAAGCCCCCA
TTTTGGTCAAGCACAGGGTGAATGTGATATTGTTCCCACAACCTTATTCTCCACTCAACA
GCCGCCTGGCTTTGGGGAAGAGGCCGCCTTCAGGTGACAGTGCAGCTGTCCAGGTGGCCG
TGCACTGAACCAGGCTGAGGGAGACAAAAACCCCGCAGACCCGCCTGCCTTTCAGCGTCC
AGTTAACTGCAGAAGTTTAGGCTCACCTCAAAGATGTCTAGTTTTTCCAAGTTACAATAC
AGCAGTTTCCTACAGAACACCCCCTTCCTCAATTGCCAAGGGGCCGCATCGCACGGCATC
AGGCCACCACTGCAGGCCAGCAGATTCCACCCCAGGAACGGTCATGAACTCAGCCTTTGT
CTCAACGAGGGGCGTAACATTTCCTTACAGTCAAGCCCCATCAACTAGAAGTGCTTATTA
CTTTTAGGATTAAAAAGTAATAACAGACTTTGACTTAATACTCTGTCTTTTCAGAGGCA
AAGTGGGTGGGTAGAGGGGAGCTTTAAAAATAGAAGTACAAAACAACATCCTGGAAACAT
ATGACCCCAGATGGAATAATGTCACATTCCCCAGTGCAGATAATGGGCTGCTGCTGGCTC
TGTGGTGTCTGTCTGCAGAAGATTTGCTCAGTCAAGGAAATTCAAGTGGTGAGACCTTTC
CACCATGGGTGGTAAGAGAAACCTGCCTTCACCAAAATCTCTGAAGGGGAAAGAAGTGGA
GAGAAAGGTTTGCTTCACTTCGGGGACTGCAGTTTGAGAAATAAAAGGGATACAGAGATA
TCTGCACTTTGTAGAAAGGGCAAGATTATTTGCTTATATCTGAAGGGAGGTGGGTGGTTT
TGCTGGATGTTTGGTCTGAAAGAGTTACTTTTGATAAAGTTAATCTAATTGTAGTTATAT
TTTCTGTGTGCTTTTTTTTAATTACTAAGAAAAAAATTGGTGAGTTCAGTAGCTTTGGTA
TTATGAGTGCAAATCATAATAGCTCCAATGTGAAAAAAAAAATCAAAAGTATAACTTGTC
ACTTAATGTTAGAAAATTGCCTAAAATGCAGTGTAATAAATAATCTCTGTACCAAATAGT
AATTTAAATGGGGTAATTTTCTGCAAGGAAAATGTACTGTTTTTATGTTTCCAACCCTCT
TGA

FIGURE 2DD

SEQ ID NO: 39_AA207220_H
GCTGTGGCTCCCCGTCCTGGTGCGGGACCTGTGCCCCGCGCTTCAGCCCTCCCCGCAAGC
CTATTGATTCCCCTGCCGCCCTTGCTCCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTC
GCGCGGCGCTCCGGCCCCACTCCCTCGGCCGCAGAGCTAGCCCGGCCGCTGGCGGAAGGG
CTGATCAAGTCGCCCAAGCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAG
CACAACCTGCGGCACCGCTACGAGTTCCTGGAGACCCTGGGCAAAGGCACCTACGGAAG
GTGAAGAAGGCGCGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAATCCGGAAGGAC
AAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTCATCA
CTCAACCACCCTCACATCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTG
ATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAG
CTCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGC
CATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGGATGCCAAT
GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG
CAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTAC
ACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGC
ACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCC
TACCGGGAGCCACCTAAACCCTCTGATTGCCTGNNTGGCCTGATCCGGTGGCTGTTGATG
GTGAACCCCACCCGCCGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGG
GGCTACGCCACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCCTGGCAGT
GACTCTGCCCGCGCCTCCATGGCTGACTGGCTCCGGCGTTCCTCCCGCCCCCTCCTGGAG
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CCTGGCCTGGAGCGCCAGCATTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCAG
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CTGCCAAAGGGCATTCTCAAGAAGAAGGTGTCAGCCTCTGCAGAAGGGGTACAGGAGGAC
CCTCCGGAGCTCAGCCCAATCCCTGCGAGCCCAGGGCAGGCTGCCCCCCTGCTCCCCAAG
AAGGGCATTCTCAAGAAGCCCCGACAGCGCGAGTCTGGCTACTACTCCTCTCCCGAGCCC
AGTGAATCTGGGGAGCTCTTGGACGCAGGCGACGTGTTTGTGAGTGGGGATCCCAAGGAG
CAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACTCAAT
GGCAAGTTCTCCCAGACAGCCTTGGAGCTCGCGGCCCCCACCACCTTCGGCTCCCTGGAT
GAACTCGCCCCACCTCGCCCCCTGGCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAG
GACAGCATCCTGTCCTCTGAGTCCTTTGACCAGCTGGACTTGCCTGAACGGCTCCCAGAG
CCCCCACTGCGGGGCTGTGTGTCTGTGGACAACCTCACGGGGCTTGAGGAGCCCCCCTCA
GAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTT
TCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCA
AAGCTCACCTGAGTGGAGTAGGCATTGCCCCAGCCCGGTCAGGCTCTCAGATGCAGCTGG
TTGCACCCCGAGGGGAGATGCCTTCTCCCCCACCTCCCAGGACCTGCATCCCAGCTCAGA
AGGCTGAGAGGGTTTGCAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAGGCAAATG
AAATGCGCCAAGGGTTCAGTGTCTGTCTTCAGCCCTGCTGAACGAAGAGGATACTAAAGA
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GGCCACAGAGA

SEQ ID NO: 40_AA426580_H, MAK_V_H
ATGCCGGCGGCGGCGGGGGACGGGCTCCTGGGGGAGCCGGCGGCGCCTGGGGGCGGCGGC
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GTGAGCGGCGTGCCCCGCGAGCGGCTCCGCGACTTCCAGCACCACAAGCGCGTGGGCAAC
TACCTCATCGGCAGCAGGAAGCTGGGCGAGGGCTCCTTTGCCAAGGTGCGCGAGGGGCTG
CACGTGCTGACCGGGGAGAAGGTGGCCATAAAAGTCATTGATAAGAAGAGAGCCAAAAAG
GACACCTATGTCACCAAAAACCTGCGGCGAGAGGGTCAGATCCAGCAGATGATCCGCCAC
CCCAATATCACTCAGCTCCTTGATATTTTAGAAACGGAAAACAGCTACTACCTGGTCATG
GAGCTGTGCCCTGGGGGCAACCTGATGCACAAGATCTATGAGAAGAAGCGGCTGGAGGAG

FIGURE 2EE

TCCGAAGCCCGCAGATACATCCGACAGCTCATCTCTGCCGTAGAGCACCTGCACCGGGCC
GGGGTGGTCCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC
AAGCTGATTGACTTTGGTTTGAGCAACTGCGCAGGGATCCTGGGTTACTCGGATCCGTTC
AGCACACAGTGTGGCAGCCCTGCCTACGCTGCACCTGAACTGCTCGCCAGGAAGAAATAC
GGCCCCAAAATCGATGTCTGGTCCATAGGTGTGAACATGTATGCCATGTTGACCGGGACG
CTGCCTTTCACGGTGGAGCCTTTCAGCCTGAGGGCTTTGTACCAGAAGATGGTAGACAAA
GAAATGAACCCCCTCCCCACTCAGCTCTCCACAGGTGCCATCAGTTTCCTGCGCTCTCTC
CTGGAACCGGATCCTGTGAAGAGGCCAAATATTCAGCAGGCACTGGCGAATCGCTGGCTT
AATGAGAATTACACGGGCAAAGTGCCCTGTAATGTCACCTATCCCAACAGGATTTCTCTG
GAAGATCTGAGCCCGAGCGTCGTGCTGCACATGACCGAGAAGCTGGGTTACAAGAACAGC
GACGTGATCAACACTGTGCTCTCCAACCGCGCCTGCCACATCCTGGCCATCTACTTCCTC
TTAAACAAGAAACTGGAGCGCTATTTGTCAGGGAAATCTGACATCCAGGACAGCCTCTGC
TACAAGACCCGGCTCTACCAGATAGAAAAGTACAGGGCCCCCAAGGAGTCCTATGAGGCC
TCTCTGGACACCTGGACACGAGATCTTGAATTCCATGCCGTGCAGGATAAAAAGCCCAAA
GAACAAGAAAAAAGAGGGGATTTTCTTCATCGACCATTCTCCAAGAAGTTGGACAAGAAC
CTGCCCTCGCACAAACAGCCCTCAGGCTCGCTTATGACACAGATTCAGAACACCAAAGCC
CTCCTGAAGGACCGGAAGGCCTCCAAGTCCAGCTTCCCCGACAAAGATTCCTTTGGCTGC
CGCAATATTTTCCGCAAAACCTCAGATTCCAATTGTGTGGCTTCTTCTTCCATGGAGTTC
ATCCCCGTGCCACCGCCCAGGACCCCGAGGATTGTGAAGAAACCGGAGCCCCATCAGCCA
GGGCCCGGAAGCACTGGCATCCCCCACAAGGAAGACCCCCTGATGCTGGACATGGTGCGC
TCCTTCGAGTCTGTGGATCGCGACGACCACGTAGAAGTGCTGTCTCCCTCTCATCACTAC
AGGATTCTGAACTCCCCGGTCAGCTTGGCTCGCAGAAATTCCAGCGAGAGGACGCTGTCC
CCGGGTCTGCCATCCGGAAGCATGTCGCCTCTCCATACTCCTTTGCATCCAACTCTGGTC
TCTTTTGCTCACGAAGATAAGAACAGCCCCCCAAAAGAGGAGGGCCTGTGTTGCCCACCT
CCGGTTCCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAATTGTGTGAAAAGCCGA
GGCCGGTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCGCCATCAGAGTCTGCAG
CCATCTGCAGATAGGCCCCTGGAGGCCAGCCTGCCCCCACTGCAGCCCCTAGCCCCTGTG
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SEQ ID NO: 41_Z36720_H
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GACACCCAGGCTGGGTGGCCCGAGGTCCTGGAGCTGGTGAGGGCCATGCAGCAGGATGCG
GCCCAGCACGGTGCCAGGCTGGAGGCCCTCTTCAGGATGGTGGCTGCGGTGGACAGGGCC
ATCGCTTTGGTGGGGGCCACGTTCCAGAAATCAAAGGTGGCGGATTTCCTCATGCAGGGG
CGTGTGCCCTGGAGGAGAGGCAGCCCAGGTGACAGCCCTGAGGAGTGGGTAAAAGAGGAG
GAGGTCTGTTTCATGCCTCCAGTTCCCCCAGCTCCGGGGGCAGCAGGACAGAGCCTGCAG
AAGGATAAGGGGGAGCTGTCTGCCGAGCAGGGGATCTGGGCCACATTGATGACGCTGGTG
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GTGCTGAGCACCAGTGGGGTGCAGTCTGATGCCAGGGAGCCTGGGGAAGAGAGCCAGAAG
GCGGACGTGCTGGAGGGGACAGCGGAGAGGCTGCCCCCCATCAGAGCGTCAGGGCTGGGA
GCTGACCCCGCCCAGGCAGTGGTCTCACCGGGCCAGGGAGATGGTGTTCCTGGCCCAGCC
CAGGCATTCCCTGGCCACCTGCCCCTGCCCACAAAGGTGGAAGCCAAGGCTCCTGAGACA
CCCAGCGAGAACCTCAGGACTGGCCTGGAATTGGCTCCAGCACCCGGCAGGGTCAATGTG
GTCTCCCCGAGCCTGGAGGTTGCACCAGGTGCAGGACAAGGAGCATCGTCCAGCAGGCCT
GACCCTGAGCCCTTAGAGGAAGGCACGAGGCTGACTCCAGGGCCTGGCCCTCAGTGCCCA
GGGCCTCCAGGGCTGCCAGCCCAGGCCAGGGCAACCCACAGTGGTGGAGAAACACCTCCA
AGGGCAGCCCTGCTGAAGGGCGCTGTGGCCCCGGGCTTCTCTCGGAGGGACCTGGTGTTT
CCTAGCATCTTCTGCGCCTGCCTAGGGATCTCCATCCACATACAAGAGATGGATACTCCT

FIGURE 2FF

GGGGAGATGCTGATGACAGGCAGGGGCAGCCTTGGACCCACCCTCACCACAGAGGCTCCA
GCAGCTGCCCAGCCAGGCAAGCAGGGCCCACCTGGGACCGGGCGCTGCCTCCAAGCCCCT
GGGACTGAGCCCGGAGAACAGACCCCTGAAGGAGCCAGAGAGCTCTCCCCGCTGCAGGAG
AGCAGCAGCCCCGGGGGAGTGAAGGCAGAGGAGGAGCAAAGGGCTGGGGCCGAGCCTGGC
ACGAGACCAAGCTTGGCCAGGAGTGACGACAATGACCACGAGGTTGGGGCCCTGGGCCTG
CAGCAGGGCAAAAGCCCAGGGGCGGGAAACCCTGAGCCTGAGCAGGACTGTGCAGCCAGG
GCTCCGGTGAGAGCTGAAGCAGTAAGGAGGATGCCCCCAGGCGCCGAGGCTGGCAGCGTG
GTTCTGGATGACAGTCCGGCCCCACCAGCTCCTTTTGAACACCGGGTAGTGAGCGTCAAG
GAGACCTCCATCTCTGCGGGTTACGAGGTGTGCCAGCACGAAGTCTTGGGAGGGGGTCGG
TTTGGCCAGGTCCACAGGTGCACAGAGAAGTCCACAGGCCTCCCACTGGCTGCCAAGATC
ATCAAAGTGAAGAGCGCCAAGGACCGGGAGGACGTGAAGAACGAGATCAACATCATGAAC
CAGCTCAGCCACGTGAACCTGATCCAGCTCTATGACGCCTTCGAGAGCAAGCACAGCTGC
ACCCTTGTCATGGAGTACGTGGACGGGGGTGAGCTCTTCGACCGGATCACAGATGAGAAG
TACCACCTGACTGAGCTGGATGTGGTCCTGTTCACCAGGCAGATCTGTGAGGGTGTGCAT
TACCTGCACCAGCACTACATCCTGCACCTGGACCTCAAGCCGGAGAACATATTGTGCGTC
AATCAGACAGGACATCAAATTAAGATCATTGACTTTGGGCTGGCCAGAAGGTACAAGCCT
CGAGAGAAGCTGAAGGTGAACTTCGGCACTCCTGAGTTCCTGGCCCCAGAAGTCGTCAAT
TATGAGTTTGTCTCATTCCCCACAGACATGTGGAGTGTGGGAGTCATCACCTACATGCTA
CTCAGTGGCTTGTCCCCATTTCTAGGGGAAACAGATGCAGAGACCATGAATTTCATTGTA
AACTGTAGCTGGGATTTTGATGCTGACACCTTTGAAGGGCTCTCGGAGGAGGCCAAGGAC
TTTGTTTCCCGGTTGCTGGTCAAAGAGAAGAGCTGCAGAATGAGTGCCACACAGTGCCTG
AAACACGAGTGGCTGAATAATTTGCCTGCCAAAGCTTCAAGATCCAAAACTCGTCTCAAA
TCCCAACTACTGCTGCAGAAATACATAGCTCAAAGAAAATGGAAGAAACATTTCTATGTG
GTGACTGCTGCCAACAGGTTAAGGAAATTTCCAACTTCTCCCTAA

SEQ ID NO: 42_SGK088_H
GGGGAGATGGCGCTGTTTGAGTGCCTGGTGGCGGGGCCCACTGACGTGGAGGTGGATTGG
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CGCAAATGCAAGCTGCTACTTACATCTGTACATGAGGACGACAGTGGCGTCTACACCTGC
AAGCTCAGCACGGCCAAAGATGAGCTGACCTGCAGTGCCCGGCTGACCGTGCGGCCCTCG
TTGGCACCCCTGTTCACACGGCTGCTGGAAGATGTGGAGGTGTTGGAGGGCCGAGCTGCC
CGTTTCGACTGCAAGATCAGTGGCACCCCGCCCCCTGTTGTTACCTGGACTCATTTTGGC
TGCCCCATGGAGGAGAGTGAGAACTTGCGGCTGCGGCAGGACGGGGGTCTGCACTCACTG
CACATTGCCCATGTGGGCAGCGAGGACGAGGGGCTCTATGCGGTCAGTGCTGTTAACACC
CATGGCCAGGCCCACTGCTCAGCCCAGCTGTATGTAGAAGAGCCCCGGACAGCCGCCTCA
GGCCCCAGCTCGAAGCTGGAGAAGATGCCATCCATTCCCGAGGAGCCAGAGCAGGGTGAG
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GCCAAGGAGGCCATGCTAGAGTGCCAGGTGACCGGCCTGCCCTACCCCACCATCAGCTGG
TTCCACAATGGCCACCGCATCCAGAGCAGCGACGACCGGCGCATGACACAGTACAGGGAT
GTCCATCGCTTGGTGTTCCCTGCCGTGGGGCCTCAGCACGCCGGTGTCTACAAGAGCGTC
ATTGCCAACAAGCTGGGCAAAGCTGCCTGCTATGCCCACCTGTATGTCACAGATGTGGTC
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GTGCAGCACCAGGTGCTGGGCTCGGACCAGTGGACGGCACTGGTCACAGGCCTGCGGGAG
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CACGGCCCAACCCTGGAGGAGGCCCCTGCCATGCTGGACAAACCAGACATCGTGTATGTG
GTGGAGGGACAGCCTGCCAGCGTCACCGTCACATTCAACCATGTGGAGGCCCAGGTCGTC
TGGAGGAGCTGCCGAGGGGCCCTCCTAGAGGCACGGGCCGGTGTGTACGAGCTGAGCCAG
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FIGURE 2GG

CTCACCTGCACCGCCCGAAACCGTCACGGCACACAGACCTGCTCGGTCACATTGGAGCTG
GCAGAGGCCCCTCGGTTTGAGTCCATCATGGAGGACGTGGAGGTGGGGCTGGGAAACT
GCTCGCTTTGCGGTGGTGGTCGAGGGAAAACCACTGCCGGACATCATGTGGTACAAGGAC
GAGGTGCTGCTGACCGAGAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGCTCC
CTGGTGGTGCTCAGCACGGGGGCCCAGGATGGAGGCGTCTACACCTGCACCGCCCAGAAC
CTGGCGGGTGAGGTCTCCTGCAAAGCAGAGTTGGCTGTGCATTCAGCTCAGACAGCTATG
GAGGTCGAGGGGGTCGGGGAGGATGAGGACCATCGAGGAAGGAGACTCAGCGACTTTTAT
GACATCCACCAGGAGATCGGCAGGGGTGCTTTCTCCTACTTGCGGCGCATAGTGGAGCGT
AGCTCCGGCCTGGAGTTTGCGGCCAAGTTCATCCCCAGCCAGGCCAAGCCAAAGGCATCA
GCGCGTCGGGAGGCCCGGCTGCTGGCCAGGCTCCAGCACGACTGTGTCCTCTACTTCCAT
GAGGCCTTCGAGAGGCGCCGGGGACTGGTCATTGTCACCGAGCTCTGCACAGAGGAGCTG
CTGGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCCTATATGCGG
CAGGTGCTAGAGGGAATACACTACCTGCACCAGAGCCACGTGCTGCACCTCGATGTCAAG
CCTGAGAACCTGCTGGTGTGGGATGGTGCTGCGGGCGAGCAGCAGGTGCGGATCTGTGAC
TTTGGGAATGCCCAGGAGCTGACTCCAGGAGAGCCCCAGTACTGCCAGTATGGCACACCT
GAGTTTGTAGCACCCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGACATCTGG
CCTGTGGGTGTTGTTGCCTTCCTCTGTCTGACAGGAATCTCCCCGTTTGTTGGGGAAAAT
GACCGGACAACATTGATGAACATCCGAAACTACAACGTGGCCTTCGAGGAGACCACATTC
CTGAGCCTGAGCAGGGAGGCCCGGGGCTTCCTCATCAAAGTGTTGGTGCAGGACCGGCTG
AGACCTACCGCAGAAGAGACCCTAGAACATCCTTGGTTCAAAACTCAGGCAAAGGGCGCA
GAGGTGAGCACGGATCACCTGAAGCTATTCCTCTCCCGGCGGAGGTGGCAGCGCTCCCAG
ATCAGCTACAAATGCCACCTGGTGCTGCGCCCCATCCCCGAGCTGCTGCGGGCCCCCCCA
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TCGGATTCTGAAGAGGAAGAGCTGGAAGAGCTGCCCTCAGTGCCCCGCCCACTGCAGCCC
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CAGGACCAGGAGGCTCCCAGCCCAGAGGCCCTCCCCTCCCCAGGCCAGGAGCCCGCAGCT
GGGGCTAGCCCCAGGCGGGGAGAGCTCCGCAGGGGCAGCTCGGCTGAGAGCGCCCTGCCC
CGGGCCGGGCCGCGGGAGCTGGGCCGGGGCCTGCACAAGGCGGCGTCTGTGGAGCTGCCG
CAGCGCCGGAGCCCCGGCCCGGGAGCCACCCGCCTGGCCCGGGGAGGCCTGGGTGAGGGC
GAGTATGCCCAGAGGCTGCAGGCCCTGCGCCAGCGGCTGCTGCGGGGAGGCCCCGAGGAT
GGCAAGGTCAGCGGCCTCAGGGGTCCCCTGCTGGAGAGCCTGGGGGGCCGTGCTCGGGAC
CCCCGGATGGCACGAGCTGCCTCCAGCGAGGCAGCGCCCCACCACCAGCCCCCACTCGAG
AACCGGGGCCTGCAAAAGAGCAGCAGCTTCTCCCAGGGTGAGGCGGAGCCCCGGGGCCGG
CACCGCCGAGCGGGGGCGCCCCTCGAGATCCCCGTGGCCAGGCTTGGGGCCCGTAGGCTA
CAGGAGTCTCCTTCCCTGTCTGCCCTCAGCGAGGCCCAGCCATCCAGCCCTGCACGGCCC
AGCGCCCCCAAACCCAGTACCCCTAAGTCTGCAGAACCTTCTGCCACCACACCTAGTGAT
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CCAGTCCGAGCCTCCAAGCCTGCACCACCCCCCAGGCCCTGCAAACCCTAGCGCTGCCC
CTCACACCCTATGCTCAGATCATTCAGTCCCTCCAGCTGTCAGGCCACGCCCAGGGCCCC
TCGCAGGGCCCTGCCGCGCCGCCTTCAGAGCCCAAGCCCCACGCTGCTGTCTTTGCCAGG
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GTGCTAGCCGAGAAAGCCCGAGTTCCCACGGTGCCCCCCAGGCCAGGCAGCAGTCTCAGT
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GAGTCGCCCCTGTCGCTGGGGCTGCGGCTGCTGAGCCGTTCGCGCTCGGAGGAGCGCGGC
CCCTTCCGTGGGGCCGAGGAGGAGGATGGCATATACCGGCCCAGCCCGGCGGGGACCCCG
CTGGAGCTGGTGCGACGGCCTGAGCGCTCACGCTCGGTGCAGGACCTCAGGGCTGTCGGA
GAGCCTGGCCTCGTCCGCCGCCTCTCGCTGTCACTGTCCCAGCGGCTGCGGCGGACCCCT
CCCGCGCAGCGCCACCCGGCCTGGGAGGCCCGCGGCGGGGACGGAGAGAGCTCGGAGGGC
GGGAGCTCGGCGCGGGGCTCCCCGGTGCTGGCGATGCGCAGGCGGCTGAGCTTCACCCTG

FIGURE 2HH

GAGCGGCTGTCCAGCCGATTGCAGCGCAGTGGCAGCAGCGAGGACTCGGGGGCGCGTCG
GGCCGCAGCACGCCGCTGTTCGGACGGCTTCGCAGGGCCACGTCCGAGGGCGAGAGTCTG
CGGCGCCTTGGCCTTCCGCACAACCAGTTGGCCGCCCAGGCCGGCGCCACCACGCCTTCC
GCCGAGTCCCTGGGCTCCGAGGCCAGCGCCACGTCGGGCTCCTCAGCCCCAGGGGAAAGC
CGAAGCCGGCTCCGCTGGGGCTTCTCTCGGCCGCGGAAGGACAAGGGGTTATCGCCACCA
AACCTCTCTGCCAGCGTCCAGGAGGAGTTGGGTCACCAGTACGTGCGCAGTGAGTCAGAC
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CCTGAGCCTACCAAGGTGACTGTGCAGAGCCTCAGCCCGGCCAAGGAGGTGGTCAGCTCC
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FIGURE 2II

GAGAGCTGGAGGCCAGCAGTCACTCACACTCGCTCTGTCCTCCTGTCCAGTGGATACAGC
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TCCCATTCATATTTATTTATTTATTGACTTTTATGAAGTTTCCCCTTCCATCCGATCCCT
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FIGURE 2JJ

AAACGCTGCAATGACATGATGAATCTAGGACGTCTGCAGGGCTTTGAGGGCACTCTGACT
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FIGURE 2KK

AAAACTCCATGTCTGGGCACGCCTGGCTGATCTTCACCTCTTTCTTCTAGGACCTTCCTC
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FIGURE 2LL

CATGTGTGCAGGTTCATTGGCTGTGGCAGGAACGAGAAGTTTAACTATGTAGTGATGCAG
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AATGCCCACAAGAACCGGGAGATGGGCCGCCACGACGACCTGTGGTCCCTCTTCTACATG
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AACAGCCATGGCCAGGCAAATGGTCTTCTCAATGCTCCAAGCCTTGGGTCACCAATTCGT

FIGURE 2MM

GTCCGCTCAGAGATTACTCAGCCAGACAGAGATATTCCACTGGTGCGAAAGTTACGTTCC
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TTCCTTGAGACCTGGTATAAAATAGTGTATTTTTCTTTTTAAAGCTTCTAAGGTACCATT
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AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAGAATCAACTGTTGCCTCT
CATACCAGGAAGCCACATCTCCCCCACACCTGATGGAAGAAAACAAGTCCTCCAGTTAAA
ATTTGATCACCTTCCAAACATTTAGGAAAATGTTCTTTCAAGTGCAAAGTAATTTAATAT
GTACACATTTTGTACAAGTGAGATAGGAATTCTCAGTGTTTCAAATGCAAATGAGCCATA

FIGURE 2NN

TGAAAATTAAGATGCCTTCTAGAATTGGTTTGCTCTGATCATTGCTGATTCCTTTCCCCA
TGCTTTTACAT

SEQ ID NO: 50_AA061797_M
GAAAATAGCCCTGCGGGAAATCCGTATGCTGAAGTTGAAACACCCAAACCTCGTGAACCT
CATCGAGGTGTTCAGAAGAAAGAGAAAGATGCATCTAGTTTTTGAGTACTGTGATCACAC
ACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTAAAAGTGT
GCTATGGCAAACCCTTCAAGCCCTTAACTTCTGTCACAAGCACAATTGTATTCATCGGGA
TGTAAAACCTGAAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTTTGG
ATTTGCACGAATTCTAATTCCAGGAGACGCCTACACAGACTATGTTGCCACCAGGTGGTA
CCGAGCCCCCGAACTTCTCGTGGGAGACACGAAGTACGGTTCCTCTGTAGACGTGTGGGC
CGTCGGCTGTGTTTTTGCAGAGCTCCTGACGGGTCAGCCACTCTGGCCGGGAAAATCCGA
CGTGGACCAGCTTTACCTGATCATCAGGACGTTGGGGAAGCTGATTCCAAGACACCAGTC
TATCTTTAGGAGTAACCAGTTTTTCCGCGGCATCAGCATACCTGAACCAGAGGACATGGA
GACTCTTGAAGAAAAATTCTCAAATGTTCAGCCTGTGGCTTTAAGTTTCATGAAGGGATG
CCTGAAGATGAATCCTGATGAGAGGCTGACCTGTGCCCAGCTGCTGGACAGTGCCTACTT
TGAGTCTTTTCAAGAGGATCAAATGAAAAGAAAAGCCCGCAGTGAGGGGAGAAGCCGAAG
GCGCCAGCAGAATCAACTGCTGCCTCTTATTCCTGGAAGCCACATCTCCCCCACACCTGA
TGGAAGGAAACAAGTCGTCCAGTTAAAGTTCGATCATCTTCCAAACATTTAGGGGACTCA
TCCTTCCCAGCACATCCTTTTAATATTGTCTACATAGGAATAAGACGGGAATCCTCAGCA
TCTCAAATACAGTGAGCGACGTGAACACCAGGGCACCTCTAATCACCACGGGCTCCTCCC
CTGTGCTTTTTCCACGCCAGCTCCATCTCCTAAAACATTCTCTTTAAATGTTGCAGTATC
AAAATGGCACATCCGAAAGAGATGCTTCCAGTTTCACCAGAGCCGGGCTTCCTCAGGCAA
TCGGTACTGTGCATCTGTGGACTTATGCTCCGACCTAGGGAAAGATTTCCACGTAGCCGT
CTCACTTCAGCCGACCAGTGGTGTCCTGAAGCAGACCCAGATCTGCTGGCTGCTGTTTGT
GGAGGGGATGGCCCTGAGCCCTCTCACTGGAGTTTCTTCTCCGTGCAGCCAGGTCTTACT
TTAGACTACATTTGTGTTATTGTGGCATGGCAATCGTGAAAGGTGGTCTAGGTTTACCCT
TGACTCCACAGCAGATGCTAGTCTCCTTCTCGTGAGGAGCTGACAAGTCTGCTTCTAAAA
CGAACTAGAGAAAATTCCAAACGTGACCAGTTAGTGGACAGACTACAAGGAATCGACCAC
CATACCACAGTAACGCCCCTGGATCCCTGGCTGCCCACCCACTCTAAGGCTATCCTGGTT
CACCATGGTTTCTCTTTCTTTTCTTCTTTTTTAATCTATTTGTACATATGAGAAAGAGGC
AGAGGGGCGAGAGAAACCTCGTGTGTGAAAATCAAAAGACAAGCAGGAGGCCAGCCTAAG
CTACATAGCAAGGCCTTTTCTCTACACCCATTCTCTAAGGTTGCTTAAACCCAAGTCCCT
GCTGCTGATTGTATAAACTATGAATAAGTTCTACATATGTAGGACATATTGTTGTCATTG
TTGAAATATCTAAGGATCTTGGTAGAAGCAGAAGTGTTCTAAATATTCTCCACACTGGTG
AGTATCTTGGCATTTCATTTCTGACCTCATCACAGATGAACACATCAAAGGATGAGTATG
TATCACTTTGCATCTTAGAATTCTACCTGTTTTAGCTGCGTTAAACCTTGTGAAAGGGCG
GGGCCATAACTGAACCTGTGGAGTTCTTGCCTGTGTGCAGGAAACCCTCTGGTTTTGTCT
CCAGCATGGAAGAAAACAGCTATAGTCACACCTACCTGAAAGTAGAAATTCAAAGTCACT
GTCCTTGACTACATATGCAGTCCAAGGCCACGCTGGGCTACACTTCTCCAGGCATGAAGG
TCCGTGTTTGTATCAAGGGGCAGGAAAGGAGAGTCCAAGGTCAAGGCCAGCCGAGGCTGC
ATAGTGAGTTGAGGCTCTTCAGCAAAAGAAAAGCAAACTAATAGGAGTCGTTGAAGGTAG
CCACCGGCCATTTCTCTAAATATCATTCTGCTGAAAAGGGGGCTTAGTTTAGTTTAGAAT
GCATTAATGTATGTAGAAGCTGGGCTATTTCAGATTATTTGAAATTGTAGCTATTGTTAA
TTAGCACTTAATAACTAACTAGCATTATGGTAGTCTAAACTATTAGAGTTTACTACAAAG
AGGTTTTGATTGAATTATATTAAACATATAATATGGATTTTAAAAATTTAAGATGTTTAA
GAAAGCTATATAAAGATTAAACATTTTTGTGGCTGTATATTTGTGTATATACCTTGGTTG
TTCTTTAAATTATTTTAATAAAAGCCAGAAACATT

FIGURE 20O

SEQ ID NO: 51_AA397553_H
ATGCCCAATTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGAACT
TTGCAGCCGTCATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCG
AAGCACAAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTTGGTGACCCCCGAAGCA
GCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATATCAGCTCTGATTCC
GACACCTTCTCCGATGACATGGCCTTCAAACTAGACCGAAGGGAGAACGACGAACGTCGT
GGATCAGATCGGAGCGACCGCCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGG
GACTTACTAAAAGCTAAACAGACCGAAAAAGAAAAAAGCCAAGAAGTCTCCAGCAAGTCG
GGATCGATGAAGGACCGGATATCGGGAAGTTCAAAGCGTTCGAATGAGGAGACTGATGAC
TATGGGAAGGCGCAGGTAGCCAAAAGCAGCAGCAAGGAATCCAGGTCATCCAAGCTCCAC
AAGGAGAAGACCAGGAAAGAACGGGAGCTGAAGTCTGGGCACAAAGACCGGAGTAAAAGT
CATCGAAAAAGGGAAACACCCAAAAGTTACAAAACAGTGGACAGCCCAAAACGGAGATCC
AGGAGCCCCCACAGGAAGTGGTCTGACAGCTCCAAACAAGATGATAGCCCCTCGGGAGCT
TCTTATGGCCAAGATTATGACCTTAGTCCCTCACGATCTCATACCTCGAGCAATTATGAC
TCCTACAAGAAAAGTCCTGGAAGTACCTCGAGAAGGCAGTCGGTCAGTCCCCCTTACAAG
GAGCCTTCGGCCTACCAGTCCAGCACCCGGTCACCGAGCCCCTACAGTAGGCGACAGAGA
TCTGTCAGTCCCTATAGCAGGAGACGGTCGTCCAGCTACGAAAGAAGTGGCTCTTACAGC
GGGCGATCGCCCAGTCCCTATGGTCGAAGGCGGTCCAGCAGCCCTTTCCTGAGCAAGCGG
TCTCTGAGTCGGAGTCCACTCCCCAGTAGGAAATCCATGAAGTCCAGAAGTAGAAGTCCT
GCATATTCAAGACATTCATCTTCTCATAGTAAAAAGAAGAGATCCAGTTCACGCAGTCGT
CATTCCAGTATCTCACCTGTCAGGCTTCCACTTAATTCCAGTCTGGGAGCTGAACTCAGT
AGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGCTGCAGCAAAGATGGATGGAAAGGAGTCC
AAGGGTTCACCTGTATTTTTGCCTAGAAAAGAGAACAGTTCAGTAGAGGCTAAGGATTCA
GGTTTGGAGTCTAAAAAGTTACCCAGAAGTGTAAAATTGGAAAAATCTGCCCCAGATACT
GAACTGGTGAATGTAACACATCTAAACACAGAGGTAAAAAATTCTTCAGATACAGGGAAA
GTAAAGTTGGATGAGAACTCCGAGAAGCATCTTGTTAAAGATTTGAAAGCACAGGGAACA
AGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGTTACTCCAAAGGAGACAGAAACA
TCAGAAAAGGAGACCCCTCCACCTCTTCCCACAATTGCTTCTCCCCCACCCCCTCTACCA
ACTACTACCCCTCCACCTCAGACACCCCCTTTGCCACCTTTGCCTCCAATACCAGCTCTT
CCACAGCAACCACCTCTGCCTCCTTCTCAGCCAGCATTTAGTCAGGTTCCTGCTTCCAGT
ACTTCAACTTTGCCCCCTTCTACTCACTCAAAGACATCTGCTGTGTCCTCTCAGGCAAAT
TCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGTAACAGCTGCTATTCCA
CACCTGAAAACTTCAACGTTGCCTCCTTTGCCCCTCCCACCCTTATTACCTGGAGGTGAT
GACATGGATAGTCCAAAAGAAACTCTTCCTTCAAAACCTGTGAAGAAAGAGAAGGAACAG
AGGACACGTCACTTACTCACAGACCTTCCTCTCCCTCCAGAGCTCCCTGGTGGAGATCTG
TCTCCCCCAGACTCTCCAGAACCAAAGGCAATCACACCACCTCAGCAACCATATAAAAAG
AGACCAAAAATTTGTTGTCCTCGTTATGGAGAAAGAAGACAAACAGAAAGCGACTGGGGG
AAACGCTGTGTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCAA
GTATATAAAGCCAGGGACAAAGACACAGGAGAACTAGTGGCTCTGAAGAAGGTGAGACTA
GACAATGAGAAAGAGGGCTTCCCAATCACAGCCATTCGTGAAATCAAAATCCTTCGTCAG
TTAATCCACCGAAGTGTTGTTAACATGAAGGAAATTGTCACAGATAAACAAGATGCACTG
GATTTCAAGAAGGACAAAGGTGCCTTTTACCTTGTATTTGAGTATATGGACCATGACTTA
ATGGGACTGCTAGAATCTGGTTTGGTGCACTTTTCTGAGGACCATATCAAGTCGTTCATG
AAACAGCTAATGGAAGGATTGGAATACTGTCACAAAAAGAATTTCCTGCATCGGGATATT
AAGTGTTCTAACATTTTGCTGAATAACAGTGGGCAAATCAAACTAGCAGATTTTGGACTT
GCTCGGCTCTATAACTCTGAAGAGAGTCGCCCTTACACAAACAAAGTCATTACTTTGTGG
TACCGACCTCCAGAACTACTGCTAGGAGAGGAACGTTACACACCAGCCATAGATGTTTGG
AGCTGTGGATGTATTCTTGGGGAACTATTCACAAAGAAGCCTATTTTTCAAGCCAATCTG
GAACTGGCTCAGCTAGAACTGATCAGCCGACTTTGTGGTAGCCCTTGTCCAGCTGTGTGG
CCTGATGTTATCAAACTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGG

FIGURE 2PP

CGTCTACGAGAAGAATTCTCTTTCATTCCTTCTGCAGCACTTGATTTATTGGACCACATG
CTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCTACAGAGCGACTTCCTT
AAAGATGTCGAACTCAGCAAAATGGCTCCTCCAGACCTCCCCCACTGGCAGGATTGCCAT
GAGTTGTGGAGTAAGAAACGGCGACGTCAGCGACAAAGTGGTGTTGTAGTCGAAGAGCCA
CCTCCATCCAAAACTTCTCGAAAAGAAACTACCTCAGGGACAAGTACTGAGCCTGTGAAG
AACAGCAGCCCAGCACCACCTCAGCCTGCTCCTGGCAAGGTGGAGTCTGGGGCTGGGGAT
GCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGAATTGGCAGTGTTATTA
AACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACATC
CACTCCAACCCAGAGATGCAGCAGCAGCTGGAAGCCCTGAACCAATCCATCAGTGCCCTG
ACGGAAGCTACTTCCCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAG
GAAGCACCCTCTGCCCCAGTGATCCTGCCTTCAGCAGAACAGATGACCCTTGAAGCTTCA
AGCACACCAGCTGACATGCAGAATATATTGGCAGTTCTCTTGAGTCAGCTGATGAAAACC
CAAGAGCCAGCAGGCAGTCTGGAGGAAAACAACAGTGACAAGAACAGTGGGCCACAGGGG
CCCCGAAGAACTCCCACAATGCCACAGGAGGAGGCAGCAGCATGTCCTCCTCACATTCTT
CCACCAGAGAAGAGGCCCCCTGAGCCCCCCGGACCTCCACCGCCGCCACCTCCACCCCCT
CTGGTTGAAGGCGATCTTTCCAGCGCCCCCCAGGAGTTGAACCCAGCCGTGACAGCCGCC
TTGCTGCAACTTTTATCCCAGCCTGAAGCAGAGCCTCCTGGCCACCTGCCACATGAGCAC
CAGGCCTTGAGACCAATGGAGTACTCCACCCGACCCCGTCCAAACAGGACTTATGGAAAC
ACTGATGGGCCTGAAACAGGGTTCAGTGCCATTGACACTGATGAACGAAACTCTGGTCCA
GCCTTGACAGAATCCTTGGTCCAGACCCTGGTGAAGAACAGGACCTTCTCAGGCTCTCTG
AGCCACCTTGGGGAGTCCAGCAGTTACCAGGGCACAGGGTCAGTGCAGTTTCCAGGGGAC
CAGGACCTCCGTTTTGCCAGGGTCCCCTTAGCGTTACACCCGGTGGTCGGGCAACCATTC
CTGAAGGCTGAGGGAAGCAGCAATTCTGTGGTACATGCAGAGACCAAATTGCAAAACTAT
GGGGAGCTGGGGCCAGGAACCACTGGGGCCAGCAGCTCAGGAGCAGGCCTTCACTGGGGG
GGCCCAACTCAGTCTTCTGCTTATGGAAAACTCTATCGGGGGCCTACAAGAGTCCCACCA
AGAGGGGGAAGAGGGAGAGGAGTTCCTTACTAA

SEQ ID NO: 52_AA789239_H
TGAAAATGGAGATGTATGAAACCCTTGGAAAAGTGGGAGAGGGAAGTTACGGAACAGTCA
TGAAATGTAAACATAAGAATACTGGGCAGATAGTGGCCATTAAGATATTTTATGAGAGAC
CAGAACAATCTGTCAACAAAATTGCGATGAGAGAAATAAAGTTTCTAAAGCAATTTCATC
ACGAAAACCTGGTCAATCTGATTGAAGTTTTTAGACAGAAAAAGAAAATTCATTTGGTAT
TTGAATTTATTGACCACACAGTATTAGATGAGTTACAACATTATTGTCATGGACTAGAGA
GTAAGCGACTTAGAAAATACCTCTTCCAGATCCTTCGAGCAATTGACTATCTTCACAGTA
ATAATGTAATCATTCATCGAGATATAAAACCTGAGAATATTTTAGTATCCCAGTCAGGAA
TTACTAAGCTCTGTGATTTTGGTTTTGCACGAACACTAGCAGCTCCTGGGGACATTTATA
CGGACTATGTGGCCACACGCTGGTATAGAGCTCCCGAATTAGTATTAAAAGATACTTCTT
ATGGAAAGTATGTGCCTGTGGATATCTGGGCTTTGGGCTGTATGATCATTGAGATGGCCA
CTGGAAATCCCTATCTTCCTAGTAGTTCTGATTTGGATTTACTCCATAAAATTGTTTTGA
AAGTGNGATTCATGCCAGAACTGAAAGCTAAATTACTGCAGGAAGCAAAAGTCAATTCAT
TAATAAAGCCAAAAGAGAGTTCTAAAGAAAATGAACTCAGGAAAGATGAAAGAAAAACAG
TTTATACCAATACACTGCTAAGTAGTTCAGTTTTGGGAAAGGAAATAGAAAAAGAGAAAA
AGCCCAAGGAGATCAAAGTCAGAGTTATTAAAGTCAAAGGAGGAAGAGGAGATATCTCAG
AACCAAAAAAGAAAGAGTATGAAGGTGGACTTGGTCAACAGGATGCAAATGAAAATGTTC
ATCCTATGTCTCCAGATACAAAACTTGTAACCATTGAACCACCAAACCCTATCAATCCCA
GCACTAACTGTAATGGCTTGAAAGAAAATCCACATTGCGGAGGTTCTGTGACAATGCCAC
CCATCAATCTAACTAACAGTAATTTGATGGCTGCAAATCTCAGTTCAAATCTCTTTCACC
CCAGTGTGAGGTTAACTGAAAGAGCAAAAAAGAGACGCACTTCTTCACAATCTATTGGAC
AAGTTATGCCTAATAGCAGGCAAGAGGATCCAGGTCCTATTCAAAGCCAAATGGAGAAGG
GTATATTTAATGAGCGAACAGGTCACAGTGACCAAATGGCAAATGAGAACAAAAGGAAGC

FIGURE 2QQ

TGAATTTTTCCAGATCTGACAGGAAAGAATTCCATTTTCCAGAATTGCCTGTCACAATAC
AGTCAAAAGATACAAAAGGAATGGAAGTTAAACAGATAAAAATGCTGAAGAGGGAGTCAA
AGAAAACAGAGTCATCTAAGATACCAACTTTACTTAACGTGGATCAAAATCAAGAAAAAC
AAGAGTTTATTCCCTTATCTCTGCTGTCTGCCTGCTGTCCTATTTTCACAAATATTTGCT
CTCAGCTAACTATCAGGGTGGAGATGGCCATTGCGAGGGGAAGAATTTGAAGAGAAACAG
GTTTTTTTTCTGGTAGTGTCTTTTCTTTTACATAGTCCAAAAAATACAAGATGACAACTC
TTCCCGTTTTATTTATCTACAATAGAAGTGTGATGTGAGTTGTTGTTAAGACAGCCATCC
ATGTGCATGAGCATCATCCAGCTTTTTTTGTTAGCAAAACATTTACTGTTTTCTTTTCCC
TTTTAAGACTCTGTTGATGTGATAATTTGATTTGGAATTATAAAGTCATCTCTTCTCTGC
CTTGAA

SEQ ID NO: 53_AA124976_M
CTGGCAGATATAGTTCATGCTTGTTTACAAATTGATCCTGCTGAGAGGACATCATCTACT
GATCTTTTGCGTCACGATTACTTTACTAGAGATGGATTTATTGAGAAATTCATACCAGAG
CTGAGAGCTAAATTATTACAGGAAGCAAAGGTTAATTCATTTATAAAGCCAAAAGAGAAT
TTTAAAGAAAATGAACCTGTGAGAGATGAGAAGAAATCAGTTTTTACCAACACCCTGCTC
TATGGAAATCCATCACTTTATGGCAAGGAAGTGGACAGAGACAAAAGGGCCAAGGAGCTC
AAAGTCAGAGTCATTAAGGCCAAAGGGGGCAAAGGAGATGTCCCAGACCAGAAGAAGCCA
GAGTATGAAGGCGACCACCGCCAGCAGGGCACAGCTGATGACACACAGCCCTCATCACTG
GACAAGAAGCCTTCTGTCTTGGAACTGACAAACCCTCTCAATCCCAGTGAGAATTCTGAC
GGTGTCAAAGAAGACCCACACGCTGGGGGTTGTATGATAATGCCACCTATCAACCTGACA
AGCAGTAATTTGTTGGCCGCAAATCTCAGTTCAAACCTTTCCCACCCCAATTCACGGTTA
ACTGAAAGAACAAAAAAGAGACGCACTTCTTCACAAACTATTGGACAGACTTTGTCTAAT
AGCAGACAAGAGGACACAGGTCCCACACAAGTCCAAACAGAGAAAGGTGCATTTAATGAG
CGAACAGGTCAGAATGACCAAATATCGAGTGGGAACAAAAGAAAGCTGAATTTTCCCAAA
TGCGACAGGAAAGAATTCCATTTCCCTGAACTGCCATTCACAGTGCAGGCGAAGGAGATG
AAAGGGATGGAAGTTAAACAGATAAAAGTGCTGAAGAGAGAATCAAAGAAAACAGATTCA
TCTAAAATACCAACTTTACTTAGTATGGACCCAAATCAAGAAAAACAAGAGGGTGGAGAT
GGCGATTGTGAGGGGAAGAATTTGAAGAGGAACAGATTTTTTTTTTCCCGATAGTGCTTT
GTCTTTTAAGTAATCTTAAAAATACAAGCTTGACAATTCCTTCCTTTTTATTTTATATAC
ACTAGAATGTACATAGGTTGCTGCTAAGATAGCCACCCATCCCATCTGCATCAACATCAT
CTATTTTTTTGGTTTTGCTAGCAAAATTTTCACAATTTTTCTCTATCTTCCAAAAACTGT
TATTTTGATGCTGTGATTTGAAATTATAAAGTCACCTCCTCTGTCTGCTTCCTTCCTTGC
CATGATTACTGAGTGGGTAGTCACATGATGTGCCCTGCTCGCACTGCTCTCAGACTGCTG
AGACTCAAACCTCATAAGCCAGGGGTCTCCTGGGAAGCACTGGCCTCTTCAAGTGGATGC
TCGATGAACCTTCTTATCTGTTGTCTTAGTAACCACTCGTTGCCATCACATGATGAAAGA
CATTCTATTGTCCCCAGTGAAGCATTTATAGTACTTACATAACATGTTACAGTGATATGA
TGTTCCTAGGTTAAACTCCTTGAGATGAAACTATTTCCTGCATTCTCTGACTCCCCTAGT
CTAATAGTTCCTTCCATTTAGCCAGAAGAATTTCCTGAAGAAGCGATGCACAACCTGGGA
AAGGTTTACTTTCTATCCTGGGCTGTTTTCTGTTGCTAAATAATATAGACTGGGTAGTTA
GTTAACAT

SEQ ID NO: 54_AA575635_M CCRK_M
AGCGCCTCAGGCCAGCTCAAGATAGCTGACTTTGGCCTGGCCCGGGTCTTCTCTCCGGAT
GGTGGTCGCCTCTACACACATCAGGTGGCCACCAGGTGGTACCGAGCTCCTGAACTCCTG
TATGGCGCTCGGCAGTATGACCAGGGCGTTGACCTATGGGCTGTGGGCTGCATCATGGGA
GAGCTGTTGAATGGGTCCCCCCTGTTCCCGGGCGAAAACGACATTGAACAACTGTGCTGT
GTGCTTCGCATCCTGGGTACCCCGAGTCCTCGAGTCTGGCCGGAGATCACAGAGCTGCCT
GACTACAACAAGATCTCCTTCGAGGAGCAGGCACCAGTGCCCCTGGAGGAGGTGCTGCCT
GATGCCTCTCCCCAGGCCTTGGACCTGCTGGGCCAGTTCCTCCTCTACCCTCCACGACAG

FIGURE 2RR

CGTATTGCAGCCTCCCAGGCCCTTCTGCATCAGTACTTCTTCACAGCGCCTCTGCCTGCC
CATCCATCCGAGCTGCCAATTCCTCAGCGCCCAGGGGGACCTGCACCCAAGGCTCACCCA
GGGCCCCCCCATGTCCACGACTTCCATGTGGATCGACCTATTGAGGAGTCACTGTTGAAC
CCAGAACTGATTCGGCCCTTCATCCCAGAGGGGTGAGATGCTGGTCCAGGCCTTCCTGCT
CGCCCTAGGAGCACCTCTTTCTGATTTGCCTCCATGGCCTCCCCACGGCTATATATACCA
CACCTGGTCCTGCTCCTGAGTGTGCTTGAGGGCTGGGCTCTGGGAGGCAGAACCGTGAGA
TGTTCATCCCAGCAGAGAAAGAGACTCACGTCCTACAGACAAAGCCTCCAGAAACTGCTA
GCTGTGTCCTTCTCCAGGGCCACCCCTCAGTGGTGCCACCCGGCCTTAGAGATGATTGTC
AGGCTCTGTCCCCTCTTCAAGGACATTGGTACTACAGCACCACCTGGTGGAAGCACAGAG
TATAAGCTGTCTTCATACTGGGGACACAGCTGGGAAGTCAGACATGTTTTAGTTTTGGTT
CCACTGGGTCAGGATTTGAGGTTCATATAAAAGCCCTGGGTGTTTCTGTCTAATTGCACC
TTGTCTGTTGCTGTTAGGGAAAGGACAATGGTGGGCCTTGATTCACAGGGGTCAGGTACT
CAGAAGGGGCCTCCTGTGAAGGCCATTTGGGTCCTCAGGCTTCCCATGCTATTCACGGGA
CTTGAGTGCTCATTTGGGAGCGAGGGTCCAGAAGCTGAGGCCCAGGGATGGACAGTCCAG
TTCCCGAAGCCCACTTCCCACATGTCGGGTGGGTCAGTCAGTGAGCCTGAGGCTGCCTTG
CAGATGCGGAAGCAGGCATTCCTGGAATCCACTCAGTAAATAAATTCCAGTGTGACTCAG

SEQ ID NO: 55_AA631990_H
GAACAACAATAACAGAATAAGGAAGAAAATCTCATGATTACCTCAATAAGTACAGAGAAA
TCTGGTCACACTCACTATCCATTCATGATTACAACTCTTCAATACTATCGCGGCCGAGGA
GGGAAGACGGCAGTTTGGCGACATTTCTCGGCCGAAGGGCCATTTGCTTTTGCGGAGATG
CGGCATTCCAAAAGAACTCACTGTCCTGATTGGGATAGCAGAGAAAGCTGGGGACATGAA
AGCTATCGTGGAAGTCACAAGCGGAAGAGGAGATCTCATAGTAGCACACAAGAGAACAGG
CATTGTAAACCACATCACCAGTTTAAAGAATCTGATTGTCATTATTTAGAAGCAAGGTCC
TTGAATGAGCGAGATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGT
GAAGGATATGTTCCTAGACATTATCACAGAGACATTGAAAGCGGGTATCGAATCCACTGC
AGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCTAAAAGGAAGCGCAATAGACACTGT
TCAAGTCATCAGTCACGTTCGNATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGC
AAAGTTGTAGAGTGCATTGATCATGGCATGGATGGCATGCATGTAGCAGTGAAAATCGTA
AAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTA
AATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCAT
CATGGTCATGTTTGTATTGTGTTTGAACTACTGGGACTTAGTACTTACGATTTCATTAAA
GAAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGC
CAGTCAATAAATTTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAAT
ATTTTGTTTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGTGATGAA
CGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAT
GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCT
TTAGGTTGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTAC
CTTGGTTTCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA
ATATTAGGACCCATACCACAACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCAC
CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGC
AAACCGTTGAAGGAATTTATGCTTTGTCATGATGAAGAACATGAGAAACTGTTTGACCTG
GTTCGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCAG
CATCCTTTCTTTGACTTATTAAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATA
CTTCTCTAGAAGAGATTACTTAAGACTGTGTCAGTCAACTAAACATTCTAATATTTTTGT
AAACATTAAATTATTTTGTACAGTTAAGTGTAAATATTGTATGTTTTGTATCAATAGCAT
AATTAACTTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAAAATTAATTTT
TCTTTTTGAAATTACCATTTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAAT
GTGATTGATCTTGCCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTTGAGTAAA
AGGAAATCTTGACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGA

FIGURE 2SS

ACTTAACTTTAAAAGTTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAACTCTAG
ATAAGCAGGTACTAGAAACCAAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATT
TTAAGTGTTGTATTCTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAA
AGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAACCACATACACACTTTATTT
AAGATTAAAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGT
GAGTCACAGATATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCC
TTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTAT
AAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAG
GATTTGATTGGAAAGCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAATTTAATTGA
TTGGTTACATAAACTTTTTGACTTCAAT

SEQ ID NO: 56_AA557536_H
AGTAAGGCCCCGCGGGCGTCCTGGCCGCCATGTGCACCGTAGTGGACCCTCGCATTGTCC
GGAGATACCTACTCAGGCGGCAGCTCGGGCAGGGGAGAACATTCCGGGAAATCACGCTCC
TCCAGGTGAGTGGCCTGGGCCCTCCAGTCCAATCCCCTTGCCCAGGTACAGATCTCTCCA
GACAGGAGAGAAACTGGCCTTCTTGGGCCCCAGAGCACAGCCCCTCCTGGCCTTCCAGCC
GCCTCCGACTCTCTCCCCAGGAGTTTGGGGACCATCCCAACATCATCAGCCTCCTTGACG
TGATCCGGGCAGAGAACGACAGGGACATTTACCTGGTGTTTGAGTTTATGGACACTGACC
TGAACGCAGTCATCCGGAAGGGCGGCCTGCTGCAGGACGTCCACGTGCGCTCCATCTTCT
ACCAGCTCCTGCGGGCCACCCGGTTCCTCCACTCGGGGCACGTTGTGCACCGGGACCAGA
AGCCGTCCAATGTGCTCCTGGATGCCAACTGCACAGTGAAGCTGTGTGACTTTGGCCTGG
CCCGCTCCCTGGGCGACCTCCCTGAGGGGCCTGAGGACCAGGCCGTGACAGAGTACGTGG
CCACACGCTGGTACCGAGCACCGGAGGTGCTGCTCTCTTCGCACCGCTACACCGCTTCCT
GCCCCAGATACACCCTTGGGGTGGACATGTGGAGTCTGGGCTGTATCCTGGGGGAGATGC
TGCGGGGGAGACCCCTGTTCCCCGGCACGTCCACCCTCCACCAGCTGGAGCTGATCCTGG
AGACCATCCCACCGCCATCTGAGGAGXXXAGGCCACGACAGACGCTGGATGCCCTCCTAC
CGCCAGACACCTCCCCAGAGGCCTTGGACCTCCTTAGGCGACTCCTGGTGTTCGCCCCGG
ACAAGCGGTTAAGCGCGACCCAGGCACTGCAGCACCCCTACGTGCAGAGGTTCCACTGCC
CCAGCGACGAGTGGGCACGAGAGGCAGATGTGCGGCCCCGGGCACACGAAGGGGTCCAGC
TCTCTGTGCCTGAGTACCGCAGCCGCGTCTATCAGATGATCCTGGAGTGTGGAGGCAGCA
GCGGCACCTCGAGAGAGAAGGGCCCGGAGGGTGTCTCCCCAAGCCAGGCACACCTGCACA
AACCCAGAGCCGACCCTCAGCTGCCTTCTAGGACACCTGTGCAGGGTCCCAGACCCAGGC
CCCAGAGCAGCCCAGGCCATGACCCTGCCGAGCACGAGTCCCCCCGTGCAGCCAAGAACG
TTCCCAGGCAGAACTCCGCTCCCCTGCTCCAAACTGCTCTCCTAGGGAATGGGGAAAGGC
CCCCTGGGGCGAAGGAAGCGCCCCCCTTGACACTCTCGCTGGTGAAGCCAAGCGGGAGGG
GAGCTGCGCCCTCCCTGACCTCCCAGGCTGCGGCTCAGGTGGCCAACCAGGCCCTGATCC
GGGGTGACTGGAACCGGGGCGGTGGGGTGAGGGTGGCCAGCGTACAACAGGTCCCTCCCC
GGCTTCCTCCGGAGGCCCGGCCCGGCCGGAGGATGTTCAGCACCTCTGCCTTGCAGGGTG
CCCAGGGGGGTGCCAGGGCTTTGCTTGGAGGCTACTCCCAAGCCTACGGGACTGTCTGCC
ACTCGGCACTGGGCCACCTGCCCCTGCTGGAGGGGCACCATGTGTGAGCCGCCCTACTCC
CTTCACCTGGCCCTCTGTTCCTGCCCCAGCNCCTTCCCCAGACCCCTCTCCAGTCTCCTG
CACCCCTTAGCCCTCCCTGCTTTGCCTGGCCCGTTGAAGTTCCAGGGAGCTTGCCCGGGT
CTCCTCGGGGGAGCAGATGAGGGCCCTGCCC

SEQ ID NO: 57_N28606_H, MOK_H
ATGAAGAACTATAAAGCAATTGGCAAAATAGGAGAGGGAACGTTTTCTGAAGTTATGAAG
ATGCAAAGCCTGAGAGATGGAAACTACTATGCATGTAAACAAATGAAGCAGCGCTTTGAA
AGTATTGAGCAAGTCAACAACCTACGAGAGATCCAAGCACTGAGGCGCCTGAATCCGCAC
CCAAACATTCTTATGTTGCATGAAGTGGTTTTTGACAGAAAATCTGGTTCTCTTGCACTA
ATATGTGAACTTATGGACATGAATATTTATGAGCTAATACGAGGGAGAAGATACCCATTA

FIGURE 2TT

TCAGAAAAAAAAATTATGCACTATATGTACCAGTTATGTAAGTCCCTGGATCATATTCAC
AGAAATGGAATATTTCACAGAGATGTAAAACCAGAAAATATACTAATAAAGCAGGATGTC
CTGAAATTAGGGGACTTTGGCTCCTGCCGGAGTGTCTATTCCAAGCAGCCGTACACGGAA
TACATCTCCACCCGCTGGTACCGGGCCCCGGAGTGTCTCCTCACTGATGGGTTCTACACG
TACAAGATGGACCTGTGGAGCGCCGGCTGTGTGTTCTACGAGATCGCCAGTCTGCAGCCC
CTCTTTCCTGGAGTAAATGAACTGGACCAAATCTCAAAAATCCACGATGTCATCGGCACA
CCCGCTCAGAAGATCCTCACCAAGTTCAAACAGTCGAGAGCTATGAATTTTGATTTTCCT
TTTAAAAAGGGATCAGGAATACCTCTACTAACAACCAATTTGTCCCCACAATGCCTCTCC
CTCCTGCACGCAATGGTGGCCTATGATCCCGATGAGAGAATCGCCGCCCACCAGGCCCTG
CAGCACCCCTACTTCCAAGAACAGAGGAAAACAGAGAAGCGGGCTCTGGGCAGCCACAGA
AAAGCTGGCTTTCCGGAGCACCCTGTGGCACCGGAACCACTCAGTAACAGCTGCCAGATT
TCCAAGGAGGGCAGAAAGCAGAAACAGTCCCTAAAGCAAGAGGAGGACCGTCCCAAGAGA
CGAGGACCGGCCTATGTCATGGAACTGCCCAAACTAAAGCTTTCGGGAGTGGTCAGACTG
TCGTCTTACTCCAGCCCCACGCTGCAGTCCGTGCTTGGATCTGGAACAAATGGAAGAGTG
CCGGTGCTGAGACCCTTGAAGTGCATCCCTGCGAGCAAGAAGACAGATCCGCAGAAGGAC
CTTAAGCCTGCCCCGCAGCAGTGTCGCCTGCCCACCATAGTGCGGAAAGGCGGAAGATAA

SEQ ID NO: 58_AB023153_H, ICK_H
ATGAATAGATACACAACAATCAGGCAGCTCGGGGATGGAACCTACGGTTCCGTCCTGCTG
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TCCTGGGAGGAATGCATGAACCAACGGGAGGTTAAGTCTTTAAAGAAGCTCAACCATGCC
AATGTAGTCAAATTAAAAGAAGTTATCAGGGAAAATGATCATCTTTATTTTATCTTCGAG
TACATGAAGGAAAATCTTTACCAGCTCATTAAAGAGAGAAATAAGTTGTTTCCTGAGTCT
GCTATAAGGAATATCATGTATCAGATATTACAAGGACTCGCATTTATTCACAAACTCGGC
TTCTTTCATCGAGACTTAAAGCCTGAGAACCTCCTCTGCATGGGACCAGAACTTGTGAAA
ATTGCAGACTTTGGTTTGGCCCGAGAAATACGATCAAAACCTCCATATACAGATTATGTA
TCTACCAGATGGTACAGGGCTCCAGAAGTACTCCTGAGGTCTACCAACTACAGCTCCCCC
ATTGACGTCTGGGCGGTGGGCTGCATCATGGCAGAAGTTTACACCCTCAGGCCACTCTTC
CCTGGAGCCAGTGAAATTGACACAATATTCAAAATTTGCCAAGTGCTGGGGACACCAAAA
AAGACTGACTGGCCTGAAGGCTATCAACTTTCAAGTGCAATGAACTTCCGTTGGCCACAG
TGTGTACCCAATAACTTAAAGACCTTGATTCCCAATGCTAGCAGTGAAGCAGTCCAGCTC
CTGAGAGACATGCTTCAGTGGGATCCCAAGAAACGACCAACAGCTAGTCAGGCACTTCGA
TATCCTTACTTCCAAGTTGGACACCCACTAGGCAGCACCACACAAAACCTTCAGGATTCA
GAAAAACCACAGAAAGGCATCCTGGAAAGGGCAGGCCCACCTCCTTATATTAAGCCAGTC
CCACCTGCCCAGCCACCAGCCAAGCCACACACACGAATTTCTTCACGACAGCATCAAGCC
AGCCAGCCCCCTCTGCATCTCACGTACCCCTACAAAGCAGAGGTCTCCAGGACAGATCAC
CCAAGCCATCTCCAGGAGGACAAGCCAAGCCCGTTGCTTTTCCCATCCCTCCACAACAAG
CATCCACAGTCGAAAATCACAGCTGGCCTGGAGCACAAAAATGGTGAGATAAAGCCAAAG
AGTAGGAGAAGGTGGGGTCTTATTTCCAGGTCAACAAAGGATTCAGATGATTGGGCTGAC
TTGGATGACTTGGATTTCAGTCCATCCCTCAGCAGGATTGACCTGAAAAACAAGAAAAGA
CAGAGTGATGACACTCTCTGCAGGTTTGAGAGTGTTTTGGACCTGAAGCCCTCTGAGCCT
GTGGGCACAGGAAACAGTGCCCCCACCCAGACGTCATATCAGCGGCGAGACACGCCCACC
CTGAGATCTGCAGCCAAGCAGCACTATTTGAAGCACTCTCGATACTTGCCTGGGATCAGT
ATAAGAAATGGCATACTCTCGAATCCAGGCAAGGAATTTATTCCACCTAATCCATGGTCT
AGTTCTGGCTTGTCTGGAAAATCTTCAGGGACAATGTCAGTAATCAGCAAAGTAAATTCA
GTTGGTTCCAGCTCTACAAGTTCTAGTGGACTGACTGGAAACTATGTCCCTTCCTTTCTG
AAAAAAGAAATCGGTTCTGCTATGCAGAGGGTACACCTAGCACCTATTCCAGACCCTTCC
CCTGGTTATTCCTCCCTGAAGGCCATGAGACCTCATCCTGGGCGACCATTCTTGGACACC
CAGCCTAGAAGCACTCCTGGGTTGATACCACGGCCTCCAGCCGCCCAGCCAGTGCATGGC
CGGACAGACTGGGCTTCCAAGTACCCATCCCGGCGGTGA

FIGURE 2UU

SEQ ID NO: 59_AA839940_M
AGCAGCAACAATGGTGGCATGAGTGCAGAGGAGGAGATAGGGCCTGGGGCTGAGCCTATG
AGAGGACCAAGCTTGGCTACAAGGGACTGGAGAGATGAGACTGTTGGGACCACAGACCTG
CAGCAAGGCATAGACCCAGGAGCAGTGAGCCCTGAGCCTGGGAAGGACCACGCAGCCCAG
GGCCCAGGAAGAACTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT
CTAGATGACAGCGCAGCACCCCCAGCCCCTTTTGAACACCGGGTAGTGAGCATCAAAGAT
ACCCTGATCTCAGCAGGCTACACGGTATCCCAACATGAAGTCTTAGGAGGGGGTCGGTTT
GGCCAGGTGCACAGGTGTACAGAGAGGTCTACAGGCCTTGCACTGGCAGCCAAGATCATC
AAAGTGAAGAACGTAAAGGACCGGGAGGATGTGAAGAATGAGGTCAACATCATGAACCAG
CTCAGCCACGTAAACTTGATCCAACTTTATGATGCGTTTGAGAGCAAGAACAGCTTCACT
CTGATCATGGAGTATGTGGATGGAGGCGAACTCTTTGACCGGATCACGGATGAGAAGTAC
CACCTCACTGAGTTGGATGTGGTCTTGTTCACGAGGCAGATCTGTGAGGGTGTGCATTAC
CTGCATCAGCACTATATCCTGCACCTGGACCTCAAGCCTGAGAACATATTGTGTGTCAGC
CAGACAGGGCATCAAATTAAGATCATTGACTTTGGGCTGGCTAGAAGATACAAGCCTCGG
GAGAAGCTAAAGGTGAACTTTGGTACTCCGGAGTTCCTGGCCCCAGAAGTTGTTAACTAT
GAGTTTGTGTCATTTCCAACAGACATGTGGAGTGTGGGAGTTATCACCTACATGCTACTC
AGTGGTTTGTCCCCATTTCTAGGGGAGACAGATGCAGAGACCATGAATTTTATTGTGAAC
TGCAGCTGGGATTTCGATGCTGATACCTTCAAAGGGCTGTCGGAGGAAGCCAAGGACTTT
GTTTCCCGGTTACTGGTCAAAGAGAAGAGCTGTAGGATGAGCGCCACACAGTGCCTGAAA
CACGAGTGGTTAAATCACCTGCCTGCCAAAGCCTCGGGCTCCAACGTTCGCCTCAGATCC
CAACAACTGCTGCAGAAATATATGGCTCAGAGTAAATGGAAGAAACATTTCCACGTGGTG
GCTGCAGTCAACAGGCTACGGAAATTTCCAACGTGTCCCTAATCTTCAACTCTGGTGTTC
CACTGGGCCTGGGAATTCTTGAGGCAACACGAAGTGGTAATATGAAGAGATTACTCAAGA
TTTTATGTAGATTGGCGCTTTGCTATTATTGATTTTTCTTATTTTGCAAAGAATGATGGA
AGGAAGCAAGAAAGAAAGAAAAGAAGAAAAGGGGGAAGAAAAGGAAAAGGCAGAAAGCAA
GGAAACAGGCTACGTTGTTGCTCTTCTTGTAGGTGAAAGTGTTTTTATTAAAAGCCCTAG
GAATGTTTTTCTGCCTCGTAAGGTCAGCAGGTCTCATATGCTGCTTGCTACCCCGCACCC
TTCCTTTTGGTAATAAGAGCAGGCACGCTCAGGATGGGCAGGGAAATCCTACTTGGCTTT
TGGTCAAATTTGAATTCTAAACTTGTCATGATTAAAGAAGCCAGTAGGGAGGGAGGTATG
GAAGAGGGAGGAATTAGGTCCAACAGTGGGGGATGAATTTGACCGAAACATTGTATAAAA
TTCTTAAAGAATTAATAAAATATATTTTTAAAGGAG

SEQ ID NO: 60_AA460132_H
GGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAACCACTTACAGGCCGGAAG
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GGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTCAGAGACAGCTGATCGGTTGGAG
CTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTACGCCGGCCGATGGCGAGGAG
CCCGCCCCGGAGGCTGAGGCTCTGGCCGCAGCCCGGGAGCGGAGCAGCCGCTTCTTGAGC
GGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGTTCCGTGGCCGCTTCCAGGGC
CGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACCGGCACCCGGCGCTGGAGGCG
CGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCGGGCGCTCCTCCGCTGTCGCCGCGCT
GGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTTCCAACTGCTTATATATGGAA
GAAATTGAAGGCTCAGTGACTGTTCGAGATTATATTCAGTCCACTATGGAGACTGAAAAA
ACTCCCCAGGGTCTCTCCAACTTAGCCAAGACAATTGGGCAGGTTTTGGCTCGAATGCAC
GATGAAGACCTCATTCATGGTGATCTCACCACCTCCAACATGCTCCTGAAACCCCCCCTG
GAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTCATTTCAGCACTTCCAGAG
GATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCCTCAGTACCCATCCCAACACT
GAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCCTCCAAAAAGGCCAGGCCA
GTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAAAGAGGTCCATGGTTGGGTAG
AAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTTTCAAAGTAAATTTGAAGAAA

FIGURE 2VV

TGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGATATTTTTAAGTGGTATGTG
ATCGTGTCATTATCATCTGCACTTCACTCAAGAGCTTACTATGTGTCTAAGTCATGTTCT
AGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTTCTCCCAGATTGTGACATGTA
TATCTCAGATACATGGGTGTGGCATTGAACCACATAATGAGAACATTATTCTCTTTTTAG
TCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTCGCTGAGCTTACTGGCCCTCT
AACCCAGTGTTTTTTTTTGTTGTTGTTGTGTACATGTTATATTTATTTTGAAACCAGTTT
AATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATACAGCATGG

SEQ ID NO: 61_SGK034_H
CAGAGAGAGAAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATG
GACACGGAGGAGGGGGTAGAGGTGGTGTGGAACGAGCTCCACTTCGGAGACAGGAAGGCC
TTCGCGGCGCACGAGGAGAAGATCCAGACCGTGTTCGAGCAGCTGGTGCTGGTGGACCAC
CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTC
ATCTTCATCACAGAGTACGTGTCATCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAG
AAGAACCACAAGGCCATGAACGCCCGGGCCTGGAAGCGCTGGTGCACGCAGATCCTGTCT
GCGCTCAGCTTCCTGCACGCCTGCAGCCCCCCAATCATCCACGGGAACCTGACCAGCGAC
ACCATCTTCATTCAGCACAACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTC
TCCAATGCACTTCCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACTTCGG
AACCTGCACTTCTTCCCCCCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATC
TTCTCCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATCCAGACCAATGGGGAC
ACCCGGGTCACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCAACATG
CGGGAGTTCATCCTTTGCTGCCTGGCCCGGGACCCTGCCCGCCGGCCCTCTGCCCACAGC
CTCCTCTTCCACCGCGTGCTCTTCGAGGTGCACTCGCTGAAGCTCCTGGCAGCCCACTGC
TTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTGGAGGAGAAGACCAAGGCCATG
GACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGCAGGCCCCCGCTGCAGTGGCGG
TACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCCTGGAGGATGTCAGGAATGGAATC
TACCCACTGATGAACTTTGCAGCCACTCGACCCCTGGGGCTGCCCCGTGTGCTGGCCCCA
CCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGAGCCCTTTGACTCTGAGACC
AGAAAGGTCATCCAGATGCAGTGCAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCAT
CTCACTCTGCTTCTGGTGCTGGAAGACCGGCTGCACCGGCAGCTGACCTACGACCTGCTC
CCAACGGACAGCGCCCAGGACCTCGCCTCGGAGCTCGTGCACTATGGCTTCCTCCACGAG
GACGACCGGATGAAGCTGGCCGCCTTCCTGGAGAGCACCTTCCTCAAGTACCGTGGGACC
CAGGCCTGACCCGGAGCCCCAGCCCCAGGGGACCATGCCGGGGTGCTGCCCGGGCAGGCC
ATGTTGGGGAGACTCCAGCACCGTGGGGCTGCCCTCCTCCATGCGCCTGGAGCACAAAG
GCCCCGGTAGTGAAGGAACCCCCCGTCTCCTGAGAGTGGGGCTGACCCTGCCTTGGGCGC
CGAGGGGTTGGGGGGTGGGTGTGGGGGAGCCGTTAGGCCTCCCAGGTCCTTAGGATCAGG
GTTGCCCCCAGAACCCCTTCCCATATCCTCCATTCTCCGCCCTGAGTTCCTACCCAGGCT
GCCTGGCTGGGGCCACTGCCTCCTCAGCATGCAGGAGGCTGCCCTGTAGGGAACCCCAGC
TCTGGGGCTTGGGGGTGAGGGTCAGCCCTGGACAGACCTCTGCCCAGGGAACTGCTCCAT
GGGGTCTGGGAGAGCAGCCATCCCCTGCTGGCACCATAGACCCACACAAGGAGCCTGCAC
AGCAAGCCAGCGGTGACACACCTGCAGGTGTCAGGCATGGCACTGGGCACAACAGGGACC
TGGCAGGAGAAACAGACCACAGAGAGGTCTGGAGTTGAGGCTGTTGTCAGCAAAGCCCCT
GGTCCCACACAGCTCTGCCCTAGAGCCACCTCTTTGACCCTTTACCCACCCTGAGACCAG
AACTTGCAGCCCCTCTGCAGATCTCCTCTGGCCACTGCAGCCCCTCCAATGGGCTTTTTC
TCTCATGCATTCCCTGGCCTGGAGGCGTCAGGGACCCCACATCCTCCCTGCTCCTCAGAC
TCACAGCCCCTCCATGTTACCTCCCGCACCTCCTCCCTGGGGCAGCTGCTCCCTGGGCCT
CTGAGGATGTCAGCTCCTGGCTCCCTGCCTCTCTCCCACTCCACTCCTGGCTCAGTCTTA
GAGATTTCTATGCCCTCATGGATTCTACCCCTGCCTTCCTGGCCTCTTGATTCTTGGCTT
GCCTCTCCTCCAATTCCAAACTTAGTGAAATGGCCTTAAGCATTTTAAACTGTATGTATA
CATTAGCGCATTCATGCCTTTCTAAACGCATTTCAAATGTCAACCAGGAAGGCACACCAC

FIGURE 2WW

TGTATTAGTTTTATACTGCCGCTGTAAAATTTACCACAAACTTAGTGACTTAACACAAAT
TTATTGCAATTCTGTAGGCTGGAAGTCTGACTATGGGTCTCACTGGACTAGAATCAAGGC
TGGCAGGCTGCCTTCCTTCCTGGAGGTTCTAGGGGAGACTCTGTCTCCTGCTCCTTCAGG
CTGCTGGCAGAATCCACATCCTTTCGGTGGCAGGGCCAAGGTCCCCACTTTCTTGCTGAC
TGTAAACTAAGGCCACTTCCAGCTTGTAGAGGCTGCCTACATTCCTTGGCTCTTGGCCCC
CTCCTCCATCTTCAGAGCTAGCAGGTTCAGTCTGTGTCACGAACCATTTCTCTGGTTCCC
TGCAGACAGGAAAGGTTGTCCCTAAGGACTCATGAGATTAGGTTGGGCCCAGCCAGATAA
TACATGATAATCTCCCTCCTCAAGGTTTTTAATATTAAACACATCTGCAGGACACATTTT
GCCATGTAAACTAACATTCACTGGTTCCAGGGATTAAGGAATGAACCTCTTTTGTTGGGG
AAGGGTGGCATTCTGCTGACCACAGCACTCCAACCAAAAGCCAAAAACCAAAGCAAGACT
TACTAACGCATATCAAATAAATTAAAGGTACAAAATCGTGAATCTCAGTTATCTTAAATA
TTCCAATACTATTTACAAAATTATTCAAATTCTCACGCCTTCCAACTCAAAATTAGCAAT
CTAAAGTAATTTCCATATCCTAGATGGAAACCCTCATGCTAAACTGTCTGATTATGCATG
GTTCTAAATGGTTTCAGTGGCAAATACATAACATTGTACTACTGATTAAACTGAACTTAA
AAGC

SEQ ID NO: 62_AA103218_M SGK034_M
CCACGCGTCCGCACCAGAGTATGGCGAAGTCAATGATGGGACTGGCTTTGTGGACATCTT
CTCCTTCGGGATGTGTGCACTGGAGATGGCTGTACTCGAGATCCAAGCCAACGGGGATAC
CAGAGTCACAGAAGAGGCCATCGCTCGAGCCAGGCACTCACTGAGTGACCCCAACATGCG
GGAATTCATCCTCTCCTGCCTGGCCCGGGACCCTGCCCGCCGACCCTCAGCCCACAACCT
CCTCTTCCACCGAGTGCTCTTTGAGGTGCACTCGCTGAAGCTGCTGGCAGCTCACTGCTT
CATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTAGAGGAAAAGACCAAGGCCATGGA
CCTCCATGCAGTTTTGGCTGAGATGCCGCAGCCCCATGGACCCCCAATGCAGTGGCGGTA
CTCAGAGGTCTCCTTCTTGGAGCTGGACAAATTCCTAGAGGATGTCAGGAACGGGATCTA
TCCACTGATGAACTTTGCGGCTGCTCGGCCCTTGGGGCTTCCCCGTGTGTTGGCCCCACC
CCCAGAGGAAGCCCAAAAGGCCAAAACTCCAACGCCAGAACCCTTTGACTCGGAGACCAG
GAAGGTGGTCCAGATGCAGTGCAACCTGGAAAGAAGCGAGGACAAGGCTCGGTGGCACCT
TACTCTGCTCTTGGTGCTTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCC
AACGGACAGTGCCCAGGACCTCGCTGCTGAACTAGTGCATTATGGCTTCCTGCACGAGGA
TGACAGGACAAAGCTAGCAGCCTTTCTGGAGACCACTTTTCTCAAGTACCGAGGGACGCA
AGCGTGACCTTCCCAGTCCTGACGGCCCAGCAGAGATACAGGGGCTCAGGGTTGTCCACT
TGGCAAAGAGCCCCCACACTGCTCAAAGCTGCCTTCTGCCTGTGTTCCCTGGAACTGAAC
ACAGGCCCTGCTAGTGAAGACACCCCCACCCCCCAGCTTTCTGCAGCAGTGTGGGACCCT
GGGGTGGTGATGGAGCCCTGAGCCTGGACGAGAGTGGATACAGGTCAGTTAGGGGAACCG
CTCCATCTGGTACTAGACAACAGCCATGCCTTCAGGTGGCATAGAAACCTAGGGAAGGAG
CCTGAACTCAGGTGTCACAGTGCTGGGCATCAGGCAGACCAGACCTGACCTGATTGGAGA
ACTGTAGACTAGATAGCTTGGAGTTGAACCCATGGCCAGGGAATTCCTTGGTCCTGCTCA
GACCAGTCCTGATCCCTTGCAGACCTGCCTTGAGCCCTCTTTCTGATCTTCCACACTCTT
GAGACCAGGACCTGTGTCCTCCCCAAAGCCCTTGGGAAGGATCTTTCTATTCATCATCCC
TCTGGCCTAGGGGCTCAGGGGTCAGGCATCCTCCACATTCCCTCCCTGGGGAAGTTGTGT
GTTTGAGTTGAGGATGTGGGTTCCTGGCTCCCTCTTTCTCCCCAGCCCAACTTGTCTCTT
TCTTACTGGTTTCAAAGTCCTGATGAACGCTTCCCCTCAGAGCCACCCTGGTTTCCTTGG
TTCTTGAACTGCCTCTCTCCCAACTTCAAACCAGGTCTTAAACGTTTTTTAAATGCATAT
ATAAATGTAATGCAGTCACGGTCCTTTTTAAACACTTTGTGTATGAAACCAGGAAAGCTC
ACTATTGTATTAGGAATAGTTCCACATTGCTGCTGTTAACAGATATCATAAACCCAGTGG
TTTGAGACGACACACACACACACACACACACACACACACACAGAGAGAGAGAGAGTTCTGTA
CATCAAGTGTGATCCAGGCTCTCACTAGATTAATACCCAGGCTAAGTTCCTTTCTGGAAG
CTGGGACTTACCTCCTGCTCCTTCAAGCTATTGGCAGAACTCACTTCCCTGCAATGGTAA
GGCAGAAATCCCTATTTTCTCAACAGCTGCCAACTAAGAACCCCTCTCAGCTTCTAGAGG

FIGURE 2XX

CCACCAACTTTTCTTAGTTCTTCTTTCTCCCCCCTCAAGACCAGCAGCGTCAAGTTGAAT
CTTTGTCCTGGGCTAGCTGACTGGCTTGCCACTGCTGGGAAGAGTTGGGGCCTTTTGTGA
GTAGGTTGGACCCACCAGGATAACCGAGGATGATCCCCTTCTCAGGGTCTATAGATGAAC
CACACCTGCGCAGTTCCTTCTGCTGTCATCCTGGGCTTTGGTGCTTGGAGAACAGCCGTG
GGCGGTGGGTGTTGTTACTGTGGTACCTACCATGCCATCTTAACCGAAACCAAGACCTAA
AATAAAACAGATTTGTCATGGGACATCTAATAAATTAAATGAACTCTG

SEQ ID NO: 63_NEK7_H, N34132_H
CACGAATCCGAGCCCGCTCGCCTCTCTCCAGCGAACCGACCATGTCTGGCGGCGCCGCAG
AGAAGCAGAGCAGCACTCCCGGTTCCCTGTTCCTCTCGCCGCCGGCTCCTGCCCCCAAGA
ACGGCTCCAGCTCCGATTCCTCCGTGGGGGAGAAACTGGGAGCCGCGGCCGCCGACGCTG
TGACCGGCAGGACCGAGGAGTACAGGCGCCGCCGCCACACTATGGACAAGGACAGCCGTG
GGGCGGCCGCGACCACTACCACCACTGAGCACCGCTTCTTCCGCCGGAGCGTCATCTGCG
ACTCCAATGCCACTGCACTGGAGCTTCCCGGCCTTCCTCTTTCCCTGCCCCAGCCCAGCA
TCCCCGCGGCTGTCCCGCAGAGTGCTCCACCGGAGCCCCACCGGGAAGAGACCGTGACCG
CCACCGCCACTTCCCAGGTAGCCCAGCAGCCTCCAGCCGCTGCCGCCCCTGGGGAACAGG
CCGTCGCGGGCCCTGCCCCCTCGACTGTCCCCAGCAGTACCAGCAAAGACCGCCCAGTGT
CCCAGCCTAGCCTTGTGGGGAGCAAAGAGGAGCCGCCGCCGGCGAGAAGTGGCAGCGGCG
GCGGCAGCGCCAAGGAGCCACAGGAGGAACGGAGCCAGCAGCAGGATGATATCGAAGAGC
TGGAGACCAAGGCCGTGGGAATGTCTAACGATGGCCGCTTTCTCAAGTTTGACATCGAAA
TCGGCAGAGGCTCCTTTAAGACGGTCTACAAAGGTCTGGACACTGAAACCACCGTGGAAG
TCGCCTGGTGTGAACTGCAGGATCGAAAATTAACAAAGTCTGAGAGGCAGAGATTTAAAG
AAGAAGCTGAAATGTTAAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCCT
GGGAATCCACAGTAAAAGGAAAGAAGTGCATTGTTTTGGTGACTGAACTTATGACGTCTG
GAACACTTAAAACGTATCTGAAAAGGTTTAAAGTGATGAAGATCAAAGTTCTAAGAAGCT
GGTGCCGTCAGATCCTTAAAGGTCTTCAGTTTCTTCATACTCGAACTCCACTTATCATTC
ACCGCGATCTTAAATGTGACAACATCTTTATCACCGGCCCTACTGGCTCAGTCAAGATTG
GAGACCTCGGTCTGGCAACCCTGAAGCGGGCTTCTTTTGCCAAGAGTGTGATAGGTACCC
CAGAGTTCATGGCCCCTGAGATGTATGAGGAGAAATATGATGAATCCGTTGACGTTTATG
CTTTTGGGATGTGCATGCTTGAGATGGCTACATCTGAATATCCTTACTCGGAGTGCCAAA
ATGCTGCGCAGATCTACCGTCGCGTGACCAGTGGGGTGAAGCCAGCCAGTTTTGACAAAG
TAGCAATTCCTGAAGTGAAGGAAATTATTGAAGGATGCATACGACAAAACAAAGATGAAA
GATATTCCATCAAAGACCTTTTGAACCATGCCTTCTTCCAAGAGGAAACAGGAGTACGGG
TAGAATTAGCAGAAGAAGATGATGGAGAAAAAATAGCCATAAAATTATGGCTACGTATTG
AAGATATTAAGAAATTAAAGGGAAAATACAAAGATAATGAAGCTATTGAGTTTTGTTTTG
ATTTAGAGAGAGATGTCCCAGAAGATGTTGCACAAGAAATGGTAGAGTCTGGGTATGTCT
GTGAAGGTGATCACAAGACCATGGCTAAAGCTATCAAAGACAGAGTATCATTAATTAAGA
GGAAACGAGAGCAGCGGCAGTTGGTACGGGAGGAGCAAGAAAACAAAAAGCAGGAAGAGA
GCAGTCTCAAACAGCAGGTAGAACAATCCAGTGCTTCCCAGACAGGAATCAAGCAGCTCC
CTTCTGCTAGCACCGGCATACCTACTGCTTCTACCACTTCAGCTTCAGTTTCTACACAAG
TAGAACCTGAAGAACCTGAGGCAGATCAACATCAACAACTACAGTACCAGCAACCCAGTA
TATCTGTGTTATCTGATGGGACGGTTGACAGTGGTCAGGGATCCTCTGTCTTCACAGAAT
CTCGAGTGAGCAGCCAACAGACAGTTTCATATGGGTTCCCAANNCATGAACAGGCACATT
CTACAGGCACAGTCCCAGGGCATATACCTTCTACTGTCCAAGCACAGTCTCAGCCCCATG
GGGTATATCCACCCTCAAGTGTGCAGCAGGGAATACAGCAGACAGCCCCTCCTCAACAGA
CAGTGCAGTATTCACTTTCACAGACATCAACCTCCAGTGAGGCCACTACTGCACAGCCAG
TGAGTCAGCCTCAAGCTCCACAAGTCTTGCCTCAAGTATCAGCTGGAAAACAGAGTACTC
AGGGAGTCTCTCAGGTTGCTCCTGCAGAGCCAGTTGCAGTAGCACAGCCCCAAGCTACCC
AGCCGACCACTTTGGCTTCCTCTGTAGACAGTGCACATTCAGATGTTGCTTCAGGTATGA
GTGATGGCAATGAGAACGTCCCATCTTCCAGTGGAAGGCATGAAGGAAGAACTACAAAAC

FIGURE 2YY

GGCATTACCGAAAATCTGTAAGGAGTCGCTCTCGACATGAAAAAACTTCACGCCCAAAAT
TAAGAATTTTGAATGTTTCAAATAAAGGAGACCGAGTAGTAGAATGTCAATTAGAGACTC
ATAATAGGAAAATGGTTACATTCAAATTTGACCTAGATGGTGACAACCCCGAGGAGATAG
CAACAATTATGGTGAACAATGACTTTATTCTAGCAATAGAGAGAGAGAGTCGTTTGTGGATC
AAGTGCGAGAAATTATTGAAAAAGCTGATGAAATGCTCAGTGAGGATGTCAGTGTGGAAC
CAGAGGGTGATCAGGGATTGGAGAGTCTACAAGGAAAGGATGACTATGGCTTTTCAGGTT
CTCAGAAATTGGAAGGAGAGTTCAAACAACCAATTCCTGCGTCTTCCATGCCACAGCAAA
TAGGCATTCCTACCAGTTCTTTAACTCAAGTTGTTCATTCTGCGGGAAGGCGGTTTATAG
TGAGTCCTGTGCCAGAAAGCCGATTACGAGAATCAAAAGTTTTCCCCAGTGAAATAACAG
ATACAGTTGCTGCCTCTACAGCTCAGAGCCCTGGAATGAACTTGTCTCACTCTGCATCAT
CCCTTAGTCTACAACAGGCCTTTTCTGAACTTAGACGTGCCCAAATGACAGAAGGACCCA
ATACAGCACCTCCAAACTTTAGTCATACAGGACCAACATTTCCAGTAGTACCTCCTTTCT
TAAGTAGCATTGCTGGAGTCCCAACCACAGCAGCAGCCACAGCACCAGTCCCTGCAACAA
GCAGCCCTCCTAATGACATTTCCACATCAGTAATTCAGTCTGAGGTTACAGTGCCCACTG
AAGAGGGGATTGCTGGAGTTGCCACCAGCACAGGTGTGGTAACTTCAGGTGGTCTCCCCA
TACCACCTGTGTCTGAATCACCAGTACTTTCCAGCGTAGTTTCAAGTATCACAATACCTG
CAGTTGTCTCAATATCTACTACATCCCCGTCACTTCAAGTCCCCACATCCACATCTGAGA
TCGTTGTTTCTAGTACAGCACTGTATCCTTCAGTAACAGTTTCAGCAACTTCAGCCTCTG
CAGGGGGCAGTACTGCTACCCCAGGTCCTAAGCCTCCAGCTGTAGTATCTCAGCAGGCAG
CAGGCAGCACTACTGTGGGAGCCACATTAACATCAGTTTCTACCACCACTTCATTCCCAA
GCACAGCTTCACAGCTGTCCATTCAGCTTAGCAGCAGTACTTCTACTCCTACTTTAGCTG
AAACCGTGGTAGTTAGCGCACACTCACTAGATAAGACATCTCATAGCAGTACAACTGGAT
TGGCTTTCTCCCTCTCTGCACCATCTTCCTCTTCCTCTCCTGGAGCAGGAGTGTCTAGTT
ATATTTCTCAGCCTGGTGGGCTGCATCCTTTGGTCATTCCATCAGTGATAGCTTCTACTC
CTATTCTTCCCCAAGCAGCAGGACCTACTTCTACACCTTTATTACCCCAAGTACCTAGTA
TCCCACCCTTGGTACAGCCTGTTGCCAATGTGCCTGCTGTACAGCAGACACTAATTCATA
GTCAGCCTCAACCAGCTTTGCTTCCCAACCAGCCCCATACTCATTGTCCTGAAGTAGATT
CTGATACACAACCCAAAGCTCCTGGAATTGATGACATAAAGACTCTAGAAGAAAAGCTGC
GGTCTCTGTTCAGTGAACACAGCTCATCTGGAGCTCAGCATGCCTCTGTCTCACTGGAGA
CCTCACTAGTCATAGAGAGCACTGTCACACCAGGCATCCCAACTACTGCTGTTGCACCAA
GCAAACTCCTGACTTCTACCACAAGTACTTGCTTACCACCAACCAATTTACCACTAGGAA
CAGTTGCTTTGCCAGTTACACCAGTGGTCACACCTGGGCAAGTTTCTACCCCAGTCAGCA
CTACTACATCAGGAGTGAAACCTGGAACTGCTCCCTCCAAGCCACCTCTAACTAAGGCTC
CGGTGCTGCCAGTGGGTACTGAACTTCCAGCAGGTACTCTACCCAGCGAGCAGCTGCCAC
CTTTTCCAGGACCTTCTCTAACCCAGTCCCAGCAACCTCTAGAGGATCTTGATGCTCAAT
TGAGAAGAACACTTAGTCCAGAGATGATCACAGTGACTTCTGCGGTTGGTCCTGTGTCCA
TGGCGGCTCCAACAGCAATCACAGAAGCAGGAACACAGCCTCAGAAGGGTGTTTCTCAAG
TCAAAGAAGGCCCTGTCCTAGCAACTAGTTCAGGAGCTGGTGTTTTTAAGATGGGACGAT
TTCAGGTTTCTGTTGCAGCAGACGGTGCCCAGAAAGAGGGTAAAAATAAGTCAGAAGATG
CAAAGTCTGTTCATTTTGAATCCAGCACCTCAGAGTCCTCAGTGCTATCAAGTAGTAGTC
CAGAGAGTACCTTGGTGAAACCAGAGCCGAATGGCATAACCATCCCTGGTATCTCTTCAG
ATGTGCCAGAGAGTGCCCACAAAACTACTGCCTCAGAGGCAAAGTCAGACACTGGGCAGC
CTACCAAGGTTGGACGTTTTCAGGTGACAACTACAGCAAACAAAGTGGGTCGTTTCTCTG
TATCAAAAACTGAGGACAAGATCACTGACACAAAGAAAGAAGGACCAGTGGCATCTCCTC
CTTTTATGGATTTGGAACAAGCTGTTCTTCCTGCTGTGATACCAAAGAAAGAGAAGCCTG
AACTGTCAGAGCCTTCACATCTAAATGGGCCGTCTTCTGACCCGGAGGCCGCTTTTTTAA
GTAGGGATGTGGATGATGGTTCCGGTAGTCCACACTCGCCCCATCAGCTGAGCTCAAAGA
GCCTTCCTAGCCAGAATCTAAGTCAAAGCCTTAGTAATTCATTTAACTCCTCTTACATGA
GTAGCGACAATGAGTCAGATATCGAAGATGAAGACTTAAAGTTAGAGCTGCGACGACTAC
GAGATAAACATCTCAAAGAGATTCAGGACCTGCAGAGTCGCCAGAAGCATGAAATTGAAT

FIGURE 2ZZ

CTTTGTATACCAAACTGGGCAAGGTGCCCCCTGCTGTTATTATTCCCCCAGCTGCTCCCC
TTTCAGGGAGAAGACGACGACCCACTAAAAGCAAAGGCAGCAAATCTAGTCGAAGCAGTT
CCTTGGGGAATAAAAGCCCCCAGCTTTCAGGTAACCTGTCTGGTCAGAGTGCAGCTTCAG
TCTTGCACCCCCAGCAGACCCTCCACCCTCCTGGCAACATCCCAGAGTCCGGGCAGAATC
AGCTGTTACAGCCCCTTAAGCCATCTCCCTCCAGTGACAACCTCTATTCAGCCTTCACCA
GTGATGGTGCCATTTCAGTACCAAGCCTTTCTGCTCCAGGTCAAGGTAATAAAGCAACCA
TCATCGTCCAAAAACAATAAAATGGAGATGTTGCCATACCTGGGACAAAAGCCTGTTAAG
GCGGGTTGGGAGACTAGCTGACCAGAACACAGCCTGTGTGTTGTACACTGAAGAATCTGG
GTGAAAAGGGAAGTGGAGTGATAATGAGAATCGGTGGGCTCACTGCTCCCATTAGGTGAA
ATTACTTTTTTTCAAGGAATTACAGTGAAAAGTTACATCTGTGTGGCCTATATGACTTGC
TCATTTGGGATTTGGAACTTAGGCTTTAATATTAGGCTGAGATTTCCTGGATGAAATTCT
AAGGTGTTTTAGCAGTTTCTGAAGCTAATACATTTTCTTAGCCATTGTAGAATTTTGTTA
CTTTTAAGTATGGGAGTGGCATACTAAAATGAATAACCTTACAATTCAGTTTTTTATCCA
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GAAAGAGCTTTTAGTCATATTAGAACAAGAATTGAAAAGACTTGGGCATCTGGGTGAGAA
GAATGAAAAAAATATAGGTACTGGCTTATGTGCCTTTGCCACAGTTTCACAGAAATTAGA
GATCAGTCTCTTCACAGGAAGAATGCACTTGATTGGTAAGGAGGGCAAACTAGCTAGCAT
TATTCGAACTAAGAAAAGCTTCCGCATTTTGCAGATGGTAGAATTAAGACCTAATATTT
CATCTCTTACATATCTGACCTTCCCCCCAGAAGCTTGTTCTTCTGTGTGCCATCTTAGTG
CATTTCACCACTCCAGCCTCAAGTTTCTAACATCTTGTAGTTGTGTTCTGTCTCTTCTCC
TCTCTCTGTTCTACCCTGTTTTTCCCCTCTCACAGGCTGTGCGAAGTTTAACTGTGCATC
TGAACAGGTGACATTCAAACCTGGTGGCAGGAGGACCCGATTTCTGAGTACGCCCTGCTT
GGCTCTTTGTGTGTAACACCTTTACTCCTTCCTTGTCCTTGTGTTTCTGCTGCTTGGATC
TGATGTTTCACGCAGTCCATTTTCATTTGTCTCTTTTTGTATATCATCTACTCAGTGGCT
TGGCTGAATTACTGTTACCCTCAGAAGTTTGGGCCCCCACATTAATTATGATAAAAAATG
TCAAAATAACAAGTTATCTACAAATTTCAATGTAACTTTCTGGTAGAAGTGCTTCTTCAT
GGATCTGTGACAGAGAGTGGATATGGTATCTAGGCAATAGATTGCTGGGTCATTTAGAAT
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GAGAGAAATCAGCCAGACACGGTGGCGTACACCTGTAATCCCAGCACTTTGGGAGGCCGA
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CCATCTCT

SEQ ID NO: 64_BCON3_H
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GGGGGAGTCCCAGACAGTACTTAGCAGTGGCTCAGACCCAAAGGTAGAATCCTCATCTTC
AGCTCCTGGCCTGACATCAGTGTCACCTCCTGTGACCTCCACAACCTCAGCTGCTTCCCC
AGAGGAAGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTGGAAGAGTCGCCCTGTGGGCG
CTGGCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATA
CCTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGTGGAATGAGGTACAGTTCTCTGA
ACGCAAGAACTACAAGCTGCAGGAGGAAAAGGTTCGTGCTGTGTTTGATAATCTGATTCA
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GGCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAA
GAAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACACA
AATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCCATCATCCATGGGAACCT
GACCTGTGACACCATCTTCATCCAGCACAACGGACTCATCAAGATTGGCTCTGTGGCTCC
TGACACTATCAACAATCATGTGAAGACTTGTCGAGAAGAGCAGAAGAATCTACACTTCTT
TGCACCAGAGTATGGAGAAGTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGG
CATGTGTGCACTGGAGATGGCAGTGCTGGAGATTCAGGGCAATGGAGAGTCCTCATATGT
GCCACAGGAAGCCATCAGCAGTGCCATCCAGCTTCTAGAAGACCCATTACAGAGGGAGTT

FIGURE 2AAA

CATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTT
CCACCCAGCATTGTTTGAAGTGCCCTCGCTCAAACTCCTTGCGGCCCACTGCATTGTGGG
ACACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACCAAAAACATGGATACTAG
TGCCGTACTGGCTGAAATCCCTGCAGGACCAGGAAGAGAACCAGTTCAGACTTTGTACTC
TCAGTCACCAGCTCTGGAATTAGATAAATTCCTTGAAGATGTCAGGAATGGGATCTATCC
TCTGACAGCCTTTGGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACC
TGTCGTGCCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAA
GGTGGTGCTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGGAGTCAAACACCACCTGAC
ACTTCTGCTGAAGTTGGAGGACAAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAA
TGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGA
CCAGAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTGCCAGGAA
CAGTACCCTCAACTCAGCCGCTGTCACCGTCTCCTCTTAGAGCTCACTCGGGCCAGGCCC
TGATCTGCGCTGTGGCTGTCCCTGGACGTGCTGCAGCCCTCCTGTCCCTTCCCCCCAGTC
AGTATTACCCTGTGAAGCCCCTTCCCTCCTTTATTATTCAGGAGGGCTGGGGGGGCTCCC
TGGTTCTGAGCATCATCCTTTCCCCTCCCCTCTCTTCCTCCCCTCTGCACTTTGTTTACT
TGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCGCCTTCTAGTTGGGGGCTAGT
CGCTGATCTGCCGGCTCCCGCCCAGCCTGTGTGGAAAGGAGGCCCACGGGCACTAGGGGA
GCCGAATTCTACAATCCCGCTGGGGCGGCCGGGGCGGGAGAGAAAGGTGGTGCTGCAGTG
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GCT

SEQ ID NO: 65_AA711829_M
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ATTGGCTCTGTGGCTCCTGACACTATCAACAATCACGTGAAGACTTGCCGGGAAGAACAG
AAGAACCTACACTTTTTTGCACCAGAGTATGGAGAAGTCACAAACGTGACAACAGCAGTG
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GGCGAGTCCTCATATGTGCCACAGGAAGCCATCAGCAGTGCCATCCAGCTACTAGAAGAC
TCATTACAGAGGGAGTTTATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGGAGACCAACA
GCCAGAGAACTTCTGTTCCACCCAGCACTGTTTGAAGTGCCCTCACTCAAGCTTCTTGCT
GCTCACTGTATCGTGGGGCACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACC
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GTTCAGACTTTGTACTCTCAGTCACCAGCCCTAGAATTAGACAAATTCCTTGAAGATGTC
AGGAATGGGATCTACCCTCTGACAGCCTTTGGGCTACCTCGGCCTCAGCAGCCACAGCAG
GAGGAGGTGACATCACCTGTTGTGCCCCCCTCTGTCAAGACTCCAACTCCTGAGCCAGCT
GAAGTGGAGACACGAAAGGTGGTGCTGATGCAGTGCAACATCGAATCTGTGGAGGAGGGA
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TGTGACCTGATGCCAAATGAGAGCATCCCGGACTTGGCAGCTGAGCTGGTGCAGCTGGGC
TTCATTAGTGAGGCTGATCAGAGCCGCCTGACTTCTCTGCTGGAGGAGACGCTCAACAAG
TTCAACTTCACCAGGAACAGTACACTCAACACAGCCACTGTCACCGTCTCCTCGTAGAGC
TCACTTGAGCCAGGCCCCTAGCCAGGCTGTGGCTGTCCCTGGGCATGCTGCAGTCCTCCT
GTCCCTTCTCCCCAGTCAGTATTACCCTTCGCGCCCATATTATTTAGGAGGGCTTTAGGG
GCTCCCTGGTTGAGTATCACCCTGCCCCTTCCCCTCTCTTCCTCCCCTCTGCACTTTGTT
TACTTGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCACCTTCTAGCTGGGGGC
TAGTAGCTGACCTGCTGCCTCCTGCCCTACTTGTGTGGACAGGAGGCCCACGGGCACTGG
GGAAGCTGAGTTCTACAATCCCGCTGGGGCGCATGGGCAGGAGAGAAAGGTGGTGCTGCA
GGGGTGGCCCCCCGGGGGGGGCATTCGAATCACCTCAGTTGCTGCTGTAATAAAGTCTAC
TTTTTGCT

FIGURE 2BBB

SEQ ID NO: 66_AA099102_H
ATGTCATCATGTGTCTCTAGCCAGCCCAGCAGCAACCGGGCCGCCCCCCAGGATGAGCTG
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GGCTGTGCTGTGGACCTCGGCTTGGCGCGGGACCGGCCCCTGGAGGCCGATGGCCAAGAG
GTCCCCCTTGACACCTCCGGGTCCCAGGCCCGGCCCCACCTCTCCGGTCGCAAGCTGTCT
CTGCAAGAGCGGTCCCAGGGTGGGCTGGCAGCCGGTGGCAGCCTGGACATGAACGGACGC
TGCATCTGCCCGTCCCTGCCCTACTCACCCGTCAGCTCCCCGCAGTCCTCGCCTCGGCTG
CCCCGGCGGCCGACAGTGGAGTCTCACCACGTCTCCATCACGGGTATGCAGGACTGTGTG
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TTGGCCTACAATGAAAATGACAATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAAG
CTGATCCGGCAGGCCGCTTTTCCACGTCGCCCTCCACCCCGAGGCACCCGGCCAGCTCCT
GGAGGCTGCATCCAGCCCAGGGGCCCCATTGAGCAGGTGTACCAGGAAATTGCCATCCTC
AAGAAGCTGGACCACCCCAATGTGGTGAAGCTGGTGGAGGTCCTGGATGACCCCAATGAG
GACCATCTGTACATGGTGTTCGAACTGGTCAACCAAGGGCCCGTGATGGAAGTGCCCACC
CTCAAACCACTCTCTGAAGACCAGGCCCGTTTCTACTTCCAGGATCTGATCAAAGGCATC
GAGTACTTACACTACCAGAAGATCATCCACCGTGACATCAAACCTTCCAACCTCCTGGTC
GGAGAAGATGGGCACATCAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAAGGGCAGT
GACGCGCTCCTCTCCAACTACGTGGGCACGCCCGCCTTCATGGCTCCCGAGTCGCTCTCT
GAGACCCGCAAGATCTTCTCTGGGAAGGCCAAGGATGTTTGGGCCATGGGTGTGACACTA
TACTGCTTTGTCTTTGGCCAGTGCCCATTCATGGACGAGCGGATCATGTGTTTACACAGT
AAGATCAAGAGTCAGGCCCTGGAATTTCCAGACCAGCCCGACATAGCTGAGGACTTGAAG
GACCTGATCACCCGTATGCTGGACAAGAACCCCGAGTCGAGGATCGTGGTGCCGGAAATC
AAGCTGCACCCCTGGGTCACGAGGCATGGGGCGGAGCCGTTGCCGTCGGAGGATGAGAAC
TGCACGCTGGTCGAAGTGACTGAAGAGGAGGTCGAGAACTCAGTCAAACACATTCCCAGC
TTGGCAACCGTGATCCTGGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTC
GAGGGCAGCCGGCGGGAGGAACGCTCACTGTCAGCGCCTGGAAACTTGCTCACCAAAAAA
CCAACCAGGGAATGTGAGTCCCTGTCTGAGCTCAAGGAAGCAAGGCAGCGAAGACAACCT
CCAGGGCACCGACCCGCCCCCCGTGGGGGAGGAGGAAGTGCTCTTGTGAGAGGCAGTCCC
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CCGGAGGAGGCCATGGAGCCCGAGTAG

SEQ ID NO: 67_5R69_17_2_H
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CCCTCAGGTAGGGATCGGGGCGCCTTGTCGCCGCCAGCCACGTGTGGCGTCCGGTACAGT
CAGCAGAGTGCAGGGTGCGGGCACCAGGAAAGGGGGCGCAGGGGAACTCCCGCGGGCCTC
GCGTTTGCAAACTTCTCGCCTGGGCAGGAGGCGGTCGTGGGAAAGAAGGTGGAAGAGCGA
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TGGAAAATTTGAAGCATATTATCACCCTTGGCCAGGTCATCCACAAACGGTGTGAAGAGA
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GCATGCCTGTTTCACCCATAAGCCAAGGAGCGTCCTGGGCACAGGAAGATCAGCAGGATG
CAGACGAAGACAGGCGAGCTTTCCAGATGCTAAGAAGAGATAATGAAAAAATAGAAGCTT
CACTGAGACGATTAGAAATCAACATGAAAGAAATCAAGGAAACTTTGAGGCAGTGTAAGT
TATCATGTGCCCTGCTGTTTCTGATGGCCCCCAAACTAGAAGTCATCAGTTTACTGGGAC

FIGURE 2CCC

CCCAGCCTCCCGCTACCCCTGCATTTGTCCATTTTCTGTGCTGGATGGCTGGAAGCAGCC
CACAGGTTTGGGGATCCATTCATGGCTAGCCCAGGCTTCTGTCCATGGAATAACATGTGG
AGAGAGCTTCTTGACCAGTAAGATACCTTCTAGCAGCTGTCAAAGTACTTAAAAACCTCT
ATGAATAGAATCAAAGCTTCAGTTCAGTTGCTGAATTTCCAAGAAGAAATTCAAATCAAA
TTTAAAATGCCCACTCATTCATTCATTCAACAAAACTGTGAGTATCTGGTTTATGCCAGA
GGCCATGCAAAGAGGTAACTAAGATGCAGAGAAGGACACTGCCTTCCAGGAGCTCACGGG
GTGGAGGAGGAAAGAGGAAAGACAGACAGTGAACACACAACAGCAAGGTTACTGAGCTTG
AACTATGTCCCTAACTACTAGATCTGAAATGACTACGCCAGATGCCAGATGCTCAAGTGC
CAAGCTCTGGGTAACAGGAATAGACATCCTTCCAGGATGAGAGAGATGAGTCTGGATGAG
GGTTAAGGCTGGAGGGACAGGCGGGATTTGAAGAGGAGGGAAAGGAAGTGGATGACACAT
TCTGTTAACTGTCCAGCTGTGTCTCTACTGGTCACTCAGAGGCACGGGAGCCGCTCCCTT
GGGCTGAGTCCATCAGAAGCCCCAGCCACCACCAGCTCTGGTTCATGTAGTAGAGCTTCC
CACTCACACATCACAAATATGCCACCTCCCTTAGGACCCCTTCCTCTGCTCATTGACTCT
TTTGTCTTCTTTCCTCTCGGGGGTGAGGTCAGATTTACCACCAAAATGCATGCAGGAGAT
CCCGCAAGAGCAAATCAAGGAGATCAAGAAGGAGCAGCTTTCAGGATCCCCGTGGATTCT
GCTAAGGGAAAATGAAGTCAGCACACTTTATAAAGGAGAATACCACAGAGCTCCAGTGGC
CATAAAAGTATTCAAAAAACTCCAGGCTGGCAGCATTGCAATAGTGAGGCAGACTTTCAA
TAAGGAGATCAAAACCATGAAGAAATTCGAATCTCCCAACATCCTGCGTATATTTGGGAT
TTGCATTGATGAAACAGTGACTCCGCCTCAATTCTCCATTGTCATGGAGTACTGTGAACT
CGGGACCCTGAGGGAGCTGTTGGATAGGGAAAAAGACCTCACACTTGGCAAGCGCATGGT
CCTAGTCCTGGGGGCAGCCCGAGGCCTATACCGGCTACACCATTCAGAAGCACCTGAACT
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AGATATCCCGTTTCAAGGTGAAGAATGTGAAGACTGGCTCAGCCAGTGGCTGTAATTCTG
AGAAGATCCGCAAGCTGGTGGCTGTGAAGCGGCAGCAGGAGCCACTGGGTGAAGACTGCC
CTTCAGAGCTGCGGGAGATCATTGATGAGTGCCGGGCCCATGATCCCTCTGTGCGGCCCT
CTGTGGATGAAATCTTAAAGAAACTCTCCACCTTTTCTAAGTAGTGTATCAAAATCTAAA
CCAAGGAGTCTCTGGACAAGAAGCTGGGAGAGGCACGAACTGGACATCTCTCTCTCTCAT
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CCTCTGACAGTAACTTTGATAGATGGTTTGTCAAATGTATCTTTCTGGGTATCCACACCT
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CATGGACATGTTGAGTGAGCATGCTGGAGAATGAGAGACCACATGAAGCAGAAACATGCT
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GAGCTAAATAAATTACTGTTGTCTTTT

SEQ ID NO: 68_H85811_H
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CGATGGCCCCCGTGTACGAAGGTATGGCCTCACATGTGCAAGTTTTCTCCCCTCACACCC
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ACATGACTGGGTACGGCTCCCACAGCAAAGTGTATAGCCAGAGCAAGAACATCCCCCTGT
CGCAGCCAGCCACCACAACCGTCAGCACCTCCTTGCCGGTCCCAAACCCAAGCCTACCTT
ACGAGCAGACCATCGTCTTCCCAGGAAGCACCGGGCACATCGTGGTCACCTCAGCAAGCA

FIGURE 2DDD

GCACTTCTGTCACCGGGCAAGTCCTCGGCGGACCACACAACCTAATGCGTCGAAGCACTG
TGAGCCTCCTTGATACCTACCAAAAATGTGGACTCAAGCGTAAGAGCGAGGAGATCGAGA
ACACAAGCAGCGTGCAGATCATCGAGGAGCATCCACCCATGATTCAGAATAATGCAAGCG
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GCGAGGGCGACTATCAGCTGGTGCAGCATGAGGTACTGTGCTCCATGACCAACACCTACG
AGGTCTTAGAGTTCTTGGGCCGAGGGACGTTTGGGCAAGTGGTCAAGTGCTGGAAACGGG
GCACCAATGAGATCGTAGCCATCAAGATCCTGAAGAACCACCCATCCTATGCCCGACAAG
GTCAGATTGAAGTGAGCATCCTGGCCCGGTTGAGCACGGAGAGTGCCGATGACTATAACT
TCGTCCGGGCCTACGAATGCTTCCAGCACAAGAACCACACGTGCTTGGTCTTCGAGATGT
TGGAGCAGAACCTCTATGACTTTCTGAAGCAAAACAAGTTTAGCCCCTTGCCCCTCAAAT
ACATTCGCCCAGTTCTCCAGCAGGTAGCCACAGCCCTGATGAAACTCAAAAGCCTAGGTC
TTATCCACGCTGACCTCAAACCAGAGAACATCATGCTGGTGGATCCATCTAGACAACCAT
ACAGAGTCAAGGTCATCGACTTTGGTTCAGCCAGCCACGTCTCCAAGGCTGTGTGCTCCA
CCTACTTGCAGTCCAGATATTACAGGGCCCCTGAGATCATCCTTGGTTTACCATTTTGTG
AGGCAATTGACATGTGGTCCCTGGGCTGTGTTATTGCAGAATTGTTCCTGGGTTGGCCGT
TATATCCAGGAGATTCGGAGTATGATCAGATTCGGTATATTTCACAAACACAGGGTTTGC
CTGCTGAATATTTATTAAGCGCCGGGACAAAGACAACTAGGTTTTTCAACCGTGACACGG
ACTCACCATATCCTTTGTGGAGACTGAAGACACCAGATGACCATGAAGCAGAGACAGGGA
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ACATGACGACAGATTTGGAAGGGAGCGACATGTTGGTAGAAAAGGCTGACCGGCGGGAGT
TCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCACTCCAATCG
AAACCCTGAACCATCCCTTTGTCACCATGACACACTTACTCGATTTTCCCCACAGCACAC
ACGTCAAATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACA
CGGTGAACCAGAGCAAAACCCCTTTCATCACGCACGTGGCCCCCAGCACGTCCACCAACC
TGACCATGACCTTTAACAACCAGCTGACCACTGTCCACAACCAGCCCTCAGCGGCATCCA
TGGCTGCAGTGGCCCAGCGGAGCATGCCCCTGCAGACAGGAACAGCCCAGATTTGTGCCC
GGCCTGACCCGTTCCAGCAAGCTCTCATCGTGTGTCCCCCCGGCTTCCAAGGCTTGCAGG
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GGCCAAGTGGGACCCAGCAGATCCTGCTTCCCCCAGCATGGCAGCAACTGACTGGAGTGG
CCACCCACACCTCAGTGCAGCATGCCACCGTGATTCCCGAGACCATGGCAGGCACCCAGC
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AGCCTGCACTATTGACCGGTCATGTGACCCTTCCAGCAGCACAGCCCTTAAATGTGGGTG
TGGCCCACGTGATGCGGCAGCAGCCAACCAGCACCACCTCCTCCCGGAAGAGTAAGCAGC
ACCAGTCATCTGTGAGAAATGTCTCCACCTGTGAGGTGTCCTCCTCTCAGGCCATCAGCT
CCCCACAGCGATCCAAGCGTGTCAAGGAGAACACACCTCCCCGCTGTGCCATGGTGCACA
GTAGCCCGGCCTGCAGCACCTCGGTCACCTGTGGGTGGGGCGACGTGGCCTCCAGCACCA
CCCGGGAACGGCAGCGGCAGACAATTGTCATTCCCGACACTCCCAGCCCCACGGTCAGCG
TCATCACCATCAGCAGTGACACGGACGAGGAGGAGGAACAGAAACACGCCCCCACCAGCA
CTGTCTCCAAGCAAAGAAAAAACGTCATCAGCTGTGTCACAGTCCACGACTCCCCCTACT
CCGACTCCTCCAGCAACACCAGCCCCTACTCCGTGCAGCAGCGTGCTGGGCACAACAATG
CCAATGCCTTTGACACCAAGGGGAGCCTGGAGAATCACTGCACGGGGAACCCCCGAACCA
TCATCGTGCCACCCCTGAAAACCCAGGCCAGCGAAGTATTGGTGGAGTGTGATAGCCTGG
TGCCAGTCAACACCAGTCACCACTCGTCCTCCTACAAGTCCAAGTCCTCCAGCAACGTGA
CCTCCACCAGCGGTCACTCTTCAGGGAGCTCATCTGGAGCCATCACCTACCGGCAGCAGC
GGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCAGGCTCAGCAGCACA
TCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCCTACATCACTCCCACCATGG
CCCAGGCTCCGTACTCCTTCCCGCACAACAGCCCCAGCCACGGCACTGTGCACCCGCATC
TGGCTGCAGCCGCTGCCGCTGCCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTG
CGCCGGCGGCCCTGGGCTCCACCGGCACCGTGGCCCACCTGGTGGCCTCGCAAGGCTCTG

FIGURE 2EEE

CGCGCCACACCGTGCAGCACACTGCCTACCCAGCCAGCATCGTCCACCAGGTCCCCGTGA
GCATGGGCCCCCGGGTCCTGCCCTCGCCCACCATCCACCCGAGTCAGTATCCAGCCCAAT
TTGCCCACCAGACCTACATCAGCGCCTCGCCAGCCTCCACCGTCTACACTGGATACCCAC
TGAGCCCCGCCAAGGTCAACCAGTACCCTTACATATAAACACTGGAGGGGAGGGAGGGAG
GGAGGGAGGGAGAGAATGGCCCGAGGGAGGAGGGAGAGAAGGAGGGAGGCGCTCCTGGGA
CCGTGGGCGCTGGCCTTTTATACTGAAGATGCCGCACACAAACAATGCAAACGGGGCAGG
GGCGGGGGGGGGGGGCAGAGGGCAGGGGGACGGGTCGGGACACCAGTGAAACTTGAACC
GGGAAGTGGGAGGACGTAGAGCAGAGAAGAGAACATTTTTAAAAGGAAGGGATTAAAGAG
GGTGGGAAATCTATGGTTTTTATTTTAAAAAAG

SEQ ID NO: 69_DYRK3_H
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GGATGCGGGGCCGCCTGGGGCCGGGCTCCCGCCCCAGCAGCGGAGTTGGGGGATGGTGTC
TATGACACCTTCATGATGATAGATGAAACCAAATGTCCCCCCTGTTCAAATGTACTCTGC
AATCCTTCTGAACCACCTCCACCCAGAAGACTAAATATGACCGCTGAGCAGTTTACAGGA
GATCATACTCAGCACTTTTTGGATGGAGGTGAGATGAAGGTAGAACAGCTGTTTCAAGAA
TTTGGCAACAGAAAATCCAATACTATTCAGTCAGATGGCATCAGTGACTCTGAAAAATGC
TCTCCTACTGTTTCTCAGGGTAAAAGTTCAGATTGCTTGAATACAGTAAAATCCAACAGT
TCATCCAAGGCACCCAAAGTGGTGCCTCTGACTCCAGAACAAGCCCTGAAGCAATATAAA
CACCACCTCACTGCCTATGAGAAACTGGAAATAATTAATTATCCAGAAATTTACTTTGTA
GGTCCAAATGCCAAGAAAAGACATGGAGTTATTGGTGGTCCCAATAATGGAGGGTATGAT
GATGCAGATGGGGCCTATATTCATGTACCTCGAGACCATCTAGCTTATCGATATGAGGTG
CTGAAAATTATTGGCAAGGGGAGTTTTGGGCAGGTGGCCAGGGTCTATGATCACAAACTT
CGACAGTACGTGGCCCTAAAAATGGTGCGCAATGAGAAGCGCTTTCATCGTCAAGCAGCT
GAGGAGATCCGGATTTTGGAGCATCTTAAGAAACAGGATAAAACTGGTAGTATGAACGTT
ATCCACATGCTGGAAAGTTTCACATTCCGGAACCATGTTTGCATGGCCTTTGAATTGCTG
AGCATAGACCTTTATGAGCTGATTAAAAAAAATAAGTTTCAGGGTTTTAGCGTCCAGTTG
GTACGCAAGTTTGCCCAGTCCATCTTGCAATCTTTGGATGCCCTCCACAAAAAATAAGATT
ATTCACTGCGATCTGAAGCCAGAAAACATTCTCCTGAAACACCACGGGCGCAGTTCAACC
AAGGTCATTGACTTTGGGTCCAGCTGTTTCGAGTACCAGAAGCTCTACACATATATCCAG
TCTCGGTTCTACAGAGCTCCAGAAATCATCTTAGGAAGCCGCTACAGCACACCAATTGAC
ATATGGAGTTTTCGCTGCATCCTTGCAGAACTTTTAACAGGACAGCCTCTCTTCCCTGGA
GAGGATGAAGGAGACCAGTTGGCCTGCATGATGGAGCTTCTAGGGATGCCACCACCAAAA
CTTCTGGAGCAATCCAAACGTGCCAAGTACTTTATTAATTCCAAGGGCATACCCCGCTAC
TGCTCTGTGACTACCCAGGCAGATGGGAGGGTTGTGCTTGTGGGGGGTCGCTCACGTAGG
GGTAAAAAGCGGGGTCCCCCAGGCAGCAAAGACTGGGGGACAGCACTGAAAGGGTGTGAT
GACTACTTGTTTATAGAGTTCTTGAAAAGGTGTCTTCACTGGGACCCCTCTGCCCGCTTG
ACCCCAGCTCAAGCATTAAGACACCCTTGGATTAGCAAGTCTGTCCCCAGACCTCTCACC
ACCATAGACAAGGTGTCAGGGAAACGGGTAGTTAATCCTGCAAGTGCTTTCCAGGGATTG
GGTTCTAAGCTGCCTCCAGTTGTTGGAATAGCCAATAAGCTTAAAGCTAACTTAATGTCA
GAAACCAATGGTAGTATACCCCTATGCAGTGTATTGCCAAAACTGATTAGCTAGTGGACA
GAGATATGCCCAGAGATGCATATGTGTATATTTTTATGATCTTACAAACCTGCAAATGGA
AAAAATGCAAGCCCATTGGTGGATGTTTTTGTTAGAGTAGACTTTTTTTAAACAAGACAA
AACATTTTTATATGATTATAAAAGAATTCTTCAAGGGCTAATTACCTAACCAGCTTGTAT
TGGCCATCTGGAATATGCATTAAATGACTTTTTATAGGTCA

FIGURE 2FFF

SEQ ID NO: 70_AA589241_M DYRK3_M
CCACGCGTCCGGAGTTGCTAGGAATGCCACCGCAGAAACTTCTGGAGCAATCCAAGCGTG
CCAAGTACTTTATTAACTCCAAAGGCTTGCCTCGATACTGCTCCGTATCTACCCAGACGG
ACGGGAGGGTGGTGCTTCTCGGGGGTCGCTCACGCAGGGGTAAAAAGCGAGGCCCGCCAG
GCAGCAAAGACTGGGCAACCGCACTGAAGGGCTGTGGTGACTACTTGTTCATAGAGTTTC
TGAAACGATGCCTCCAGTGGGACCCCTCTGCCCGCCTCACCCCGGCTCAAGCATTAAGAC
ATCCTTGGATTAGCAAGTCTACACCCAAACCTCTCACCATGGACAAGGTGCCAGGGAAGC
GGGTAGTTAACCCTACAAATGCTTTCCAGGGACTGGGTTCCAAGCTGCCTCCAGTCGTTG
GGATAGCCAGTAAGCTTAAAGCTAACCTAATGTCCGAAACCAGTGGTAGTATACCTCTGT
GCAGTGTATTGCCAAAGCTGATTAGCTAGTGGACCACTCAGAGACTGATACATATCATAT
GTATTTTTAATTACCTTGCAAACATGCAAATGGAAAACGGAATAATTGAAGCCCATTCAC
TGATGGATATGTTTTTGTTAGACTTTTTTTAACAAGGCAGAACATTTTTATATGACTAT
AAAAGAACGCTTCAAGGGCTAATGTCAAACCAGCTTGTATTGGCCATCTGGAGTATACAT
TAAATGACTTTTTCATAGGTC

SEQ ID NO: 71_5R72_16_2_H
GTCGAGGCGCAGCGCTGCCATGGCTGGGGGCCGTGGGGCCCCCGGGCGCGGCCGGGACGA
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CGGCGCGGACTTCCAAGACCTGCGGCCGGACGCTTGCGGACCGGTCAAAGAGCCCCCTGA
AATCAATTTAGTTTTGTACCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGA
TTTGAGGGTTAAATGCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAA
TGCCAAAGGTCTATCAAATGAAAGTGTCAATTTGTTAAAATCTCGCCTAGAAGAACTGGC
CAAGAAACACTGTGGGGAGGTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCT
CAGCGAGCATAACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGC
TCAGGAGGAGCAGCAGAGGCTGTTGGAGGCCAAGCGGAAAGAAGAGCAGGAGCAACGTGA
AATCCTGCATGAGATTCAGAGAAGGAAAGAAGAGATAAAAGAAGAGAAAAAAAGGAAAGA
AATGGCTAAGCAGGAACGTTTGGAAATTGCTAGTTTGTCAAACCAAGATCATACCTCTAA
GAAGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGT
AGGAAATGGTAAACATCGGGCAAACTCCTCAGGAAGGTCTAGGCGAGAACGTCAGTATTC
TGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATTCTGTATTTCAATATGGGGAG
TCCTGATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACTTGGAAA
ATTAGTCTACAATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTTGTATGAGTGGGT
CCTTCAGTGGCAGAAAAAAATGGGTCCATTCCTTACCAGTCAAGAAAAAGAGAAGATTGA
TAAGTGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAG
CCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATCGT
GGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGCACACCTGAGCCACTC
AGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTCAGGCCTTGA
TTATCTGCACAGCAATTCTGTGGTGCATAAGGTCCTGAGTGCATCTAATGTCTTGGTGGA
TGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTG
CAAGGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAATGCTCTGCCTTATAA
AACGGGGAAGAAAGGAGATGTTTGGCGTCTTGGCCTTCTGCTGCTGTCCCTCAGCCAAGG
ACAGGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGA
TTTTCTAAAGAAATGTGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTT
GAAACACAGCTTTATAAATCCCCAGCCAAAAATGCCTCTAGTGGAACAAAGTCCTGAAGA
TTCTGGAGGACAAGATTATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGC
CTTCTTTAGTGAGACACAGAGACAGTTTTCCCGATACTTCATTGAGTTTGAAGAATTACA
ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTG
CTGCTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAA
GGGCGAAGTGACACTGCTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC
CTGGATCGAGCGGCACGAGCGGCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCC

FIGURE 2GGG

CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA
CAGCGTAGAGGCCGCCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC
GGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTCCAGCGATGACGA
GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCCAGTCCTTCCTGCCTGCTTCAGA
TTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAGTCAGAATCAGGA
TGAAGATTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGC
TGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTTACGAGACACCAT
TGACCAGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTCGAGAGATTCTGGA
TGGATTAGCTTATATCCATGAGAAAGGAATGATTCACCGGGATTTGAAGCCTGTCAACAT
TTTTTTGGATTCTGATGACCATGTGAAAATAGGTGATTTTGGTTTGGCGACAGACCATCT
AGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCC
TTCAGGTCACTTAACTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGG
AAGCACCAAATCTGCATACAACCAGAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTT
TGAGATGTCCTATCACCCCATGGTCACGGCTTCAGAAAGGATCTTTGTTCTCAACCAACT
CAGAGATCCCACTTCGCCTAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCA
GAAATCAGTCATCTCCTGGCTGTTGAACCACGATCCAGCAAAACGGCCCACAGCCACAGA
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CAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGCAT
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AAAACGATACTGCATAGAACGTGTGTTCAGGCCGCGCAAGTTAGATCGATTTCATCCCAA
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TGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAG
AAATTACAGTATTTATTTGAACCATACCATGTTATTGAAAGCAATACTCTTACACTGTGG
GATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGACAGAGAA
GCTGACGAGGAGAGAAGTGGAAGCTAAATTTTGTAATCTGTCTTTGTCTTCTAATAGTCT
GTGTCGACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAAT
AAATTCATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGA
CCTAGAGGAGGTTGTTGGACTGTTGAAGAAACTCGGCATCAAGTTACAGGTCTTGATCAA
TTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTT
CATCAAACGAAGGCAAAGGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGATATGACCT
GCTGATTCCCCAGTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCATTGGGGT
CAGCATAGCTATAGACAAGATATCTGCTGCTGTCCTCAACATGGAGGAATCTGTTACAAT
AAGCTCTTGTGACCTCCTGGTTGTAAGTGTTGGTCAGATGTCTATGTCCAGGGCCATCAA
CCTAACCCAGAAACTCTGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACA
GTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGT
CTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTCGAGAAGGAAAGGCAGACAGA
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CACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTGCAGTGCAAAATCTGAAGGG
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GAGTGTGCTAGCCCCGGAGAAGCTGTCAGCCAGCACTAGGAGGCGCTATGAAACTCAGGT
ACAAACTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAAGCAGTGAAATTGAAAT
TCTGGCTGTGGATCTACCCAAAGAAACAATATTACAGTTTTTATCATTAGAGTGGGATGC
TGATGAACAGGCATTTAACACAACTGTGAAGCAGCTGCTGTCACGCCTGCCAAAGCAAAG
ATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAAGGTGTCTGT
GCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAACCCTAAAGAAC
TGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGAATAATGGAATGTTGTACAT

FIGURE 2HHH

TCATCATAATTTAAAATTAAATTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAA
TCCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAG
CCT

SEQ ID NO: 73_R43524_H, HRI_H
ATGCTGGGGGGCAACTCCGGGGTCCGCAAGCGCGAAGAGGAGGGCGACGGGGCTGGGGCT
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TCTGATGTTCCAGCAGAAATCCAGGTGTTAAAAGAACCCCTACAACAGCCAACCTTCCCT
TTTGCAGTTGCAAACCAACTCTTGCTGGTTTCTTTGCTGGAGCACTTGAGCCACGTGCAT
GAACCAAACCCACTTCGTTCAAGACAGGTGTTTAAGCTACTTTGCCAGACGTTTATCAAA
ATGGGGCTGTTGTCTTCTTTCACTTGTAGTGACGAGTTTAGCTCATTGAGACTACATCAC
AACAGAGCTATTACACACTTAATGAGGTCTGCTAAAGAGAGAGTTCGTCAGGATCCTTGT
GAGGATATTTCTCGTATCCAGAAAATCAGATCAAGGGAAGTAGCCTTGGAAGCACAAACT
TCACGTTACTTAAATGAATTTGAAGAACTTGTCATCTTAGGAAAAGGTGGATACGGAAGA
GTATACAAGGTCAGGAATAAATTAGATGGTCAGTATTATGCAATAAAAAAAATCCTGATT
AAGGGTGCAACTAAAACAGTTTGCATGAAGGTCCTACGGGAAGTGAAGGTGCTGGCAGGT
CTTCAGCACCCCAATATTGTTGGCTATCACACCGCGTGGATAGAACATGTTCATGTGATT
CAGCCACGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTGGAAGTGCTCTCCGACCAG
GAAGAGGACAGAGAGCAATGTGGTGTTAAAAATGATGAAAGTAGCAGCTCATCCATTATC
TTTGCTGAGCCCACCCCAGAAAAAGAAAAACGCTTTGGAGAATCTGACACTGAAAATCAG
AATAACAAGTCGGTGAAGTACACCACCAATTTAGTCATAAGAGAATCTGGTGAACTTGAG
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GGGAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGCTTCACCCGAA
CAGTTGGAAGGATCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTGGTCCTG
CTAGAGCTCTTTCAGCCGTTTGGAACAGAAATGGAGCGAGCAGAAGTTCTAACAGGTTTA
AGAACTGGTCAGTTGCCGGAATCCCTCCGTAAAAGGTGTCCAGTGCAAGCCAAGTATATC
CAGCACTTAACGAGAAGGAACTCATCGCAGAGACCATCTGCCATTCAGCTGCTGCAGAGT
GAACTTTTCCAAAATTCTGGAAATGTTAACCTCACCCTACAGATGAAGATAATAGAGCAA
GAAAAAGAAATTGCAGAACTAAAGAAGCAGCTAAACCTCCTTTCTCAAGACAAAGGGGTG
AGGGATGACGGAAAGGATGGGGGCGTGGGATGA

SEQ ID NO: 74_17000057519457_H
CACAAGAGCCCTTCCTGCAGGGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGT
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GGATTGCCGAAGAAGTCCCAGGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTCAG
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GGAGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGT
TCCGTGGCCGCTTCCAGGGCCGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACC
GGCACCCGGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCGGGCGC
TCCTCCGCTGTCGCCGCGCTGGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTT
CCAACTGCTTATATATGGAAGAAATTGAAGGCTCAGTGACTGTTCGAGATTATATTCAGT
CCACTATGGAGACTGAAAAAACTCCCCAGGGTCTCTCCAACTTAGCCAAGACAATTGGGC

FIGURE 2III

AGGTTTTGGCTCGAATGCACGATGAAGACCTCATTCATGGTGATCTCACCACCTCCAACA
TGCTCCTGAAACCCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTT
TCATTTCAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCC
TCAGTACCCATCCCAACACTGAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCT
CCTCCAAAAAGGCCAGGCCAGTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAA
AGAGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTT
TCAAAGTAAATTTGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAG
ATATTTTTAAGTGGTATGTGATCGTGTCATTATCATCTGCACTTCACTCAAGAGCTTACT
ATGTGTCTAAGTCATGTTCTAGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTT
CTCCCAGATTGTGACATGTATATCTCAGATACATGGGTGTGGCATTGAACCACATAATGA
GAACATTATTCTCTTTTTAGTCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTC
GCTGAGCTTACTGGCCCTCTAACCCAGTGTTTTTTTTTGTTGTTGTTGTGTACATGTTAT
ATTTATTTTGAAACCAGTTTAATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATA
CAGCATGGAAAATATCAGTGTATTGTTTTATGAAACTTTCACGTGTATATATAGACCAAG
GATATGTGCTGAGTTTTGATGTCAAATATATTTCTCTTTCAGGGTCATGATCAAAAAATG
AAAAGTCTGCTTAACTCCAATTTCTCTTTTAAAAAAGCAGACTTACAGCTTTCAGGCAAC
TGAAATTCATGTTAACATGTTTTTATTTTTATTGCTTTGTATTTTTGTGGTTACCTTCTA
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TATTTTGAGTGCCTTTTGTGTTCCTTGGCACCCTGTTGGGTATTGGGTACTTGGCACCCT
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TCATTCACCACAGTCAGCATGCCCCAAGTGCCCAGCATGGGGCGGATGGCCAGGAATGAG
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GCTTACTGCATGCCAGGCATTGGGCTGGGAATTTTTATATTGGATCTAAAATAACTCTTA
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SEQ ID NO: 75_AA013524_M
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GCCCCAGTCGTCTTCTTTGTGGACTATGCGTCTAACTGCTTATATATGGAAGAAATCGAA
GACTCGGTGACTGTTCGGGATTATATCCAATCCACTATGGAGACTGAAAAGGACCCCCAG
TGCCTCTTGGACCTGGCCAGGAGGATGGGGCAGGTTCTGGCCGGAATGCACGACCAAGAC
CTCATTCACGGGGACCTCACCACCTCCAACATGCTCCTGAGGCGGCCCCTGGCGCAGCTG
CACATCGTGCTCATCGACTTTGGGCTGAGCTTTGTCTCAGGACTGCCGGAAGATAAAGGC

FIGURE 2JJJ

GTCGACCTCTATGTCCTGGAGAAGGCCTTCCTCAGCACGCACCCCCACACCGAGACCGCG
TTTGAAGCCTTTCTGAAGAGTTACGGGCCTCGTCCAAGAAGTCCAGTCCAGTGCTGAAG
AAGTTAGATGAGGTGCGCCTGAGAGGGCGAAAGCGGTCCATGGTCGGGTAGTGGAGCTGT
GGTGAACTGGCTCACGGTGAAGGATGATGTAGACGAGGCTGGACCCCTCAGCAAAGCATG
GGTTGTTAAGTGGTCTGTGATCGTGCTGGGCCACCACCATCCATGGCTCACTGTTCTCAG
GGGCTTCATGTACATGAGGTTTATTCTGGGCAGAACTGGGTAGGTAGCCCAGGCTAGCCT
TGAATTTATGGCAACATCCTACCTCAGCTTGCTTGGAAGAGGTTATAAGCCACCATACCT
GACTTTGCACTGATTCTGTCAGAAAC

SEQ ID NO: 76_17000139801197_H, IRAKM_H
ATGGCGGGGAACTGTGGGGCCCGCGGCGCGCTGTCGGCGCACACGCTGCTGTTCGACCTG
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TGGCGCGGCCTGGCAGAGAGACTTTCAAGCAGCTGGCTGGATGTTCGTCATATTGAAAAG
TATGTAGACCAAGGTAAAAGTGGAACAAGAGAATTACTTTGGTCCTGGGCACAGAAAAAC
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TTAATTACAAACTATGGAGCAGTGTTGAGTCCTTCAGAGAAGAGTTATCAGGAAGGTGGA
TTTCCAAATATATTATTCAAGGAAACAGCCAATGTCACCGTGGATAATGTTCTTATTCCT
GAACATAATGAAAAAGGAGTACTGCTTAAATCTTCCATCAGCTTTCAAAATATCATAGAA
GGAACTAGAAATTTCCACAAAGACTTCCTAATTGGAGAAGGAGAGATTTTTGAGGTATAC
AGAGTGGAGATTCAAAACCTAACATATGCTGTCAAATTATTTAAACAGGAGAAAAAAATG
CAGTGTAAGAAGCATTGGAAGAGGTTTTTATCTGAGCTTGAAGTTTTACTACTGTTTCAT
CACCCAAACATACTAGAGTTGGCTGCATATTTTACAGAGACTGAGAAGTTCTGTCTGATT
TATCCATACATGAGAAATGGAACACTTTTTGACAGATTGCAGTGTGTAGGTGACACGGCC
CCACTCCCTTGGCACATTCGAATCGGTATATTAATAGGAATATCCAAAGCCATTCACTAC
CTGCACAACGTTCAACCATGCTCGGTCATCTGTGGCAGTATATCAAGTGCAAACATCCTT
TTGGATGATCAGTTTCAACCCAAACTAACTGATTTTGCCATGGCACACTTCCGGTCCCAC
CTAGAACATCAGAGTTGTACCATAAATATGACCAGCAGCAGCAGTAAACATCTGTGGTAC
ATGCCAGAAGAGTACATCAGACAGGGGAAACTTTCCATTAAAACAGATGTCTACAGCTTT
GGAATTGTAATAATGGAAGTTCTAACAGGATGTAGAGTAGTGTTAGATGATCCAAAACAT
ATCCAGCTGCGGGATCTCCTTAGAGAATTGATGGAGAAGAGAGGCCTGGATTCATGTCTC
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TTGGCAGGCCGGTGTGCTGCAACGCGGGCAAAGTTAAGACCATCAATGGATGAAGTTTTA
AATACTCTTGAAAGTACTCAAGCCAGCTTGTATTTTGCTGAAGATCCTCCCACATCACTA
AAGTCCTTCAGGTGTCCTTCTCCTCTATTCCTGGAGAATGTACCAAGTATTCCAGTGGAA
GATGATGAAAGCCAGAATAACAATTTACTACCTTCTGATGAAGGCCTGAGGATAGACAGA
ATGACTCAGAAAACTCCTTTTGAATGCAGCCAGTCTGAGGTTATGTTTCTGAGCTTGGAC
AAAAAGCCAGAGAGCAAGAGAAATGAGGAAGCTTGCAACATGCCCAGTTCTTCTTGTGAA
GAAAGTTGGTTCCCAAAGTATATAGTTCCATCCCAGGACTTAAGGCCCTATAAGGTAAAT
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SEQ ID NO: 77_AA840598_M IRAKM_M
ATGTGGAAGAGATTTTTATCAGAACTGGAAGTTCTACTCCTGTTCCGTCACCCCCACATA
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CACGTTCGAATCAGCGTATTGATAGGAATAGCCAAAGCCATCCAATACTTGCACAACACT
CAGCCGTGCGCCGTCATCTGTGGCAACGTTTCCAGTGCAAACATACTCTTGGATGACCAG
CTCCAACCCAAACTAACGGATTTTGCTGCAGCGCACTTCCGACCCAATCTAGAGCAGCAG
AGTTCTACCATAAATATGACCGGCGGTGGCAGGAAACATCTGTGGTACATGCCAGAAGAA

FIGURE 2KKK

TACATCAGACAGGGAAGACTTTCCGTTAAAACTGATGTCTACAGCTTCGGAATCGTGATC
ATGGAGGTTCTAACGGGCTGCAAAGTGGTGCTGGATGACCCGAAACACGTTCAGCTGCGG
GACCTCCTCATGGAACTGATGGAGAAAAGAGGCCTAGACTCCTGCCTGTCCTTCTTAGAC
AGGAAGATACCACCCTGTCCTCGGAACTTCTCTGCAAAGCTCTTCTCTCTGGCGGGCCGG
TGTGTGGCAACGAAGGCCAAGTTAAGACCCACGATGGACGAAGTCCTGTCCTCTCTGGAG
AGCACCCAGCCTAGCTTGTATTTTGCAGAAGACCCTCCCACGTCCTTGAAGTCCTTCAGG
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CAGAATAACCATTCAGTACCTCCCAAGGAAGTTTTGGGGACAGATAGAGTGACTCAGAAA
ACCCCCTTTGAATGCAGCCAGTCTGAGGTCACCTTTCTAGGCTTGGACCGAAACAGAGGG
AACAGGGGAAGTGAAGCGGATTGCAACGTGCCCAGTTCTTCTCATGAGGAATGCTGGTCC
CCAGAGCTTGTGGCGCCATCCCAGGACTTAAGTCCTACTGTGATCAGTTTGGGCTCGTCT
TGGGAAGTACCAGGCCATTCTTATGGGAGCAAGCCAATGGAGAAGAGGTGTTCCTCTGGG
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TTTTACAGCCAGTTGCTACTCTTGTTTATCGCTGGTTAACCGGTCTGTCCGGAAGTGAGC
CAAGTCATCCTTGCTAGGGCTTTTTCTGTGTAGAGAGGGAATTCCAGTCCAAAGTCTGCT
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GGGGAGACCCAGATGACACTGACCACAGAGGGTCCCTCCACCCCCCGCCTCTACATTGGC
CGAACACAGTATACGGTCACCATGCATGACCCAAGAGCCCCAGCCCTGCGCTGGAACACC
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GACACCCAGCTGCTAATGACGCTGTATGTGGGGAAGGATGAAACTGGCTTCTATGTCTCT
AAAGCACTGGTCCACACAGGAGTGGCCCTGGTGCCTCGTGGACTGACCCTGGCCCCCGCA
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FIGURE 2LLL

AGCACTGCTGTTAGATACCCCTCAGGCAGTGTGGCCCTCCCAAGCCAGTGGCTGCTCATT
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TAATATGGAAGAACTGGATGAATCATACCAGAAAGTAATTGAACTCTTCTCTGTATGCAC

FIGURE 2MMM

TAATGAAGACCCTAAAGATCGTCCTTCTGCTGCACACATTGTTGAAGCTCTGGAAACAGA
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FIGURE 2NNN

ATAGCTGCTGATGGAGTATTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCAT
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TGA

SEQ ID NO: 83_AI375137_H
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FIGURE 2OOO

GGCAAATTTGAAGTTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAG
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FIGURE 2PPP

TTTACAGGATGTCTTGCTTCATCGTAAACCTAAACTGGGACAGGAACTGGGCCGGGGCCA
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GAACAATGTGCGGAGGGGGGCTCGCCCAGAACGTCTTCCTGTGTTTGATGAGGAGTGCTG
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SEQ ID NO: 85_W20810_M
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SEQ ID NO: 86_AA744236_H
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FIGURE 2QQQ

CAGTCAATAAGAGACCCAGCATCTATCCCTCCTGAAGAGATGTCTCCAGAATTCACAACT
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ATGTAAAGCTACTGTTAAATGTAACTCCGACTGTAAGACCAGATGCAGATCAAATGACAA
AGATTCCCTTCTTTGATGATGTTGGTGCAGTAACACTGCAATATTTTGATACCTTATTCC
AAAGAGATAATCTTCAGAAATCACAGTTTTTCAAAGGACTGCCAAAGGTTCTACCAAAAC

FIGURE 2RRR

TGCCCAAGCGTGTCATTGTGCAGAGAATTTTGCCTTGTTTGACTTCAGAATTTGTAAACC
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GGGTCCTTACCTCTGCCTTCAGCCGAGCCACTAGGGACCCGTTTGCACCGTCCCGGGTTG
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FIGURE 2SSS

ACAGTCGACAGGTCAAGGCTGAGCTGGCCCGGAAGAAGCGCGAGGAGCGGCGGCGGAGA
TGGAGGCCAAACGCGCCGAGAGGAAGGTGGCCAAGGGCCCCATGAAGCTGGGAGCCCGGA
AGCTGGACTGAACCGTGGCGGTGGCCCTTCCCGGCTGCGGAGAGCCCGCCCCACAGATGT
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CGCAAGCGCTTTGTGGCCCTCAAAGTGGTGAAGAGTGCGGGGCATTACACGGAGACAGCT
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FIGURE 2TTT

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FIGURE 2UUU

ACCGGGACCTTAAGTGTGAGAACGCCTTGTTGCAGGGCTTCAACCTGAAGCTGACCGACT
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AGCCCAACACCATGGGGAAGGGAGATGTCTTAGAGGCAGCACCAACCACCACAGCCTACC
ATTCCCTCATGGATGAATATGGTTATGAGGTGGGCAAGGCCATTGGCCATGGCTCCTATG
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ACGGGGCCTGCTCTGAGCCCCTTGCTGGCAAGTGGTTCTCCCAGCTGACCCTGGGCATTG
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TCCCAGCTAACCATACCATCTCCCAGGAGTGCAAGGTCCAACTGCTCATTGCCTGTGTGG
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AGATGCTACGCCAAGCCACTAAGCGTGCCACCATTCTGGACATCATCAAGGATTCCTGGG
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AGCTCCACAACACCACTAAACAGCACCAATCCTTGCAAATTACGACCTGAAAATGGCTGA
GGGAGGGGGCTAAGAGAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTACCAA
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CCACGACCTGGACATCGTCCACCGGGACCTCAAGTGCGAGAACCTTCTCCTCGACAAGGA
CTTCAACATCAAGCTGTCTGACTTTGGCTTCTCCAAGCGCTGCCTGCGGGACAGCAATGG
GCGCATCATCCTCAGCAAGACCTTCTGCGGGTCGGCAGCATATGCAGCCCCCGAGGTGCT
GCAGAGCATCCCCTACCAGCCCAAGGTGTATGACATCTGGAGCCTGGGCGTGATCCTGTA

FIGURE 2VVV

CATCATGGTCTGCGGCTCCATGCCCTATGACGACTCCGACATCAGGAAGATGCTGCGTAT
CCAGAAGGAGCACCGTGTGGACTTCCCGCGCTCCAAGAACCTGACCTGCGAGTGCAAGGA
CCTCATCTACCGCATGCTGCAGCCCGACGTCAGCCAGCGGCTCCACATCGATGAGATCCT
CAGCCACTCGTGGCTGCAGCCCCCCAAGCCCAAAGCCACGTCTTCTGCCTCCTTCAAGAG
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SEQ ID NO: 95_AA883975_H
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CTGTCCATCCTGCGGGGCGTGCGACACCCGCACATCGTGCACGTCTTCGAGTTCATCGAG
GTGTGCAACGGGAAACTGTACATCGTGATGGAAGCGGCCGCCACCGACCTGCTGCAAGCC
GTGCAGCGCAACGGGCGCATCCCCGGAGTTCAGGCGCGCGACCTCTTTGCGCAGATCGCC
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GTGCTGCTGAGCCCGGACGAGCGCCGCGTCAAGCTCACCGACTTCGGCTTCGGCCGCCAG
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CCCCGGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC
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SEQ ID NO: 96_AA905446_H
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CGGGAAAATCTGCCTGGTGATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGCGTGCT
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TCTGAGCATCTCGGCCGATTGCCAGGACCTGCTCAAGAGGCTCCTGGAACCCGATATGAT
CCTCCGGCCTTCAATTGAAGAAGTTAGTTGGCATCCATGGCTAGCAAGCACTTGATAAAA
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FIGURE 2WWW

SEQ ID NO: 97_H29974_H
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GAAGCCAGACAACATCCTCATCACAGAGCGGTCTGGCACCCCCATCCTCAAAGTGGCCGA
CTTTGGACTAAGCAAGGTCTGTGCTGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGA
CAACAAAAATGTGAATGTGAATAAGTACTGGCTGTCCTCAGCCTGCGGTTCGGACTTCTA
CATGGCTCCTGAAGTCTGGGAGGGACACTACACAGCCAAGGCGGACATCTTTGCCCTGGG
CATTATCATCTGGGCAATGATAGAAAGAATCACTTTTATTGACTCTGAGACCAAGAAGGA
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GATCAAGCAGCTCTTGAAAGATATGTTAGCTGCTAACCCACAGGACCGGCCTGATGCCTT
TGAACTTGAAACCAGAATGGACCAGGTCACATGTGCTGCTTAAAATTCAGGGCTAAGCAT
TTTGGGTGATTTTAAACTAGGTCGATTCCTCGGGACCCACAGTCTCACCACGTCTCCTCC
AGAGGACGGCAGAGGGTACAGGTGGTGGCCTGGCCGGTTGGCGATCTCCCGACAGCTGGA
TCCGGCAATGTGAAGCTTTTGTTTGGGTTTCCCCGCTTCTTTTTAGTTTTGCTTTATTTN
TNNCCTTTTCTTTTCTTTTTTTNTTTNCCACNTNCCTTTTTTTAAATTTAAACCATTGAG
ACTTCAGAAGAGCAGGACACAATGCTGTGGACAGGCACCAATTTCTTTAAAGAAATTCAA
TGTGGGCAAGGCATATGTGTAAATTTCACTTTTACTTTTTATAAGGGGTTAGGGAGCTAT
TTTTGGTTTTGTCCTTCACTTTCCCTCTGTCTTCCTTCTTTATACTTTTCTCAGTTCTAC
TTATGACACCTCACTTCCCTAGAGAAGGCCTGCCTCCCCATAGGGAATCTGGGGGTANCT
TCTGGAACGGGGCGTGAGGANACAAGGAGCCTCTGGGCCACNCCTCCCTACCAGATGCAG
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GAGGTGAAGAACCGCC

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CGCAGTGGGGCCAGGGTGGCAGTCAAGAAGATCCGCTGCGACGCTCCCGAGAACGTGGAG
TTGGCACTAGCAGAATTCTGGGCCCTCACCAGTCTCAAGCGGCGGCACCAGAATATCGTG
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ATCATCTGGGCAATGATAGAAAGAATTACCTTTATTGACTCTGAAACCAAGAAGGAGCTC
CTGGGGACCTACATTAAGCAAGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCTAGAA
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FIGURE 2XXX

AAGCAGCTCTTGAAAGACATGTTAGCTGCTAACCCACAGGACCGACCTGATGCTTTTGAA
CTTGAAACCCGAATGGACCAGGTCACATGTGCTGCTTAAACTCCAGGGCTGAACGTCTTG
GGTGTTTTTAAACTAGGTCGATCCTTCGGGACCCACAGTCTCATCGTGTCTCGGACAGGA
TGGCAGAGGGTACAGGTGGTGGTGATCTCCTGACAGCTGGACCTCCCACAATGTGAAGCT
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SEQ ID NO: 99_AA215311_H
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GCAGTGAAGAAAATTCGATGTCACGCACCTGAAAATGTTGAACTAGCCCTTCGTGAGTTC
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AAAAAATGATTATTGATAGAAGTTTGGCAGGAAAATTCTTTAAGAGCTAACAAGAGAAGA
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AAACATATATGTATATATTTATGTATATGTAAGTATGTGAATGTGCGCATTTTGCATTCC
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CCTAATGAAATCATATTAAGTNGTTTTTCCTNNTTTTTTTGTAATATACAGCTTTTTTTT
TAAGGCATCATTTTCGAGGGTCTAAAATTATCTGGTAAAACAAATGAAATTAAGTGATCC
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CATGCAGTCATATGGCAGCAGGTTGGTGATT

SEQ ID NO: 100_AA018361_H
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GCAACCCGCCGGAACCGCCGCCCGCAGCGAGGAAGCGCCCGCGCGGGCGCAGGCGGCCGG
AATGGCGGGGCCCGGCTGGGGTCCCCCGCGCCTGGACGGCTTCATCCTCACCGAGCGCCT
GGGCAGCGGCACGTACGCCACGGTGTACAAGGCCTACGCCAAGAAGGACACTCGTGAAGT

FIGURE 2YYY

GGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAGGCATCGGTGGAGAACCTCCT
CACGGAGATTGAGATCCTCAAGGGCATTCGACATCCCCACATTGTGCAGCTGAAAGACTT
TCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTGCGCAGGGGGCGACCTGTC
TCGCTTCATCCATACCCGCAGGATTCTGCCTGAGAAGGTGGCGCGTGTCTTCATGCAGCA
ATTAGCTAGCGCCCTGCAATTCCTGCATGAACGGAATATCTCTCACCTGGATCTGAAGCC
ACAGAACATTCTACTGAGCTCCTTGGAGAAGCCCCACCTAAAACTGGCAGACTTTGGTTT
CGCACAACACATGTCCCCGTGGGATGAGAAGCACGTGCTCCGTGGCTCCCCCCTCTACAT
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GCTGGAAGAGAAGATCCGTAGCAACCGGGTCATCGAGCTCCCCTTGCGGCCCCTGCTCTC
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CATCTGGAGCAGAGGGGCACTAACCCAGGCTGACGCCAAGAATGAAGTGGCCCACTGCAG
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SEQ ID NO: 101_AA311714_H
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GATAAGTGCAGAAGGCCTGAAATAACCAACTGGGTCCGTCTCACCCGTGAAATAAAACAC
AAGAATATTGTAACTTTTCATGAATGGTATGAAACAAGCAACCACCTCTGGCTAGTGXAT
GAAAACCTCCCAGAAGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGGATTACAT
CATCTTCATAAACTTGGCATTCTCTTTTGTGACATTTCTCCTAGGAAGATACTCTTGGAA

FIGURE 2ZZZ

GGGCCTGGCACACTGAAGTTTAGCAACTTTTGCTTGGCAAAAGTGGAAGGTGAAAATTTG
GAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGAGGTGATAATGGGGAAAATGTC
CTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCAGAAGTT
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TCCAAGGAGCTTTTGCAGAACTCTCAGAGTAGACAAGCAAAAGGGCACAAGAGTGGTCAA
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SEQ ID NO: 102_SGK384_H
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FIGURE 2AAAA

TAGACGCTTACCAGAGGGTTTTCCATTCACTCCGAGACACTGTGATGTCGCAGACGAAAG
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AACCCACTAGTTCCTCAGAGACAATTTCTTCTCATTCAGAAAGCCCTGTTGGAAGCTGGG
GATGTTTTAACTCCGTGGCAGGGCACTTGCCTAGTTGTGTGCAAAGCCTTGGATCTGACC
CATGGCATGTGCACACACACAAATGCTCAAAGAAAATCCCAGACGCCAGAAGTGTGCCCC
TTTCTTGTCAATAAGGTCATTGTCAGTACCGGAGATGATTTTTTTTATGAAGCGTTTATG
CTGACTCGTGTCACTGAGCCAAGTGTGCATGGTCGTTAGCTACTTTGTGGGTTCTTCTTT
CTTTCTACCCTACTTCTTCCCTTTCCACCCCCTAACACTAGATAGGAGAGAGGAGAGAGA
AAGGAAAGTGGGCACTGTTATATTGTTGGACGACTTCTTGCTGATTAAGGGGTGTCGAGT
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GTCCCCCTGTACCGGAAAGTACAAAGTCTGCTCTGGGCTTGCATGCCTGAACACTTTAAA
ACACTGTGGAGCCAGGAATAATGGTACCCACCTGTAATCCCAGCACCTGGGAGACAGGAG
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CAATAAAAAAACAAAAAGGTC

SEQ ID NO: 104_SGK071_2_H
GAGGTGGTGGCTGTGCAGATGATGGTGGAATGCATGGATGACCATTACGCCAGTCAGGCC
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TCTGAGTGGATGCAGAATGTGCTGGGCCAGGTGCTGGACGCGCTGGAATACCTGCACCAT
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FIGURE 2BBBB

GAGTCAGAGTCACTGTCAGAGGAGCTGCAGAACGCTGGGCTGCTGGAGCACATCCTGGAG
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AAGGCCCTGCTCCAGGAGATCAAGGAGCGCTTCACCTCCAGCCTGGTGAGTGACAGCAGC
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GGGGGACTGGAATAG

SEQ ID NO: 105_AA118352_M SGK071_M
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TCCTGAACGACACAGAAGCCATGCAACTGCGGAAGGCCATCCGCCATCATCCAGGCAGCC
TGAAGCCCATCCTGAAAACCATGGAGGAGAAGCAAATCCCTGGTACAGATGTCTACTATT
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TGCAAGTCACCTTCATGAGCAACTCCTTCAAAAGCTCCTCTGTTGCGCTGAATATGCAGC
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TCAGCATCATAAAGCAGCATGGGCGGATCCTGGATATTCTGCTCAGCACCTGCTCCCTTC
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CGGAGGACGTGGAAATAGCAGAGGCTGGCTGTGCGGTGCTCTGGCTGCTGTCCTTGTTGG
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GCATCAAAGACCTAGTCCAGGTGATCCGGGGGCGCTTTACCTCCAGCCTGGAGCTGATTT
CTTACGCTGATGAGATACTCCAGGTACTGGAAGCAAATGCACAACCTGGCCTCCAGGAGG
ATCAGCTTGAGCCTCCTGCAGGGCAGGAAGCCCCACTGCAGGGAGAGCCCCTCTTCAGGC
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SEQ ID NO: 106_018653.9_H
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FIGURE 2CCCC

CGCCTCCTTCCTGCTGGCTCCGTCCTCAACGTGCTCTTCGCTCCGGGTCGGAGCCTCCG
AGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCGGGTGCGGGCCGTCGCGGGGGCCGC
GGGGAGCTGGCCCGGCAGATCCGGGCGCGCTACGAGGAGGTGCAGCGCTATTCCCGCGGG
GGCCCCGGGCCCGGGGCGGGCCGGCCGGAGCGGCGGCGCCTGATGGACCTGGCTCCGGGC
GGGCCCGGCCTGCCGCGCCCCCGGCCCCCTTGGGCCCGGCCCCTGTCCGACGGCGCCCCA
GGCTGGCCCCCGGCTCCCGGCCCAGGCTCCCCCGGCCCGGGCCCGCGCCTGGGCTGCGCC
GCGCTTCGCAACGTGTCCGGCGCGCAGTACATGGGCTCAGGCTACACCAAGGCCGTGTAC
CGGGTCCGCCTGCCCGGCGGTGCCGCGGTGGCGCTCAAGGCGGTGGACTTTAGCGGCCAC
GATCTGGGCAGCTGCGTGCGCGAGTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGCTGCGGCACCCCAACGTGCTGCAG
CTCTATGGCTACTGCTACCAGGACAGCGAGGACATCCCAGACACCCTGACCACCATCACG
GAGCTGGGCGCCCCTGTAGAAATGATCCAGCTGCTGCAAACTTCCTGGAGGATCGATTC
CGAATCTGCCTGAGCCTGGGCCGCCTCCTCCACCACCTGGCCCACTCCCCACTGGGCTCC
GTCACTCTGCTGGACTTCCGCCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATA
CTCGAGTTTCCGGCCAGGAACTTCACCCTGCCCTGCTCAGCCCAGGGCTGGTGCGAGGGC
ATGAACGAGAAGCGGAACCTCTATAATGCCTACAGGTTTTTCTTCACATACCTCCTGCCT
CACAGTGCCCCGCCTTCACTGCGTCCTCTGCTGGACAGCATCGTCAACGCCACAGGAGAG
CTCGCCTGGGGGGTGGACGAGACCCTGGCCCAGCTGGAGAAGGTGCTGCACCTGTACCGG
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCA
GACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGC
CTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCCAGTGT
CGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGCAGCTGGTCTTTTTCAAG
ACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGC
TGACCTATCTGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGGCTTGCCTGTG
GAGGGAGTGACTTGCACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCAGACAAAGCT
AACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAAT
GTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTAT
GACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGC
TGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAATAGTGTGAGA
ATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCACATGCCACAGCAGGCGGTGGGGGCTGCG
TGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGG
AGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAG
GGGACACTCCCAGGCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCTCAGCATGAGCCA
AGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGG
GGCCTTTCTGCCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCC
CCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTAT
TTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCC
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SEQ ID NO: 107_AA396601_M
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GCTGCTATCGCCTGGCGGCCCACAAGCTGCTCAAAGAGATGGTGCTGCTGGAGCGGCTGC
GGCACCCCAACGTGCTGCAGCTCTATGGCTATTGCTACCAGGACAGTGAGGGCATCCCAG
ACACGCTGACCACCATCACAGAGCTGGGTGCCCCTGTGGAGATGATCCAGCTGTTGCAGA
CTTCCTGGAGGATCGATTCCGAATCTGCCTCAGCCTTGGCCGCCTCCTCCACCACCTGG
CCCACTCCCCGCTGGGCTCGGTCACCCTGCTTGACTTCCGCCCTCGGCAGTTTGTGCTAG
TGAACGGGGAGCTGAAAGTGACAGACCTGGATGATGCCCGCGTGGAAGAGACACCGTGCA

FIGURE 2DDDD

CCAGCAGTGCCGACTGCACGCTAGAGTTTCCAGCCAGGAACTTCAGCCTGCCCTGCTCGG
CCCAGGGCTGGTGCGAGGGCATGAATGAGAAACGGAACCTCTACAATGCCTACAGGTTCT
TCTTCACATACCTCCTGCCACACAGTGCCCCGCCTTCCCTCCGACCTCTCCTGGATAGCA
TCGTCAATGCCACGGGAGAGCTCGCCTGGGGGGTGGATGAGACCCTGGCCCAGCTGGAGA
CAGCGCTACACTTGTTCCGAAGTGGGCAGTACCTGCAGAACTCTACAAGCAGCAGGGCTG
AGTACCAGCGCATCCCGGACAGTGCCATCACACAGGAGGACTATCGCTGCTGGCCATCCT
ATCACCACGGCGGCTGCCTCCTGTCCGTGTTCAACCTGGCTGAGGCTATAGATGTCTGTG
AGAGCCATGCTCAGTGTCGTGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGA
AGCTGGTCTTTTTTAAGACTGGATGGAACCAAGTGGTCCCTGATGCCGGCAAGACCACAT
ATGTGAAGGCCCCTGGTTGACTGGTTGTGGGCTCAGCTGACCAGCTGGGCTTGCCTGCTG
CAGGCGTGACTTGCATCCCACCTGGGAACCCCTGCAGACAAAAGCTAGCTCCCAGAGCAA
CTGATGTGACCAGGACAAAACGTGCAATATGCAAAAATGTTAAAATGTGAGTTTGCCAGC
TTCAGTCCCAGACTGGTTGGAACCCGATTGCCTCTCTGGAGCTGTAGGCTGTGAGCAGGG
CTCAGGCTGGTCTTAACTGGGACAGTCCCGTGGGCAGCCCATTACTGCATTCATGCTTTG
AGAATGTAGCCAGAACACTGCTGCTGCATAAGCCACCGTGGGCAGGAGCTGCCTGGGGAC
AACCAGTCTCAGAGTGCTCTCTCAGCTCAGCTCCGCTCCAAATGGAGAGCGCGGGATGCG
GAGATGTGAGTGAACCAGCACTGGGAAGAAGGCTCTCGGGCCTCTCCCTAGAGGTTGCTC
CTAGGCCAGCCCCGAGGCCGTGGGCAGCAGTGCTCGCATCCATATGAGCCAAGACTAGAG
TGGAGGAGCAGATTGCATTTGAGCCAGGACTGGGGTGGGGGTAGGGTCGGGGCCTCTCTG
CCTCATTTGCTTTCAGTGAAAGCCAGGGAGCAGCCGCAGCCAGGCTCCTCCCACTCCTGG
AGGCCAGGCTCCTCCCCCTCCTGGAGGCCAGGCTCCTCCCCCTCCTGGAGTTTGCGTACC
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CAATTAATAAAATGATGTTTTGTGAC

SEQ ID NO: 108_VRK3_H
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AAGAAAGTGAAATGGTCCAGCACCGTCACCTCTCCCCGATTATCCCTCTTCTCAGATGGT
GACAGTTCTGAGTCTGAAGATACTCTGAGTTCCTCTGAGAGATCCAAAGGCTCCGGGAGC
AGACCCCCAACCCCCAAAAGCAGCCCTCAGAAGACCAGGAAGAGCCCTCAGGTGACCAGG
GGTAGCCCTCAGAAGACCAGCTGTAGCCCTCAGAAGACCAGGCAGAGCCCTCAGACGCTG
AAGCGGAGCCGAGTGACCACCTCACTTGAAGCTTTGCCCACAGGGACAGTGCTGACAGAC
AAGAGTGGGCGACAGTGGAAGCTGAAGTCCTTCCAGACCAGGGACAACCAGGGCATTCTC
TATGAAGCTGCACCCACCTCCACCCTCACCTGTGACTCAGGACCACAGAAGCAAAAGTTC
TCACTCAAACTGGATGCCAAGGATGGGCGCTTGTTCAATGAGCAGAACTTCTTCCAGCGG
GCCGCCAAGCCTCTGCAAGTCAACAAGTGGAAGAAGCTGTACTCGACCCCACTGCTGGCC
ATCCCTACCTGCATGGGTTTCGGTGTTCACCAGGACAAATACAGGTTCTTGGTGTTACCC
AGCCTGGGGAGGAGCCTTCAGTCGGCCCTGGATGTCAGCCCAAAGCATGTGCTGTCAGAG
AGGTCTGTGCTGCAGGTGGCCTGCCGGCTGCTGGATGCCCTGGAGTTCCTCCATGAGAAT
GAGTATGTTCATGGAAATGTGACAGCTGAAAATATCTTTGTGGATCCAGAGGACCAGAGT
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GCCTACGTGGAAGGCAGCAGGAGCCCTCACGAGGGGGACCTTGAGTTCATTAGCATGGAC
CTGCACAAGGGATGCGGGCCCTCCCGCCGCAGCGACCTCCAGAGCCTGGGCTACTGCATG
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ATGAAGCAAAAACAGAAGTTTGTTGATAAGCCGGGGCCCTTCGTGGGACCCTGCGGTCAC
TGGATCAGGCCCTCAGAGACCCTGCAGAAGTACCTGAAGGTGGTGATGGCCCTCACGTAT
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CGTGTGTCTCCATATGACCCCATTGGCCTCCCGATGGTGCCCTAG

FIGURE 2EEEE

SEQ ID NO: 109_S71575_M VRK3_M
CCATCCCCACCTGTATCGGCTTTGGCATTCACCAGGACAAGTACAGGTTCCTAGTATTCC
CCAGCCTGGGGAGGAGCCTTCAGTCAGCCCTGGATGACAACCCAAAGCATGTGGTATCAG
AGAGATGTGTGCTTCAGGTGGCCTGCAGGCTGCTGGATGCTCTGGAGTATCTCCATGAAA
ATGAGTATGTTCACGGGAACCTGACAGCTGAGAATGTCTTTGTGAATCCAGAGGATCTGA
GCCAGGTGACCCTGGTGGGCTATGGCTTCACCTACCGATACTGCCCAGGTGGCAAACACG
TGGCCTACAAAGAAGGCAGCAGGAGTCCACACGATGGGGACTTGGAGTTCATTAGCATGG
ACCTGCACAAGGGATGCGGACCCTCCCGCCGCAGCGATCTCCAGACCTTGGGCTACTGTA
TGCTCAAGTGGCTTTATGGGTCCCTGCCATGGACAAATTGCCTTCCCAACACCGAAAAGA
TAACTAGGCAGAAGCAGAAGTATCTGGACAGCCCCGAGCGCCTCGTGGGACTGTGTGGCC
GCTGGAACAAGGCCTCAGAGACCCTGCGGGAGTACCTGAAGGTGGTGATGGCCCTCAATT
ATGAGGAGAAGCCACCCTATGCCACGCTGAGGAACAGCCTAGAAGCTCTGCTGCAGGATA
TGCGGGTGTCACCCTATGACCCTCTGGACCTCCAGATGGTGCCTTAGATGGAATCCAGAG
CTTCCGACTTGCAGCTTGAAGTAGAACATGAAGTAGTGTGACTGGAGGCCTGTTTGAACT
CATAGCTCCTAAAAGAATCCCTTGAATGTGCATTCTCACCGCTCCCTTAGGACATATGAA
TCAGCACTTGTGTTGGGGAACCTGAGTCATGTCATGTAATGTGAAACTCCTCCCTGTCTC
AGCTCTGGCAGCTGTGGATGGAGGTAAGTGGATGCTGGCGGCGGCGGCGGCAGCAGCCAC
TCCACTCCCTATGGCATTTCTGTGATGGCATAATAAACTGTTTTTAATC

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CTCTTCATCCAGAAACTGGGGGAGGGTGGGTTCAGCTATGTGGACCTAGTGGAAGGGTTA
CATGATGGACACTTCTACGCCCTGAAGCGAATCCTGTGTCACGAGCAGCAGGACCGGGAG
GAGGCCCAGCGAGAAGCCGACATGCATCGCCTCTTCAATCACCCCAACATCCTTCGCCTC
GTGGCTTACTGTCTGAGGGAACGGGGTGCTAAGCATGAGGCCTGGCTGCTGCTACCATTC
TTCAAGAGAGGTACGCTGTGGAATGAGATAGAAAGGCTGAAGGACAAAGGCAACTTCCTG
ACCGAGGATCAAATCCTTTGGCTGCTGCTGGGGATCTGCAGAGGCCTTGAGGCCATTCAT
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CGCCAGGCTCTGACCCTGCAGGACTGGGCAGCCCAGCGGTGCACCATCTCCTACCGAGCC
CCAGAGCTCTTCTCTGTGCAGAGTCACTGTGTCATCGATGAGCGGACTGATGTCTGGTCC
CTAGGCTGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTGTTCCAA
AAGGGTGACAGTGTGGCCCTTGCTGTGCAGAACCAACTCAGCATCCCACAAAGCCCCAGG
CATTCTTCAGCATTGCGGCAGCTCCTGAACTCGATGATGACCGTGGACCCGCATCAGCGT
CCTCACATTCCTCTCCTCCTCAGTCAGCTGGAGGCGCTGCAGCCCCCAGCTCCTGGCCAA
CATACTACCCAAATCTGA

SEQ ID NO: 111_H05721_H
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CGGCTTGGGGCGGCCGGGCCCGGCGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGC
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CTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTTGCAGCGGCAGTTCGTGGTGCGGGC
CTGGGGCTGCGCGGGCCCTTGCGGCCGGGCAGTCTTTCTGGCCTTCGGGCTAGGGCTGGG
CCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTCAGGAGATCCA
GGCAATTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGGACACGAGACGCTTGCA
GGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGCTGC
TGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGGTGACAAAGAGCACCGG
GTTGCTTCCAGGGAGAGGCCCAGGTACCAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCC

FIGURE 2FFFF

GGGGGCCCCTGCCTTCCCCTTGGCCATCAAGATGATGTGGAACATCTCGGCAGGTTCCTC
CAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCTT
GGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAGGTCCCAAGCAACTAGC
CCCTCACCCCAACATCATCCGGGTTCTCCGCGCCTTCACCTCTTCCGTGCCGCTGCTGCC
AGGGGCCCTGGTCGACTACCCTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGG
CCATGGCCGGACGCTGTTCCTCGTTATGAAGAACTATCCCTGTACCCTGCGCCAGTACCT
TTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGCTGCAGCTGCTGGAAGG
CGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGAAATCCGACAACATCCT
TGTGGAGCTGGACCCAGACGGCTGCCCCTGGCTGGTGATCGCAGATTTTGGCTGCTGCCT
GGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGTACGTGGATCGGGGCGG
AAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCCTGGCCCCAGGGCAGTGAT
TGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCGGGCT
TGTCAATCCCTTCTACGGCCAGGGCAAGGCCCACCTTGAAAGCCGCAGCTACCAAGAGGC
TCAGCTACCTGCACTGCCCGAGTCAGTGCCTCCAGACGTGAGACAGTTGGTGAGGGCACT
GCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCGCAAATGTGCTTCATCT
AAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGG
CTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGCTCACAGAGAAGTGTTG
TGTGGAAACAAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGTGTGAAACGCTCTGCCA
GGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGT
GAATTACTAAAAGAACATGGCATCCTCTGTGTCGTGATGGTCTGTGAATGGTGAGGGTGG
GAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAAAAGGCCTCGGGCTTGG
CAAATGGAAGAACTTGAGTGAGAGTTCAGTCTGCAGTCCTCTGCTCACAGACATCTGAAA
AGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATC
CACAGAGAGGATCCAGGCCAAGGCACTGGCTGTCAGTGGCAGAGTTTGGCTGTGACCTTT
GCCCCTAACACGAGGAACTCGTTTGAAGGGGGCAGCGTAGCATGTCTGATTTGCCACCTG
GATGAAGGCAGACATCAACATGGGTCAGCACGTTCAGTTACGGGAGTGGGAAATTACATG
AGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATC
TCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTGGGGATTTAAACTTGAG
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ACTCTGAAGGTGAGAATATTTTGTGGGCAGGTATCAACATTGGGGAAGAGATTTCATGTC
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CAGTAAAGGTTGTCTTCAACTGACAAAA

SEQ ID NO: 112_AI086865_H
AATGAGATGGAGAAGTACGAGCGGATCCGAGTGGTGGGGAGAGGTGCCTTCGGGATTGTG
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CAGATGACCAAGGAAGAGCGGCAGGCAGCCCAGAATGAGTGCCAGGTCCTCAAGCTGCTC
AACCACCCCAATGTCATTGAGTACTACGAGAACTTCCTGGAAGACAAAGCCCTTATGATC
GCCATGGAATATGCACCAGGCGGCACTCTGGCTGAGTTCATCCAAAAGCGCTGTAATTCC
CTGCTGGAGGAGGAGACCATCCTGCACTTCTTCGTGCAGATCCTGCTTGCACTGCATCAT
GTGCACACCCACCTCATCCTGCACCGAGACCTCAAGACCCAGAACATCCTGCTTGACAAA
CACCGCATGGTCGTCAAGATCGGTGATTTCGGCATCTCCAAGATCCTTAGCAGCAAGAGC
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ATCTGGGCCCTGGGCTGTGTCCTCTACGAGCTGGCCAGCCTCAAGAGGGCTTTCGAGGCT
GCGAACTTGCCAGCACTGGTGCTGAAGATCATGAGTGGCACCTTTGCACCTATCTCTGAC
CGGTACAGCCCTGAGCTTCGCCAGCTGGTCCTGAGTCTACTCAGCCTGGAGCCTGCCCAG
CGGCCACCACTCAGCCACATCATGGCACAGCCCCTCTGCATCCGTGCCCTCCTCAACCTC
CACACCGACGGCAGAGAAGTCCGTGGCCCCCAGCAACACAGGGAGCAGGACCACCAGTGT
CCGCTGCAGAGAGGCATCATCATGACATTCGGCAGCGGCAGCAATGGGTGCCTAGGCCAT

FIGURE 2GGGG

GGCAGCCTCACTGACATCAGCCAGCCCACCATTGTGGAGGCTTTGTTGGGCTATGAAATG
GTGCAGCAAGTGGAGGAGGCCCTGAGCTTCACACTACTAGGCTCTGCACCCCTGGACCAG
GAGCCTCTGCTGAGTATAGACCTGGGCACTGCTCACTCAGCTGCTGTGACTGGTGAGGAG
GACTTGGGCTCTGGAGATGTAAACAGGTTACCCAGCTGGGAGAGAGGACATCTGCTGGCT
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AAGTGCTGCTGGAGACACAAGCAGTGCACTGGGCACATCATCTACCCTTTCGCCTCTGAC
TGTGTCCGCCACAGCCTGCACCTACACTCTGTCAACCACTGCAACTGTAATTCTAGGCTG
AAGGACTCTTCAGAGGATAGCAGCAGCTCCCGGGGCGCGGGCCCAACCTGCTCCCATGTC
ATCGAGTCCCCTTGCTTTGAGCTCACACCGGAGGAGGAGCATGTGGAGCGATTCCGGTAT
GGCTGGTGCAAAAGCTACAGACCTGTCTCTGTGGCAGTGATCCACCATCCACTCTACCAT
GAGTGTGGGGCAGATGATCTAAATGXXAAGAAGAGGAAGAGGAGGAGGAGGAAAAGCAAG
CCCCCCATCCCGACACAGGTGGGGCCCGCCACCGCCTCCCCTGACCTAGGCACCAGCATG
GCCACTGGTACCCCTGACTCCACAGCGCCCATCACCATCTGGCGCTCTGAGAGCCCCACA
GGGAAGGGTCAGGGCAGCAAGGTGATCAAGAAGGTAAAGAAGAAAAAGGAAAAAGAGAAA
GACAAGGAGGAGATGGATGAGAAGGCAAAGCTGAAGAAAAAAGCCAAGAAAGGCCAGTTG
ACTAAGAAGAAAAGCCCGGTTAAATTGGAGCCTTCCCCGCCAGACGTGAGCCGATCATTA
AGCGCAAGACAGCTGGCCAGGATGTCCGAGTCCAGCCCAGAAAGCCGGGAAGAGCTGGAG
AGCGAGGACAGTTACAATGGCCGGGGGCAGGGAGAACTGTCCAGCGAGGATATTGTGGAA
TCATCATCGCCCAGGAAGAGAGAGAACACAGTCCAGGCCAAAAAGACAGGGGCAAAGCCC
TCACAAGCCAGGAAGGTAAACAAGAGAAAATCTCCCCCAGGATCAAACCCCAACCTCAGT
TGAGGCCAGGGTGGTCAGGGTGCAGAATAAATGCCATCGAGCCTGTGGCTGGCCCTCTGC
TGCTGTTCTCTCCCTCCAACCTGGCTGTTTCTTGCGGGGCAAGGGGTGGGCTCAGGGCTG
CAGGGGTTTCTCAAAGGCAATCCAGCTTTCACAAAGGAAGCCCATGGAAGGCAGGTGGG
AGGGAAAGGAAGGGGCACAGCCCTATTTCTTCCTACCTGCTAGGACAAGGTGGAAGAGTG
TATCTGGGGTGGGAAGGAGGGCTTCCCCTCTCTGCTGCGAGAGACTGGTCTGTGTGAAAT
CCACTTCTGGGACAGGCAGTACTGTCTGCAGCGATACCCCCAATAAACGGAACTTTTTAA
CCC

SEQ ID NO: 113_AA836348_H
ATGTCGGTGCTGGGCGAGTACGAGCGACACTGCGATTCCATCAACTCGGACTTTGGGAGC
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GGCGGCGGCGCGGCGGAGCAGGAGGAACTGCACTACATCCCCATCCGCGTCCTGGGCCGC
GGCGCCTTCGGGGAAGCCACGCTGTACCGCCGCACCGAGGATGACTCACTGGTTGTGTGG
AAGGAAGTCGATTTGACCCGGCTGTCTGAGAAGGAACGTCGTGATGCCTTGAATGAGATA
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GTTTCAGCAGTGAGCTGCATCCATAAAGCTGGAATCCTTCATAGAGATATAAAGACATTA
AATATTTTTCTGACCAAGGCAAACCTGATAAAACTTGGAGATTATGGCCTAGCAAAGAAA
CTTAATTCTGAGTATTCCATGGCTGAGACGCTTGTGGGAACCCCATATTACATGTCTCCA
GAGCTCTGTCAAGGAGTAAAGTACAATTTCAAGTCTGATATCTGGGCAGTTGGCTGCGTC
ATTTTTGAACTGCTTACCTTAAAGAGGACGTTTGATGCTACAAACCCACTTAACCTGTGT
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TTGATCCAAATGGTTCATTCGTGCCTTGACCAGGATCCTGAGCAGAGACCTACTGCAGAT
GAACTTCTAGATCGCCCTCTTCTCAGGAAACGCAGGAGGTCAAGCACTGTGACTGAAGCA
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ACCCCCCAGAAACTGGATGTTATCAAGAGTGGCTGTAGTGCCCGGCAGGTCTGTGCAGGG
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GGAGGCACTAAACTCCATGGTCAGCTGGGCCATGGAGACAAAGCCTCCTATCGACAGCCA
AAGCATGTGGAAAAGTTGCAAGGCAAAGCTATCCGTCAGGTGTCATGTGGTGATGATTTC

FIGURE 2HHHH

ACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTCGGATCAGATTATTATGGCTGC
ATGGGGGTGGACAAAGTTGCTGGCCCTGAAGTGCTAGAACCCATGCAGCTGAACTTCTTC
CTCAGCAATCCAGTGGAGCAGGTCTCCTGTGGAGATAATCATGTGGTGGTTCTGACACGA
AACAAGGAAGTCTATTCTTGGGGCTGTGGCGAATATGGACGACTGGGTTTGGATTCAGAA
GAGGATTATTATACACCACAAAAGGTGGATGTTCCCAAGGCCTTGATTATTGTTGCAGTT
CAATGTGGCTGTGATGGGACATTTCTGTTGACCCAGTCAGGCAAAGTGCTGGCCTGTGGA
CTCAATGAATTCAATAAGCTGGGTCTGAATCAGTGCATGTCGGGAATTATCAACCATGAA
GCATACCATGAAGTTCCCTACACAACGTCCTTTACCTTGGCCAAACAGTTGTCCTTTTAT
AAGATCCGTACCATTGCCCCAGGCAAGACTCACACAGCTGCTATTGATGAGCGAGGCCGG
CTGCTGACCTTTGGCTGCAACAAGTGTGGGCAGCTGGGCGTTGGGAACTACAAGAAGCGT
CTGGGAATCAACCTGTTGGGGGGACCCCTTGGTGGGAAGCAAGTGATCAGGGTCTCCTGC
GGTGATGAGTTTACCATTGCTGCCACTGATGAGAAAGTATTGAATTCTAAGACCATCCGT
TCCAATAGCAGTGGCTTATCCATTGGAACTGTGTTTCAGAGCTCTAGCCCGGGAGGAGGC
GGCGGGGGCGGCGGTGGTGAAGAAGAGGACAGTCAGCAGGAATCTGAAACTCCTGACCCA
AGTGGAGGCTTCCGAGGAACAATGGAAGCAGACCGAGGAATGGAAGGTTTAATCAGTCCC
ACAGAGGCCATGGGGAACAGTAATGGGGCCAGCAGCTCCTGTCCTGGCTGGCTTCGAAAG
GAGCTGGAAAATGCAGAATTTATCCCCATGCCTGACAGCCCATCTCCTCTCAGTGCAGCG
TTTTCAGAATCTGAGAAAGATACCCTGCCCTATGAAGAGCTGCAAGGACTCAAAGTGGCC
TCTGAAGCTCCTTTGGAACACAAACCCCAAGTAGAAGCCTCGGTAACTGAGCTTTTTGCC
TTTGAATCACAACTAGTCACCTCGGCTGAATCCTGCAGTAACCTGTGCTGGGAAGGGAAC
ACCACTGACTCCTCCTGCGTGTGCGTGCAGCTCTCTGCAGGTGGAGGTTGA

SEQ ID NO: 114_R86668_H, MKK6_H
ATGAACTTGCTGCTCTCCTACCGCGATGTGCAGGACTACTCGGCCATCATTGAGCTGGTG
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CGTATCTACAAGGACATGTTCTTCAGCTCGGGTTTCCAGGATGCTGGGCACCGGGAGCAG
GCCTATCACTGGTATCGCAAGGCTTTTGACGTAGAGCCCAGCCTTCACTCAGGCATCAAT
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TACTGGGATGTGGGTTTCTACCTGGGAGCCCAGATCCTCGCCAATGACCCCACCCAGGTG
GTGCTGGCTGCAGAGCAGCTGTATAAGCTCAATGCCCCCATATGGTACCTGGTGTCCGTG
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CCACGCCGTGCCCACTTCTGGCTCCACTTCTTGCTACAGTCCTGCCAACCATTCAAGACA
GCCTGTGCCCAGGGCGACCAGTGCTTGGTGCTGGTCCTGGAGATGAACAAGGTGCTGCTG
CCTGCAAAGCTCGAGGTTCGGGGTACTGACCCAGTAAGCACAGTGACCCTGAGCCTGCTG
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GACGTCCAGCTGTGCTTCCCCAGCGTAGGGCACTGCCAGTGGTTCTGCGGCCTGATCCAG
GCCTGGGTGACGAACCCGGATTCCACGGCGCCCGCGGAGGAGGCGGAGGGCGCGGGGGAG
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AGACGCCTGCGCCACAAGAACATAGTGCGCTATCTGGGCTCAGCTAGCCAGGGCGGCTAC
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TGGGGACCCCTGAAGGACAACGAGAGCACCATCAGTTTCTACACCCGCCAGATCCTGCAG
GGACTTGGCTACTTGCACGACAACCACATCGTGCACAGGGACATAAAAGGGGACAATGTG
CTGATCAACACCTTCAGTGGGCTGCTCAAGATTTCTGACTTCGGCACCTCCAAGCGGCTG
GCAGGCATCACACCTTGCACTGAGACCTTCACAGGAACTCTGCAGTATATGGCCCCAGAA

FIGURE 2IIII

ATCATTGACCAGGGCCCACGCGGGTATGGGAAAGCAGCTGACATCTGGTCACTGGGCTGC
ACTGTCATTGAGATGGCCACAGGTCGCCCCCCCTTCCACGAGCTCGGGAGCCCACAGGCT
GCCATGTTTCAGGTGGGTATGTACAAGGTCCATCCGCCAATGCCCAGCTCTCTGTCGGCC
GAGGCCCAAGCCTTTCTCCTCCGAACTTTTGAGCCAGACCCCCGCCTCCGAGCCAGCGCC
CAGACACTGCTGGGGGACCCCTTCCTGCAGCCTGGGAAAAGGAGCCGCAGCCCCAGCTCC
CCACGACATGCTCCACGGCCCTCAGATGCCCCTTCTGCCAGTCCCACTCCTTCAGCCAAC
TCAACCACCCAGTCTCAGACATTCCCGTGCCCTCAGGCACCCTCTCAGCACCCACCCAGC
CCCCCGAAGCGCTGCCTCAGTTATGGGGGCACCAGCCAGCTCCGGGTGCCCGAGGAGCCT
GCGGCCGAGGAGCCTGCGTCTCCGGAGGAGAGTTCGGGGCTGAGCCTGCTGCACCAGGAG
AGCAAGCGTCGGGCCATGCTGGCCGCAGTATTGGAGCAGGAGCTGCCAGCGCTGGCGGAG
AATCTGCACCAGGAGCAGAAGCAAGAGCAGGGGGCCCGTCTGGGCAGAAACCATGTGGAA
GAGCTGCTGCGCTGCCTCGGGGCACACATCCACACTCCCAACCGCCGGCAGCTCGCCCAG
GAGCTGCGGGCGCTGCAAGGACGGCTGAGGGCCCAGGGCCTTGGGCCTGCGCTTCTGCAC
AGACCGCTGTTTGCCTTCCCGGATGCGGTGAAGCAGATCCTCCGCAAGCGCCAGATCCGT
CCACACTGGATGTTCGTTCTGGACTCACTGCTCAGCCGTGCTGTGCGGGCAGCCCTGGGT
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GACCAGGGCCTGGTGCAGTGGCTACAGGAACTGAATGTGGATTCAGGCACCATCCAAATG
CTGTTGAACCATAGCTTCACCCTCCACACTCTGCTCACCTATGCCACTCGAGATGACCTC
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CGAGCAGGATCCACACCAGTCACCTCTGGACCCTGA

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TCCATCAACGGCCTGCTAGAGGATTTTGACAACATCTCGGTGACTCGCTCCAACTCCCTA
AGGAAAGAAAGCCCACCCACCCCAGATCAGGGAGCCTCCAGCCACGGTCCAGGCCACGCG
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CTGAGCTCCCTCAGCCTCTCATCCAGCACCTACCCGCCGCCCAGCTGGGGCTCCTCCTCC
GACCAGCAGCCCTCCAGGGTGTCCCATGAACAGTTTCGGGCGGCCCTGCAGCTGGTGGTC
AGCCCAGGAGACCCCAGGGAATACTTGGCCAACTTTATCAAAATCGGGGAAGGCTCAACC
GGCATCGTATGCATCGCCACCGAGAAACACACAGGGAAACAAGTTGCAGTGAAGAAAATG

FIGURE 2JJJJ

GACCTCCGGAAGCAACAGAGACGAGAACTGCTTTTCAATGAGGTCGTGATCATGCGGGAT
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GTGGTCATGGAGTTTCTAGAAGGTGGTGCCTTGACAGACATTGTGACTCACACCAGAATG
AATGAAGAACAGATAGCTACTGTCTGCCTGTCAGTTCTGAGAGCTCTCTCCTACCTTCAT
AACCAAGGAGTGATTCACAGGGACATAAAAAGTGACTCCATCCTCCTGACAAGCGATGGC
CGGATAAAGTTGTCTGATTTTGGTTTCTGTGCTCAAGTTTCCAAAGAGGTGCCGAAGAGG
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CCAAGAGTGAAGGACCTACACAAGGTTTCTTCAGTGCTCCGGGGATTCCTAGACTTGATG
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SEQ ID NO: 116_SURTK106_H
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GTGCCGCGGGAGCAACTCTCTGAAGTTCTGGAGCAGATTTGCAGTGGTAGCTGTGGGCCC
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GCTTTAAAAGAACCAGCTGGGCTCCATGAGGTACAAGATTTCTTAGGGCGAATCCAATTC
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AGTTCTTCAGTCCTGAGCCCTACATGTGGGGCTGGAGGAGAACTATAACGGAAAAACCTC
TGAGTTTCACCTTAGGTATAGATAAAAGAAAGATGGTCCCCTTTTATCTGATTCTGAGAC
AGGTAAATTCTGTTTGTTACTACGTTTAATTAGAAGGTGGAGGAGTCATTTCATGATTAA

FIGURE 2KKKK

GAACATTCAACATGTATTGTTCATTAAGCTAGCTTCCTAGTTCCGATTAGACTAAGGAGA
CTAAGCCTAGAGAGTCAATGTTAGAACAGTGAAAAGAATTCTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGCACAATAAATAGGAAATGTAGAAACCAAGCAAGAAGGCTTAGTAGCTCA
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CAGAGAAAGAAAATCATGAAGAGACCCAGCAGCTGCTCACATGCCATGTACAACATCATG
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AGAACAGAGAGAAGGAACTTTCTGTGGCCCACCAAGGGAGAAAAAAGGACATGGATCTTG
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TCCTTTCATTGAACTCTGAGGCAGGTGGACCATGCATGATACTAAGTTTAATTAGAAGCA
GGAGGAGTCATTTCATGATTAGGAACATTGTTCATCCCATTTGTTTGCCAGTTCCTGTAA
GACTAAGGAGAATCAGCCTATAGAGCCAAAGCTAGAACCAGGGATAAAAAGTGTGTGTGT
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AAGAGGTACAGAGAAGAAGTAATCTTATAGGAATGGATGGTAGCTTCTAATTTTTAACCA
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GTTATTTTACTAGGAAAATTAGAGAACCTATAGTTTCCAAAAAGAGATTCTTTATGTGCA
AAATGAGATAACTCTCTACCTCACAGGGTTGGTGTGAGGAACAATGAGAATATGTATTTG
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GTGCTCGACTATGTCAACGGGGGAGAGCTCTTCTTCCACCTGCAGCGGGAGCGCCGGTTC
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TCCCTCAACATCATTTACAGGGATCTGAAACCAGAGAACATTCTCTTGGACTGCCAGGGA
CACGTGGTGCTGACGGATTTTGGCCTCTGCAAGGAAGGTGTAGAGCCTGAAGACACCACA

FIGURE 2LLLL

TCCACATTCTGTGGTACCCCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGCCTTAT
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CCGCCCTTCTACAGCCAAGATGTATCCCAGATGTATGAGAACATTCTGCACCAGCCGCTA
CAGATCCCCGGAGGCCGGACAGTGGCCGCCTGTGACCTCCTGCAAAGCCTTCTCCACAAG
GACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTTTCTTGAGATTAAGAACCATGTATTC
TTCAGCCCCATAAACTGGGATGACCTGTACCACAAGAGGCTAACTCCACCCTTCAACCCA
AATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTCACCCAGGAAGCTGTG
TCCAAGTCCATTGGCTGTACCCCTGACACTGTGGCCAGCAGCTCTGGGGCCTCAAGTGCA
TTCCTGGGATTTTCTTATGCGCCAGAGGATGATGACATCTTGGATTGCTAGAAGAGAAGG
ACCTGTGAAACTACTGAGGCCAGCTGGTATTAGTAAGGAATTACCTTCAGCTGCTAGGAA
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AAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAGGACAGGTCATCAGATACTCAGAGGC
TGTATCTCTGCCCTGCCAACCTTGACAAATGGCTTCCAATGTTAGGTTTGCTACAAGATG
GTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAGGGAAGGGAAAATGGAGGAAAGGGGA
GAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAAAAGCTCCCCCCAATGACTTTTGCTT
CCATCTCACTAACCACCCACCCCTACCTGGAATGGAGGCTGGGAAATGTGGCTTATTTGC
TGGGTACGTGACTATCCCTAATAACAAAGGGGTTTTGACCCTAAGACATTAGGGGAGAAT
GTTGGGTAGGCAGCCAGCCCTCTTTTACCATAGGGCCTCCTGGTGTTTGGATTTTGATCT
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TATGTTGAAAAA

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ATTCCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGCCCCCCCACATCCAT
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SEQ ID NO: 121_TESK2_H
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FIGURE 2MMMM

CCCACCGCCTCCGCAGGCTAAGGAGCCGCTGCCACCAACGAGCTGTGAGGGTTACTATGC
TCCCTCTTTGCCGCCGTCTCCTCCTCTTGCCCGCGCAGGCACCCCTCTGGCTGCTCAGTC
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ACACATTGAGCAGTAACCGGGCAAACATGCTGAAAGAAGTACAGCTCATGAATAGACTCT
CCCATCCCAACATCCTTAGGTATATCAACTCCGGGAACCTGGAACAGTTGCTAGACAGTA
ACCTGCATTTGCCTTGGACTGTGAGGGTAAAACTGGCCTATGACATAGCAGTGGGCCTCA
GCTACCTTCACTTCAAAGGCATTTTTCATCGGGACCTCACATCTAAGAACTGCCTGATAA
AGAGGGATGAGAATGGTTACTCTGCAGTGGTAGCTGACTTTGGCCTGGCTGAGAAGATCC
CCGATGTCAGCATGGGGAGTGAGAAGCTGGCCGTGGTGGGTTCCCCATTCTGGATGGCAC
CTGAGGTTCTCCGAGATGAGCCCTATAATGAAAAGGCAGATGTGTTCTCTTATGGTATCA
TCCTCTGCGAGATCATCGCCCGCATCCAGGCCGATCCGGACTATCTTCCCCGCACAGAGA
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TGCAACTTACTTTCAACTGCTGTAACATGGATCCCAAACTGCGCCCATCTTTTGTGGAGA
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